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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:40:16 ; Search time 67.6736 Seconds
(without alignments)
1144.220 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_202

Perfect score: 1032
Sequence: 1 HPELTIVKVKQABDQAGARVG.....IDMWEADKVAQPLRLSALPA 202

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 1710399

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:*

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20: /cgn2_6/ptodata/2/pubpaa/US11B_PUBCOMB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1032	100.0	263	15 US-10-668-778-2 Sequence 2, Appli
2	1032	100.0	286	10 US-09-919-901-7 Sequence 7, Appli
3	1032	100.0	286	10 US-09-919-901-14 Sequence 14, Appli
4	1032	100.0	286	10 US-09-919-901-21 Sequence 21, Appli
5	1032	100.0	286	11 US-09-837-306-354 Sequence 354, App
6	1032	100.0	286	14 US-10-191-966-7 Sequence 7, Appli
7	1032	100.0	286	14 US-10-191-966-14 Sequence 14, Appli
8	1032	100.0	286	14 US-10-191-966-21 Sequence 21, Appli
9	1032	100.0	286	15 US-10-045-674-523 Sequence 523, App
10	1032	100.0	286	16 US-10-416-708A-73 Sequence 73, Appli
11	1032	100.0	2307	10 US-09-919-901-2 Sequence 2, Appli

ALIGNMENTS

12	1032	100.0	2307	10 US-09-919-901-9 Sequence 9, Appli
13	1032	100.0	2307	10 US-09-919-901-16 Sequence 16, Appli
14	1032	100.0	2307	14 US-10-191-966-2 Sequence 2, Appli
15	1032	100.0	2307	14 US-10-191-966-9 Sequence 9, Appli
16	1032	100.0	2307	14 US-10-191-966-16 Sequence 16, Appli
17	1031	99.9	286	14 US-10-231-013-9 Sequence 9, Appli
18	1031	99.9	286	16 US-10-842-534-9 Sequence 9, Appli
19	1031	99.9	1293	14 US-10-251-385-292 Sequence 292, App
20	1031	99.9	1967	16 US-10-477-044-1 Sequence 1, Appli
21	1027	99.5	265	9 US-09-772-114-6 Sequence 6, Appli
22	1027	99.5	265	14 US-10-280-482-2 Sequence 2, Appli
23	1027	99.5	265	17 US-10-656-029-2 Sequence 2, Appli
24	1027	99.5	285	9 US-09-772-114-7 Sequence 7, Appli
25	1027	99.5	286	14 US-10-016-668-5 Sequence 5, Appli
26	1027	99.5	286	14 US-10-280-482-4 Sequence 4, Appli
27	1027	99.5	286	17 US-10-656-029-4 Sequence 2, Appli
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32	1024	99.2	584	9 US-10-890-675-2 Sequence 2, Appli
33	1020	98.8	265	9 US-09-772-114-8 Sequence 8, Appli
34	1020	98.8	265	14 US-10-280-482-6 Sequence 6, Appli
35	1020	98.8	265	16 US-10-622-088-114 Sequence 114, App
36	1020	98.8	265	17 US-10-656-029-6 Sequence 6, Appli
37	1020	98.8	265	17 US-10-877-952-154 Sequence 154, App
38	1019	98.7	264	9 US-09-772-114-9 Sequence 9, Appli
39	1019	98.7	264	14 US-10-280-482-8 Sequence 8, Appli
40	1019	98.7	264	17 US-10-656-029-8 Sequence 8, Appli
41	1012.5	98.1	262	14 US-10-177-725-3 Sequence 3, Appli
42	1012.5	98.1	262	15 US-10-393-449-3 Sequence 3, Appli
43	1004	97.3	498	17 US-10-491-653-146 Sequence 146, App
44	993	96.2	284	15 US-10-052-188-2 Sequence 2, Appli
45	463	44.9	94	9 US-09-925-298-760 Sequence 760, App

RESULT 1

US-10-668-778-2

Sequence 2, Application US/10668778

Publication No. US20040038117A1

GENERAL INFORMATION:

APPLICANT: Ballint, Robert F.

APPLICANT: Her, Jeng-Horng

TITLE OF INVENTION: Interaction-Activated Proteins

FILE REFERENCE: 021167-000700US

CURRENT APPLICATION NUMBER: US/10/668, 778

PRIOR FILING DATE: 2003-09-22

PRIOR APPLICATION NUMBER: US/09/526, 106

PRIOR FILING DATE: 2000-03-15

PRIOR APPLICATION NUMBER: US 60/124,339

PRIOR FILING DATE: 1999-03-15

PRIOR APPLICATION NUMBER: US 60/135,926

PRIOR FILING DATE: 1999-05-25

PRIOR APPLICATION NUMBER: US 60/175,968

PRIOR FILING DATE: 2000-01-13

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 263

TYPE: PRT

ORGANISM: Escherichia coli

FEATURE:

OTHER INFORMATION: TEM-1 beta-lactamase

US-10-668-778-2

Query Match 100.0%; Score 1032; DB 15; Length 263;
Best Local Similarity 100.0%; Pred. No. 1.3e-99;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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Db 144 KELTAFILNMGDHYRLDRMBEPLNEAIPNDRDITTPVAMATTIRKLLTGELITLASRQ 203
Qy 181 QLIDWMEADKVAQPLIRSLPA 202
Db 204 QLIDWMEADKVAQPLIRSLPA 225
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RESULT 5
US-09-837-306-354
; Sequence 354, Application US/09837306
; Publication No. US20040029113A1
; GENERAL INFORMATION:

APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROOKEY, KRISTIN L.
APPLICANT: HOET, RENE
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC
TITLE OF INVENTION: PACKAGES THAT COLLECTIVELY DISPLAY THE MEMBERS OF A
TITLE OF INVENTION: DIVERSE FAMILY OF PEPTIDES, POLYPEPTIDES OR PROTEINS
FILE REFERENCE: DYAK/002
CURRENT APPLICATION NUMBER: US/09/837,306
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 60/198,069
PRIOR FILING DATE: 2000-04-17
NUMBER OF SEQ ID NOS: 428
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 354
LENGTH: 286
TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: PC855
US-09-837-306-354

Query Match 100.0%; Score 1032; DB 11; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.5e-99;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HPEITLVKVDADQAGRVGYIELDLSGKILSFRRPFRPFMMSTFKVLLCGAVLSRID 60
Db 24 HPEITLVKVDADQAGRVGYIELDLSGKILSFRRPFRPFMMSTFKVLLCGAVLSRID 83
Qy 61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLLTDGMTVRELCSAATITMSDNTANLLTTIGSP 120
Db 84 AGOEOLGRRIHYSQNDLVEYSPVTEKHLLTDGMTVRELCSAATITMSDNTANLLTTIGSP 143
Qy 121 KELTAFILNMGDHYRLDRMBEPLNEAIPNDRDITTPVAMATTIRKLLTGELITLASRQ 180
Db 144 KELTAFILNMGDHYRLDRMBEPLNEAIPNDRDITTPVAMATTIRKLLTGELITLASRQ 203
Qy 181 QLIDWMEADKVAQPLIRSLPA 202
Db 204 QLIDWMEADKVAQPLIRSLPA 225

RESULT 6
US-10-191-966-7
; Sequence 7, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT

FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: :
US-10-191-966-7

Query Match 100.0%; Score 1032; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.5e-99;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HPEITLVKVDADQAGRVGYIELDLSGKILSFRRPFRPFMMSTFKVLLCGAVLSRID 60
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Qy 61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLLTDGMTVRELCSAATITMSDNTANLLTTIGSP 120
Db 84 AGOEOLGRRIHYSQNDLVEYSPVTEKHLLTDGMTVRELCSAATITMSDNTANLLTTIGSP 143
Qy 121 KELTAFILNMGDHYRLDRMBEPLNEAIPNDRDITTPVAMATTIRKLLTGELITLASRQ 180
Db 144 KELTAFILNMGDHYRLDRMBEPLNEAIPNDRDITTPVAMATTIRKLLTGELITLASRQ 203
Qy 181 QLIDWMEADKVAQPLIRSLPA 202
Db 204 QLIDWMEADKVAQPLIRSLPA 225

RESULT 7
US-10-191-966-14
; Sequence 14, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: :
US-10-191-966-14

Query Match 100.0%; Score 1032; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.5e-99;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HPEITLVKVDADQAGRVGYIELDLSGKILSFRRPFRPFMMSTFKVLLCGAVLSRID 60
Db 24 HPEITLVKVDADQAGRVGYIELDLSGKILSFRRPFRPFMMSTFKVLLCGAVLSRID 83

QY 61 AGOELGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGP 120
DB 84 AGOELGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGP 143
QY 121 KELTAFLLNMGDHVTYRLDRMEPELNEALPNDERDITMPVAAATTKLLTSELTLASRQ 180
DB 144 KELTAFLLNMGDHVTYRLDRMEPELNEALPNDERDITMPVAAATTKLLTSELTLASRQ 203
QY 181 QLIDMEADKVAAGPLRSALPA 202
DB 204 QLIDMEADKVAAGPLRSALPA 225

RESULT 8
US-10-191-966-21

Sequence 21, Application US/10191966
Publication No. US20030175692A1
GENERAL INFORMATION:
APPLICANT: Poter, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-10-191-966-21

Query Match 100.0%; Score 1032; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.5e-99;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 84 AGOELGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGP 143
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QY 181 QLIDMEADKVAAGPLRSALPA 202
DB 204 QLIDMEADKVAAGPLRSALPA 225

RESULT 9
US-10-045-674-523

Sequence 523, Application US/10045674
Publication No. US2003023233A1
GENERAL INFORMATION:
APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROONEY, KRISTIN L.
APPLICANT: HOET, RENE
APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.

TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: DVAX/002 CIP2
CURRENT APPLICATION NUMBER: US/10/045,674
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 60/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 523
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Vector pCESS
US-10-045-674-523

Query Match 100.0%; Score 1032; DB 15; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.5e-99;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKKAEDQAGRVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKKAEDQAGRVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 83
QY 61 AGOELGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGP 120
DB 84 AGOELGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGP 143
QY 121 KELTAFLLNMGDHVTYRLDRMEPELNEALPNDERDITMPVAAATTKLLTSELTLASRQ 180
DB 144 KELTAFLLNMGDHVTYRLDRMEPELNEALPNDERDITMPVAAATTKLLTSELTLASRQ 203
QY 181 QLIDMEADKVAAGPLRSALPA 202
DB 204 QLIDMEADKVAAGPLRSALPA 225

RESULT 10
US-10-416-708A-73

Sequence 73, Application US/10416708A
Publication No. US20040161753A1
GENERAL INFORMATION:
APPLICANT: Wise, John G.
APPLICANT: Fromknecht, Kacia
TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING
FILE REFERENCE: 37779-0004
CURRENT APPLICATION NUMBER: US/10/416,708A
CURRENT FILING DATE: 2004-01-28
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn version 3.2
SEQ ID NO 73
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Construct
US-10-416-708A-73

Query Match 100.0%; Score 1032; DB 16; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.5e-99;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKKAEDQAGRVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKKAEDQAGRVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 83

QY 61 AGOBLGRRIHYSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGOBLGRRIHYSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAMATTIRKLLTGELTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAMATTIRKLLTGELTLASRQ 203
QY 181 QUIDMMEADKVAAGPILRSALPA 202
DB 204 QUIDMMEADKVAAGPILRSALPA 225

RESULT 11

US-09-919-901-2
; Sequence 2, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, Karen E.
; APPLICANT: Potte, Roberta L.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; PRIOR FILING DATE: 2001-08-02
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-09-919-901-2

Query Match 100.0%; Score 1032; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 2.6e-98;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADADQAGRVGYIELDLSNGKILSPRPERPMMSTPFVLLCGAVLSRID 60
DB 2045 HPELVKVKADADQAGRVGYIELDLSNGKILSPRPERPMMSTPFVLLCGAVLSRID 2104
QY 61 AGOBLGRRIHYSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTAANLLTTIGSP 120
DB 2105 AGOBLGRRIHYSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTAANLLTTIGSP 2164
QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAMATTIRKLLTGELTLASRQ 180
DB 2165 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAMATTIRKLLTGELTLASRQ 2224
QY 181 QUIDMMEADKVAAGPILRSALPA 202
DB 2225 QUIDMMEADKVAAGPILRSALPA 2246

RESULT 12

US-09-919-901-9
; Sequence 9, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, Karen B.
; APPLICANT: Potte, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901

; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-09-919-901-9

Query Match 100.0%; Score 1032; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 2.6e-98;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADADQAGRVGYIELDLSNGKILSPRPERPMMSTPFVLLCGAVLSRID 60
DB 2045 HPELVKVKADADQAGRVGYIELDLSNGKILSPRPERPMMSTPFVLLCGAVLSRID 2104
QY 61 AGOBLGRRIHYSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTAANLLTTIGSP 120
DB 2105 AGOBLGRRIHYSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTAANLLTTIGSP 2164
QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAMATTIRKLLTGELTLASRQ 180
DB 2165 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAMATTIRKLLTGELTLASRQ 2224
QY 181 QUIDMMEADKVAAGPILRSALPA 202
DB 2225 QUIDMMEADKVAAGPILRSALPA 2246

RESULT 13

US-09-919-901-16
; Sequence 16, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potte, Karen E.
; APPLICANT: Jackson, Roberta L.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; PRIOR FILING DATE: 2001-08-02
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-09-919-901-16

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Best Local Similarity 100.0%; Pred. No. 2.6e-98;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2165 KETAFIHNMGDHYTRLDRWPEPELNEAI PNDERDITMPVAMATTLRKLLTGELLTLASRQ 2224
Qy 181 QIIMMEADKVAAGPLRSALPA 202
Db 2225 QIIMMEADKVAAGPLRSALPA 2246

RESULT 14
US-10-191-966-2
; Sequence 2, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-2

Query Match 100.0%; Score 1032; DB 14; Length 2307;
Best Local Similarity 100.0%; Pred. No. 2,6e-98;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2165 KETAFIHNMGDHYTRLDRWPEPELNEAI PNDERDITMPVAMATTLRKLLTGELLTLASRQ 2224
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Db 2225 QIIMMEADKVAAGPLRSALPA 2246

RESULT 15
US-10-191-966-9
; Sequence 9, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933

; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
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; TYPE: PRT
; ORGANISM: Artificial Sequence
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US-10-191-966-9

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Best Local Similarity 100.0%; Pred. No. 2,6e-98;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 AGGOLGRRHYSNDLVEYSPVTEKHLTDGTVRELCSAAITMSDNTAANLLTTIGCP 120
Db 2105 AGGOLGRRHYSNDLVEYSPVTEKHLTDGTVRELCSAAITMSDNTAANLLTTIGCP 2164
Qy 121 KETAFIHNMGDHYTRLDRWPEPELNEAI PNDERDITMPVAMATTLRKLLTGELLTLASRQ 180
Db 2165 KETAFIHNMGDHYTRLDRWPEPELNEAI PNDERDITMPVAMATTLRKLLTGELLTLASRQ 2224
Qy 181 QIIMMEADKVAAGPLRSALPA 202
Db 2225 QIIMMEADKVAAGPLRSALPA 2246

Search completed: June 10, 2005, 11:09:06
Job time : 67.6736 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:40:16 ; Search time 63.6534 Seconds
(without alignments)
1144.220 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_190

Perfect score: 975

Sequence: 1 HPELVIVKVKADBDQIGARVG.....GELLTLASRQLIDWWEADK 190

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 1710399

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA.*
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20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	975	100.0	263	US-10-668-778-2	Sequence 2, Appli
2	975	100.0	286	US-09-919-901-7	Sequence 7, Appli
3	975	100.0	286	US-09-919-901-14	Sequence 14, Appli
4	975	100.0	286	US-09-919-901-21	Sequence 21, Appli
5	975	100.0	286	US-09-837-306-354	Sequence 354, App
6	975	100.0	286	US-10-191-966-7	Sequence 7, Appli
7	975	100.0	286	US-10-191-966-14	Sequence 14, Appli
8	975	100.0	286	US-10-191-966-21	Sequence 21, Appli
9	975	100.0	286	US-10-045-674-523	Sequence 523, App
10	975	100.0	286	US-10-416-708A-73	Sequence 73, Appli
11	975	100.0	2307	US-09-919-901-2	Sequence 2, Appli

12	975	100.0	2307	10	US-09-919-901-9	Sequence 9, Appli
13	975	100.0	2307	14	US-09-919-901-16	Sequence 16, Appli
14	975	100.0	2307	10	US-10-191-966-2	Sequence 2, Appli
15	975	100.0	2307	14	US-10-191-966-9	Sequence 9, Appli
16	975	100.0	2307	14	US-10-191-966-16	Sequence 16, Appli
17	974	99.9	286	14	US-10-231-013-9	Sequence 9, Appli
18	974	99.9	286	16	US-10-842-534-9	Sequence 9, Appli
19	974	99.9	1293	14	US-10-251-385-292	Sequence 292, App
20	974	99.9	1967	16	US-10-477-044-1	Sequence 1, Appli
21	970	99.5	265	9	US-09-772-114-6	Sequence 6, Appli
22	970	99.5	265	14	US-10-280-482-2	Sequence 2, Appli
23	970	99.5	265	17	US-10-656-029-2	Sequence 2, Appli
24	970	99.5	285	9	US-09-772-114-7	Sequence 7, Appli
25	970	99.5	286	14	US-10-016-668-5	Sequence 4, Appli
26	970	99.5	286	14	US-10-280-482-4	Sequence 4, Appli
27	970	99.5	286	17	US-10-656-029-4	Sequence 26, Appli
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32	967	99.2	584	17	US-10-890-675-2	Sequence 8, Appli
33	963	98.8	265	9	US-09-772-114-8	Sequence 6, Appli
34	963	98.8	265	14	US-10-280-482-6	Sequence 114, App
35	963	98.8	265	16	US-10-622-088-114	Sequence 6, Appli
36	963	98.8	265	17	US-10-656-029-6	Sequence 154, App
37	963	98.8	265	17	US-10-877-952-154	Sequence 9, Appli
38	962	98.7	264	14	US-10-280-482-8	Sequence 8, Appli
39	962	98.7	264	14	US-10-656-029-8	Sequence 3, Appli
40	955.5	98.0	262	14	US-10-177-725-3	Sequence 3, Appli
41	955.5	98.0	262	17	US-10-393-449-3	Sequence 146, App
42	955.5	98.0	498	15	US-10-491-653-146	Sequence 2, Appli
43	947	97.1	284	15	US-10-062-188-2	Sequence 760, App
44	936	96.0	284	15	US-09-925-298-760	
45	463	47.5	94	9	US-09-925-298-760	

ALIGNMENTS

RESULT 1
US-10-668-778-2
Sequence 2, Application US/10668778
Publication No. US20040038317A1
GENERAL INFORMATION:
APPLICANT: Ballint, Robert F.
APPLICANT: Her, Jeng-Hong
TITLE OF INVENTION: Interaction-Activated Proteins
FILE REFERENCE: 021167-000700US
CURRENT APPLICATION NUMBER: US/10/668,778
CURRENT FILING DATE: 2003-09-22
PRIOR APPLICATION NUMBER: US/09/526,106
PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: US 60/124,339
PRIOR FILING DATE: 1999-03-15
PRIOR APPLICATION NUMBER: US 60/135,926
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 60/175,968
PRIOR FILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 263
TYPE: PRT
ORGANISM: Escherichia coli
FEATURE:
OTHER INFORMATION: TEM-1 beta-lactamase
US-10-668-778-2

Query Match 100.0%, Score 975, DB 15, Length 263;
Best Local Similarity 100.0%, Pred. No. 9e-95;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 AGQEOIGRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
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QY 181 QLIDMMEADK 190
DB 181 QLIDMMEADK 190
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RESULT 2

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US-09-919-901-7
; Sequence 7, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-09-919-901-7
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Best Local Similarity 100.0%; Pred. No. 1e-94;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 181 QLIDMMEADK 190
DB 204 QLIDMMEADK 213
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RESULT 3

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US-09-919-901-14
; Sequence 14, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
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; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-09-919-901-14
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Best Local Similarity 100.0%; Pred. No. 1e-94;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 204 QLIDMMEADK 213
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RESULT 4

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US-09-919-901-21
; Sequence 21, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-09-919-901-21
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Query Match 100.0%; Score 975; DB 10; Length 286;
Best Local Similarity 100.0%; Pred. No. 1e-94;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 204 QUIDMWEADK 213

RESULT 5
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; Sequence 354, Application US/09837306
; Publication No. US20040029113A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, ROBERT C.
; APPLICANT: COHEN, EDWARD H.
; APPLICANT: NASTRI, HORACIO G.
; APPLICANT: ROOKEY, KRISTIN L.
; APPLICANT: HOEF, RENE
; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC
; TITLE OF INVENTION: PACKAGES THAT COLLECTIVELY DISPLAY THE MEMBERS OF A
; TITLE OF INVENTION: DIVERSE FAMILY OF PEPTIDES, POLYPEPTIDES OR PROTEINS
; FILE REFERENCE: DYKA/002
; CURRENT APPLICATION NUMBER: US/09/837,306
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/198,069
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 354
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: PCB55
US-09-837-306-354

Query Match 100.0%; Score 975; DB 11; Length 286;
Best Local Similarity 100.0%; Pred. No. 1e-94;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 24 HPEITLVKVDADQAGRVGYIELDLSGKILSFRRPFRPFMMSTFKVLLCGAVLSRID 83
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Db 84 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 143
Qy 121 KELLTAFLNMGDHYRLDRWPELNEAIPNDRDITMPVAMATTIRKLLTGELTLASRQ 180
Db 144 KELLTAFLNMGDHYRLDRWPELNEAIPNDRDITMPVAMATTIRKLLTGELTLASRQ 203
Qy 181 QUIDMWEADK 190
Db 204 QUIDMWEADK 213

; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-7

Query Match 100.0%; Score 975; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 1e-94;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 61 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 120
Db 84 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 143
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Qy 181 QUIDMWEADK 190
Db 204 QUIDMWEADK 213

RESULT 7
US-10-191-966-14
; Sequence 14, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: JACKSON, ROBERTA L.
; APPLICANT: PATICK, AMY K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-14

Query Match 100.0%; Score 975; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 1e-94;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HPEITLVKVDADQAGRVGYIELDLSGKILSFRRPFRPFMMSTFKVLLCGAVLSRID 60
Db 24 HPEITLVKVDADQAGRVGYIELDLSGKILSFRRPFRPFMMSTFKVLLCGAVLSRID 83

QY 61 AGOGLGRIRIHYSONDLVEYSPTVEKHLTDGVTVELCSAAITMSDNTAANLLTTIGP 120
DB 84 AGOGLGRIRIHYSONDLVEYSPTVEKHLTDGVTVELCSAAITMSDNTAANLLTTIGP 143
QY 121 KETLAFILNMGDHVTRLDRWPEBELNEAIPNDRDITTPVANAATTLRKLLTGELLTLASRQ 180
DB 144 KETLAFILNMGDHVTRLDRWPEBELNEAIPNDRDITTPVANAATTLRKLLTGELLTLASRQ 203
QY 181 OLIDMMEADK 190
DB 204 OLIDMMEADK 213

RESULT 8
US-10-191-966-21

Sequence 21, Application US/10191966
Publication No. US2003073692A1

GENERAL INFORMATION:

APPLICANT: Potes, Karen E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patrick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT

TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

FILE REFERENCE: 0125-0005A

CURRENT FILING DATE: 2002-07-10

PRIOR FILING DATE: 1999-03-08

PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 21

LENGTH: 286

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION:

US-10-191-966-21

Query Match 100.0%; Score 975; DB 14; Length 286;

Best Local Similarity 100.0%; Pred. No. 1e-94;

Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGARVGITIEDLNSGKILSFRRPFRPMMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKVKADBDQAGARVGITIEDLNSGKILSFRRPFRPMMSTFVLLCGAVLSRID 83
QY 61 AGOGLGRIRIHYSONDLVEYSPTVEKHLTDGVTVELCSAAITMSDNTAANLLTTIGP 120
DB 84 AGOGLGRIRIHYSONDLVEYSPTVEKHLTDGVTVELCSAAITMSDNTAANLLTTIGP 143
QY 121 KETLAFILNMGDHVTRLDRWPEBELNEAIPNDRDITTPVANAATTLRKLLTGELLTLASRQ 180
DB 144 KETLAFILNMGDHVTRLDRWPEBELNEAIPNDRDITTPVANAATTLRKLLTGELLTLASRQ 203
QY 181 OLIDMMEADK 190
DB 204 OLIDMMEADK 213

RESULT 9
US-10-045-674-523

Sequence 523, Application US/10045674

Publication No. US2003023233A1

GENERAL INFORMATION:

APPLICANT: LADNER, ROBERT C.

APPLICANT: COHEN, EDWARD H.

APPLICANT: NASTRI, HORACIO G.

APPLICANT: ROONEY, KRISTIN L.

APPLICANT: HOET, RENE

APPLICANT: HOOGENDOORN, HENDRICUS R. J. M.

FILE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: DMAX/002 CIP2
CURRENT APPLICATION NUMBER: US/10/045,674
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 60/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 523
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Vector pCESS

US-10-045-674-523

Query Match 100.0%; Score 975; DB 15; Length 286;

Best Local Similarity 100.0%; Pred. No. 1e-94;

Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGARVGITIEDLNSGKILSFRRPFRPMMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKVKADBDQAGARVGITIEDLNSGKILSFRRPFRPMMSTFVLLCGAVLSRID 83
QY 61 AGOGLGRIRIHYSONDLVEYSPTVEKHLTDGVTVELCSAAITMSDNTAANLLTTIGP 120
DB 84 AGOGLGRIRIHYSONDLVEYSPTVEKHLTDGVTVELCSAAITMSDNTAANLLTTIGP 143
QY 121 KETLAFILNMGDHVTRLDRWPEBELNEAIPNDRDITTPVANAATTLRKLLTGELLTLASRQ 180
DB 144 KETLAFILNMGDHVTRLDRWPEBELNEAIPNDRDITTPVANAATTLRKLLTGELLTLASRQ 203
QY 181 OLIDMMEADK 190
DB 204 OLIDMMEADK 213

RESULT 10
US-10-416-708A-73

Sequence 73, Application US/10416708A

Publication No. US20040161753A1

GENERAL INFORMATION:

APPLICANT: Wise, John G.

APPLICANT: Fromknecht, Katja

TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING

TITLE OF INVENTION: SPECIFICITIES

FILE REFERENCE: 37779-0004

CURRENT APPLICATION NUMBER: US/10/416,708A

CURRENT FILING DATE: 2004-01-28

NUMBER OF SEQ ID NOS: 89

SOFTWARE: PatentIn version 3.2

SEQ ID NO 73

LENGTH: 286

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic Construct

US-10-416-708A-73

Query Match 100.0%; Score 975; DB 16; Length 286;

Best Local Similarity 100.0%; Pred. No. 1e-94;

Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGARVGITIEDLNSGKILSFRRPFRPMMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKVKADBDQAGARVGITIEDLNSGKILSFRRPFRPMMSTFVLLCGAVLSRID 83

Qy 61 AGOELGRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANLLTTIGP 120
Db 84 AGOELGRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANLLTTIGP 143
Qy 121 KELTAFILNMGDHTRLDRWEPELNEAIPNDRDITMPVAAATTIRKLLTGELLTLASRQ 180
Db 144 KELTAFILNMGDHTRLDRWEPELNEAIPNDRDITMPVAAATTIRKLLTGELLTLASRQ 203
Qy 181 OLIDMEADK 190
Db 204 OLIDMEADK 213

RESULT 11

US-09-919-901-2

Sequence 2, Application US/09919901
Publication No. US20030082518A1
GENERAL INFORMATION:
APPLICANT: Potte, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REFORER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT FILING DATE: 2001-08-02
CURRENT FILING DATE: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 2307
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-09-919-901-2

Query Match 100.0%; Score 975; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 1.8e-93;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPEITLVKVKDADQAGAVGYIELDLSNGKILSPRPERPMMSTFKVLLCGAVLSRID 60
Db 2045 HPEITLVKVKDADQAGAVGYIELDLSNGKILSPRPERPMMSTFKVLLCGAVLSRID 2104
Qy 61 AGOELGRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANLLTTIGP 120
Db 2105 AGOELGRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANLLTTIGP 2164
Qy 121 KELTAFILNMGDHTRLDRWEPELNEAIPNDRDITMPVAAATTIRKLLTGELLTLASRQ 180
Db 2165 KELTAFILNMGDHTRLDRWEPELNEAIPNDRDITMPVAAATTIRKLLTGELLTLASRQ 2224
Qy 181 OLIDMEADK 190
Db 2225 OLIDMEADK 2234

RESULT 12

US-09-919-901-9

Sequence 9, Application US/09919901
Publication No. US20030082518A1
GENERAL INFORMATION:
APPLICANT: Potte, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REFORER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901

Qy 121 KELTAFILNMGDHTRLDRWEPELNEAIPNDRDITMPVAAATTIRKLLTGELLTLASRQ 180
Db 144 KELTAFILNMGDHTRLDRWEPELNEAIPNDRDITMPVAAATTIRKLLTGELLTLASRQ 203
Qy 181 OLIDMEADK 190
Db 204 OLIDMEADK 213

RESULT 13

US-09-919-901-16

Sequence 16, Application US/09919901
Publication No. US20030082518A1
GENERAL INFORMATION:
APPLICANT: Potte, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REFORER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT FILING DATE: 2001-08-02
CURRENT FILING DATE: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 2307
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-09-919-901-16

Query Match 100.0%; Score 975; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 1.8e-93;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPEITLVKVKDADQAGAVGYIELDLSNGKILSPRPERPMMSTFKVLLCGAVLSRID 60
Db 2045 HPEITLVKVKDADQAGAVGYIELDLSNGKILSPRPERPMMSTFKVLLCGAVLSRID 2104
Qy 61 AGOELGRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANLLTTIGP 120
Db 2105 AGOELGRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANLLTTIGP 2164
Qy 121 KELTAFILNMGDHTRLDRWEPELNEAIPNDRDITMPVAAATTIRKLLTGELLTLASRQ 180
Db 2165 KELTAFILNMGDHTRLDRWEPELNEAIPNDRDITMPVAAATTIRKLLTGELLTLASRQ 2224
Qy 181 OLIDMEADK 190
Db 2225 OLIDMEADK 2234

RESULT 13

US-09-919-901-16

Sequence 16, Application US/09919901
Publication No. US20030082518A1
GENERAL INFORMATION:
APPLICANT: Potte, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REFORER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT FILING DATE: 2001-08-02
CURRENT FILING DATE: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 2307
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-09-919-901-16

Db 2105 AGOBLGRRIHYSQNDLVEYSPVTEKHLTDGWTRELCSSAII TMSDNTAANILLTTIGSP 2164
QY 121 KETAFALNMGDHVTRLDRWEPPELNEAIPNDRDITMPVAMATTLRKLLTGSELLTLASRQ 180
Db 2165 KETAFALNMGDHVTRLDRWEPPELNEAIPNDRDITMPVAMATTLRKLLTGSELLTLASRQ 2224
QY 181 QLIDWMEADK 190
Db 2225 QLIDWMEADK 2234

RESULT 14
US-10-191-966-2
; Sequence 2, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Pottes, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patlick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-2

Query Match 100.0%; Score 975; DB 14; Length 2307;
Best Local Similarity 100.0%; Pred. No. 1.8e-93;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDABDQIGARVGYIELDLSGKILSFRRPFRPMMSTFVLLCGAVLSRID 60
Db 2045 HPEITLVKVDABDQIGARVGYIELDLSGKILSFRRPFRPMMSTFVLLCGAVLSRID 2104
QY 61 AGOBLGRRIHYSQNDLVEYSPVTEKHLTDGWTRELCSSAII TMSDNTAANILLTTIGSP 120
Db 2105 AGOBLGRRIHYSQNDLVEYSPVTEKHLTDGWTRELCSSAII TMSDNTAANILLTTIGSP 2164
QY 121 KETAFALNMGDHVTRLDRWEPPELNEAIPNDRDITMPVAMATTLRKLLTGSELLTLASRQ 180
Db 2165 KETAFALNMGDHVTRLDRWEPPELNEAIPNDRDITMPVAMATTLRKLLTGSELLTLASRQ 2224
QY 181 QLIDWMEADK 190
Db 2225 QLIDWMEADK 2234

RESULT 15
US-10-191-966-9
; Sequence 9, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Pottes, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patlick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933

; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-9

Query Match 100.0%; Score 975; DB 14; Length 2307;
Best Local Similarity 100.0%; Pred. No. 1.8e-93;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDABDQIGARVGYIELDLSGKILSFRRPFRPMMSTFVLLCGAVLSRID 60
Db 2045 HPEITLVKVDABDQIGARVGYIELDLSGKILSFRRPFRPMMSTFVLLCGAVLSRID 2104
QY 61 AGOBLGRRIHYSQNDLVEYSPVTEKHLTDGWTRELCSSAII TMSDNTAANILLTTIGSP 120
Db 2105 AGOBLGRRIHYSQNDLVEYSPVTEKHLTDGWTRELCSSAII TMSDNTAANILLTTIGSP 2164
QY 121 KETAFALNMGDHVTRLDRWEPPELNEAIPNDRDITMPVAMATTLRKLLTGSELLTLASRQ 180
Db 2165 KETAFALNMGDHVTRLDRWEPPELNEAIPNDRDITMPVAMATTLRKLLTGSELLTLASRQ 2224
QY 181 QLIDWMEADK 190
Db 2225 QLIDWMEADK 2234

Search completed: June 10, 2005, 11:09:06
Job time : 64.6534 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:40:16 ; Search time 60.6383 Seconds

(without alignments)
1144.220 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_181

Perfect score: 925
Sequence: 1 HPELVKVKQADQDQGVG.....ATTLKLTGSLTLASRQ 181

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 38334425 residues

Total number of hits satisfying chosen parameters: 1710399

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing:

Maximum Match 0%
Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	925	100.0	263	15	US-10-668-778-2
2	925	100.0	286	10	US-09-919-901-7
3	925	100.0	286	10	US-09-919-901-14
4	925	100.0	286	10	US-09-919-901-21
5	925	100.0	286	11	US-09-837-306-354
6	925	100.0	286	14	US-10-191-966-7
7	925	100.0	286	14	US-10-191-966-14
8	925	100.0	286	15	US-10-191-966-21
9	925	100.0	286	15	US-10-045-674-523
10	925	100.0	286	16	US-10-416-708A-73
11	925	100.0	2307	10	US-09-919-901-2

12	925	100.0	2307	10	US-09-919-901-9	Sequence 9, Appli
13	925	100.0	2307	14	US-09-919-901-16	Sequence 16, Appli
14	925	100.0	2307	10	US-10-191-966-2	Sequence 2, Appli
15	925	100.0	2307	14	US-10-191-966-9	Sequence 9, Appli
16	925	100.0	2307	14	US-10-191-966-16	Sequence 16, Appli
17	924	99.9	286	14	US-10-231-013-9	Sequence 9, Appli
18	924	99.9	286	16	US-10-842-534-9	Sequence 9, Appli
19	924	99.9	1293	14	US-10-251-385-292	Sequence 292, App
20	924	99.9	1967	16	US-10-477-044-1	Sequence 1, Appli
21	920	99.5	265	9	US-09-772-114-6	Sequence 6, Appli
22	920	99.5	265	14	US-10-280-482-2	Sequence 2, Appli
23	920	99.5	265	17	US-10-656-029-2	Sequence 2, Appli
24	920	99.5	285	9	US-09-772-114-7	Sequence 7, Appli
25	920	99.5	286	14	US-10-016-668-5	Sequence 5, Appli
26	920	99.5	286	14	US-10-280-482-4	Sequence 4, Appli
27	920	99.5	286	17	US-10-656-029-4	Sequence 4, Appli
28	920	99.5	286	17	US-10-877-952-26	Sequence 26, Appli
29	920	99.5	286	17	US-10-877-952-71	Sequence 71, Appli
30	917	99.1	264	15	US-10-877-952-18	Sequence 18, Appli
31	917	99.1	362	15	US-10-469-199-2	Sequence 2, Appli
32	917	99.1	584	17	US-10-890-675-2	Sequence 2, Appli
33	913	98.7	265	9	US-09-772-114-8	Sequence 8, Appli
34	913	98.7	265	14	US-10-280-482-6	Sequence 6, Appli
35	913	98.7	265	16	US-10-622-088-114	Sequence 114, App
36	913	98.7	265	17	US-10-656-029-6	Sequence 6, Appli
37	913	98.7	265	17	US-10-877-952-154	Sequence 154, App
38	912	98.6	264	9	US-09-772-114-9	Sequence 9, Appli
39	912	98.6	264	14	US-10-280-482-8	Sequence 8, Appli
40	912	98.6	264	17	US-10-656-029-8	Sequence 8, Appli
41	910	98.4	498	17	US-10-491-653-146	Sequence 146, App
42	905.5	97.9	262	14	US-10-177-725-3	Sequence 3, Appli
43	905.5	97.9	262	15	US-10-393-449-3	Sequence 3, Appli
44	886	95.8	284	15	US-10-062-188-2	Sequence 2, Appli
45	463	50.1	94	9	US-09-925-298-760	Sequence 760, App

ALIGNMENTS

RESULT 1

US-10-668-778-2

Sequence 2, Application US/10668778

Publication No. US20040038317A1

GENERAL INFORMATION:

APPLICANT: Ballint, Robert F.

APPLICANT: Her, Jeng-Hong

TITLE OF INVENTION: Interaction-Activated Proteins

FILE REFERENCE: 021167-000700US

CURRENT APPLICATION NUMBER: US/10/668,778

PRIOR FILING DATE: 2003-09-22

PRIOR APPLICATION NUMBER: US/09/526,106

PRIOR FILING DATE: 2000-03-15

PRIOR APPLICATION NUMBER: US 60/124,339

PRIOR FILING DATE: 1999-03-15

PRIOR FILING DATE: 1999-05-25

PRIOR APPLICATION NUMBER: US 60/135,926

PRIOR FILING DATE: 2000-01-13

PRIOR APPLICATION NUMBER: US 60/175,968

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 263

TYPE: PRT

ORGANISM: Escherichia coli

FEATURE:

OTHER INFORMATION: TEM-1 beta-lactamase

US-10-668-778-2

Query Match 100.0%; Score 925; DB 15; Length 263;

Best Local Similarity 100.0%; Pred. No. 2.1e-90;

Matches 181; Conservative 0; Mismatches 0; Indels 0;

QY 1 HPEITLVKVKADBDQAGAVGYIETDLSNGKILIESFRPEERPPMSTFVLLCGAVLSRID 60
Db 1 HPEITLVKVKADBDQAGAVGYIETDLSNGKILIESFRPEERPPMSTFVLLCGAVLSRID 60
QY 61 AGOQOLGRRHYSONDLVEYSPVTEKHLTDGWTVELCSAITSNDTNAAILTTTIGP 120
Db 61 AGOQOLGRRHYSONDLVEYSPVTEKHLTDGWTVELCSAITSNDTNAAILTTTIGP 120
QY 121 KELTAFILNMGDHYTRLDRWPELNEAIPNDRDITTMVAMATTLRKLLTGELLTLASRQ 180
Db 121 KELTAFILNMGDHYTRLDRWPELNEAIPNDRDITTMVAMATTLRKLLTGELLTLASRQ 180
QY 181 Q 181
Db 181 Q 181

RESULT 2

US-09-919-901-7
; Sequence 7, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-09-919-901-7

Query Match 100.0%; Score 925; DB 10; Length 286;
Best Local Similarity 100.0%; Pred. No. 2,4e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGAVGYIETDLSNGKILIESFRPEERPPMSTFVLLCGAVLSRID 60
Db 24 HPEITLVKVKADBDQAGAVGYIETDLSNGKILIESFRPEERPPMSTFVLLCGAVLSRID 83
QY 61 AGOQOLGRRHYSONDLVEYSPVTEKHLTDGWTVELCSAITSNDTNAAILTTTIGP 120
Db 84 AGOQOLGRRHYSONDLVEYSPVTEKHLTDGWTVELCSAITSNDTNAAILTTTIGP 143
QY 121 KELTAFILNMGDHYTRLDRWPELNEAIPNDRDITTMVAMATTLRKLLTGELLTLASRQ 180
Db 144 KELTAFILNMGDHYTRLDRWPELNEAIPNDRDITTMVAMATTLRKLLTGELLTLASRQ 203
QY 181 Q 181
Db 204 Q 204

RESULT 3

US-09-919-901-14
; Sequence 14, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.

; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-09-919-901-14

Query Match 100.0%; Score 925; DB 10; Length 286;
Best Local Similarity 100.0%; Pred. No. 2,4e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGAVGYIETDLSNGKILIESFRPEERPPMSTFVLLCGAVLSRID 60
Db 24 HPEITLVKVKADBDQAGAVGYIETDLSNGKILIESFRPEERPPMSTFVLLCGAVLSRID 83
QY 61 AGOQOLGRRHYSONDLVEYSPVTEKHLTDGWTVELCSAITSNDTNAAILTTTIGP 120
Db 84 AGOQOLGRRHYSONDLVEYSPVTEKHLTDGWTVELCSAITSNDTNAAILTTTIGP 143
QY 121 KELTAFILNMGDHYTRLDRWPELNEAIPNDRDITTMVAMATTLRKLLTGELLTLASRQ 180
Db 144 KELTAFILNMGDHYTRLDRWPELNEAIPNDRDITTMVAMATTLRKLLTGELLTLASRQ 203
QY 181 Q 181
Db 204 Q 204

RESULT 4

US-09-919-901-21
; Sequence 21, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-09-919-901-21

Query Match 100.0%; Score 925; DB 10; Length 286;
Best Local Similarity 100.0%; Pred. No. 2,4e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEITLVKVKADBDQAGAVGYIETDLSNGKILIESFRPEERPPMSTFVLLCGAVLSRID 60

Db 24 HPEVLVKVDAEDQAGAVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
Qy 61 AGQEQGRIRHYSQNDLVEYSPVTEKHLTDGVTVELCSAATMSDNTAANLLTTIGSP 120
Db 84 AGQEQGRIRHYSQNDLVEYSPVTEKHLTDGVTVELCSAATMSDNTAANLLTTIGSP 143
Qy 121 KELTAFILNMGDHYRLDRWPELNEALPNDERDTTMAPVAMATTIRKLLTGBLLTLASRQ 180
Db 144 KELTAFILNMGDHYRLDRWPELNEALPNDERDTTMAPVAMATTIRKLLTGBLLTLASRQ 203
Qy 181 Q 181
Db 204 Q 204

RESULT 5
US-09-837-306-354
; Sequence 354, Application US/09837306
; Publication No. US20040029113A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, ROBERT C.
; APPLICANT: COHEN, EDWARD H.
; APPLICANT: NASTRI, HORACIO G.
; APPLICANT: ROOKEY, KRISTIN L.
; APPLICANT: HOET, RENE
; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC
; TITLE OF INVENTION: PACKAGES THAT COLLECTIVELY DISPLAY THE MEMBERS OF A
; TITLE OF INVENTION: DIVERSE FAMILY OF PEPTIDES, POLYPEPTIDES OR PROTEINS
; FILE REFERENCE: DVA/002
; CURRENT APPLICATION NUMBER: US/09/837,306
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/198,069
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 354
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: pC855
US-09-837-306-354

Query Match 100.0%; Score 925; DB 11; Length 286;
Best Local Similarity 100.0%; Pred. No. 2,4e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HPEVLVKVDAEDQAGAVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
Db 24 HPEVLVKVDAEDQAGAVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
Qy 61 AGQEQGRIRHYSQNDLVEYSPVTEKHLTDGVTVELCSAATMSDNTAANLLTTIGSP 120
Db 84 AGQEQGRIRHYSQNDLVEYSPVTEKHLTDGVTVELCSAATMSDNTAANLLTTIGSP 143
Qy 121 KELTAFILNMGDHYRLDRWPELNEALPNDERDTTMAPVAMATTIRKLLTGBLLTLASRQ 180
Db 144 KELTAFILNMGDHYRLDRWPELNEALPNDERDTTMAPVAMATTIRKLLTGBLLTLASRQ 203
Qy 181 Q 181
Db 204 Q 204

RESULT 6
US-10-191-966-7
; Sequence 7, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: JACKSON, ROBERTA L.
; APPLICANT: PATICK, AMY K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT

; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-7

Query Match 100.0%; Score 925; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 2,4e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HPEVLVKVDAEDQAGAVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
Db 24 HPEVLVKVDAEDQAGAVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
Qy 61 AGQEQGRIRHYSQNDLVEYSPVTEKHLTDGVTVELCSAATMSDNTAANLLTTIGSP 120
Db 84 AGQEQGRIRHYSQNDLVEYSPVTEKHLTDGVTVELCSAATMSDNTAANLLTTIGSP 143
Qy 121 KELTAFILNMGDHYRLDRWPELNEALPNDERDTTMAPVAMATTIRKLLTGBLLTLASRQ 180
Db 144 KELTAFILNMGDHYRLDRWPELNEALPNDERDTTMAPVAMATTIRKLLTGBLLTLASRQ 203
Qy 181 Q 181
Db 204 Q 204

RESULT 7
US-10-191-966-14
; Sequence 14, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: JACKSON, ROBERTA L.
; APPLICANT: PATICK, AMY K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-14

Query Match 100.0%; Score 925; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 2,4e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HPEVLVKVDAEDQAGAVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
Db 24 HPEVLVKVDAEDQAGAVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83

QY 61 AGOELGRIRHYSONDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 120
 DB 84 AGOELGRIRHYSONDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 143
 QY 121 KELTAFHNMGDHVTRLDRWPELNEALPNDERDTTVPVAAATTLRKLLTGBLLTLASRQ 180
 DB 144 KELTAFHNMGDHVTRLDRWPELNEALPNDERDTTVPVAAATTLRKLLTGBLLTLASRQ 203
 QY 181 Q 181
 DB 204 Q 204

RESULT 8

US-10-191-966-21
 ; Sequence 21, Application US/10191966
 ; Publication No. US20030175692A1

GENERAL INFORMATION:
 ; APPLICANT: Potts, Karen E.
 ; APPLICANT: Jackson, Roberta L.
 ; APPLICANT: Patrick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
 ; FILE REFERENCE: 0125-0005A
 ; CURRENT APPLICATION NUMBER: US/10/191,966
 ; PRIOR FILING DATE: 2002-07-10
 ; PRIOR APPLICATION NUMBER: US/09/263,933
 ; PRIOR FILING DATE: 1999-03-08
 ; PRIOR APPLICATION NUMBER: 09/129,611
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 21

LENGTH: 286
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION:
 US-10-191-966-21

Query Match 100.0%; Score 925; DB 14; Length 286;
 Best Local Similarity 100.0%; Pred. No. 2,4e-90;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKQADBDQAGARVGYIELDNGSKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
 DB 24 HPEITLVKQADBDQAGARVGYIELDNGSKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
 QY 61 AGOELGRIRHYSONDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 120
 DB 84 AGOELGRIRHYSONDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 143
 QY 121 KELTAFHNMGDHVTRLDRWPELNEALPNDERDTTVPVAAATTLRKLLTGBLLTLASRQ 180
 DB 144 KELTAFHNMGDHVTRLDRWPELNEALPNDERDTTVPVAAATTLRKLLTGBLLTLASRQ 203
 QY 181 Q 181
 DB 204 Q 204

RESULT 9

US-10-045-674-523
 ; Sequence 523, Application US/10045674
 ; Publication No. US2003023233A1

GENERAL INFORMATION:
 ; APPLICANT: LADNER, ROBERT C.
 ; APPLICANT: COHEN, EDWARD H.
 ; APPLICANT: NASTRI, HORACIO G.
 ; APPLICANT: ROOKEY, KRISTIN L.
 ; APPLICANT: HOET, RENE
 ; APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.

TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
 ; TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
 ; TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
 ; FILE REFERENCE: DVAX/002 CIP2
 ; CURRENT APPLICATION NUMBER: US/10/045,674
 ; PRIOR FILING DATE: 2001-10-25
 ; PRIOR APPLICATION NUMBER: 60/198,069
 ; PRIOR FILING DATE: 2000-04-17
 ; PRIOR APPLICATION NUMBER: 09/837,306
 ; PRIOR FILING DATE: 2001-04-17
 ; NUMBER OF SEQ ID NOS: 635
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 523
 ; LENGTH: 286
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Vector pCESS
 ; OTHER INFORMATION: protein sequence
 US-10-045-674-523

QY 1 HPEITLVKQADBDQAGARVGYIELDNGSKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
 DB 24 HPEITLVKQADBDQAGARVGYIELDNGSKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
 QY 61 AGOELGRIRHYSONDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 120
 DB 84 AGOELGRIRHYSONDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 143
 QY 121 KELTAFHNMGDHVTRLDRWPELNEALPNDERDTTVPVAAATTLRKLLTGBLLTLASRQ 180
 DB 144 KELTAFHNMGDHVTRLDRWPELNEALPNDERDTTVPVAAATTLRKLLTGBLLTLASRQ 203
 QY 181 Q 181
 DB 204 Q 204

Query Match 100.0%; Score 925; DB 15; Length 286;
 Best Local Similarity 100.0%; Pred. No. 2,4e-90;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10
 US-10-416-708A-73
 ; Sequence 73, Application US/10416708A
 ; Publication No. US20040161753A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wise, John G.
 ; APPLICANT: Fromknecht, Katja
 ; TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING
 ; TITLE OF INVENTION: SPECIFICITIES
 ; FILE REFERENCE: 37779-0004
 ; CURRENT APPLICATION NUMBER: US/10/416,708A
 ; PRIOR FILING DATE: 2004-01-28
 ; NUMBER OF SEQ ID NOS: 89
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 73
 ; LENGTH: 286
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic Construct
 US-10-416-708A-73

QY 1 HPEITLVKQADBDQAGARVGYIELDNGSKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
 DB 24 HPEITLVKQADBDQAGARVGYIELDNGSKILSFRRPFRPMMSTFKVLLCGAVLSRID 83

Qy 61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANLLTTTIGSP 120
Db 84 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANLLTTTIGSP 143
Qy 121 KETLAFILNMGDHVTRLDRWPELNEALPNDERDITMPVAMATTIRKLLTGELTLASRQ 180
Db 144 KETLAFILNMGDHVTRLDRWPELNEALPNDERDITMPVAMATTIRKLLTGELTLASRQ 203
Qy 181 Q 181
Db 204 Q 204

RESULT 11

US-09-919-901-2
; Sequence 2, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, Robert E.
; APPLICANT: Potte, Karen E.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-09-919-901-2

Query Match 100.0%; Score 925; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 4.2e-89;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPEITVKYKADBDQAGRVGYIELDNGSKLIESRPERPFPMSTFKVLLCGAVLSRID 60
Db 2045 HPEITVKYKADBDQAGRVGYIELDNGSKLIESRPERPFPMSTFKVLLCGAVLSRID 2104
Qy 61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANLLTTTIGSP 120
Db 2105 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANLLTTTIGSP 2164
Qy 121 KETLAFILNMGDHVTRLDRWPELNEALPNDERDITMPVAMATTIRKLLTGELTLASRQ 180
Db 2165 KETLAFILNMGDHVTRLDRWPELNEALPNDERDITMPVAMATTIRKLLTGELTLASRQ 2224
Qy 181 Q 181
Db 2225 Q 2225

RESULT 12

US-09-919-901-9
; Sequence 9, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, Robert E.
; APPLICANT: Potte, Karen E.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901

; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-09-919-901-9

Query Match 100.0%; Score 925; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 4.2e-89;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPEITVKYKADBDQAGRVGYIELDNGSKLIESRPERPFPMSTFKVLLCGAVLSRID 60
Db 2045 HPEITVKYKADBDQAGRVGYIELDNGSKLIESRPERPFPMSTFKVLLCGAVLSRID 2104
Qy 61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANLLTTTIGSP 120
Db 2105 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANLLTTTIGSP 2164
Qy 121 KETLAFILNMGDHVTRLDRWPELNEALPNDERDITMPVAMATTIRKLLTGELTLASRQ 180
Db 2165 KETLAFILNMGDHVTRLDRWPELNEALPNDERDITMPVAMATTIRKLLTGELTLASRQ 2224
Qy 181 Q 181
Db 2225 Q 2225

RESULT 13

US-09-919-901-16
; Sequence 16, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potte, Karen E.
; APPLICANT: Jackson, Robert E.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 16
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-09-919-901-16

Query Match 100.0%; Score 925; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 4.2e-89;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPEITVKYKADBDQAGRVGYIELDNGSKLIESRPERPFPMSTFKVLLCGAVLSRID 60
Db 2045 HPEITVKYKADBDQAGRVGYIELDNGSKLIESRPERPFPMSTFKVLLCGAVLSRID 2104
Qy 61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANLLTTTIGSP 120

Db 2105 AGOELGRIRHYSQNDLVEYSPTVEKHLTDGWTVELCSAAITMSDNTAANILLTTIGP 2164
QY 121 KETLAFHNMGDHYTRLDRWEPBELNEAIPNDRDITMPVAMATTLRKLLTGSELLTLASRQ 180
Db 2165 KETLAFHNMGDHYTRLDRWEPBELNEAIPNDRDITMPVAMATTLRKLLTGSELLTLASRQ 2224
QY 181 Q 181
Db 2225 Q 2225

RESULT 14
US-10-191-966-2
Sequence 2, Application US/10191966
Publication No. US20030175692A1
GENERAL INFORMATION:
APPLICANT: Pottes, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
PRIOR FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 2307
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-10-191-966-2

Query Match 100.0%; Score 925; DB 14; Length 2307;
Best Local Similarity 100.0%; Pred. No. 4.2e-89;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKDAEDQAGRVGYIELDLSGKILSFRRPFRPPMSTFVLLCGAVLSRID 60
Db 2045 HPEITLVKVKDAEDQAGRVGYIELDLSGKILSFRRPFRPPMSTFVLLCGAVLSRID 2104
QY 61 AGOELGRIRHYSQNDLVEYSPTVEKHLTDGWTVELCSAAITMSDNTAANILLTTIGP 120
Db 2105 AGOELGRIRHYSQNDLVEYSPTVEKHLTDGWTVELCSAAITMSDNTAANILLTTIGP 2164
QY 121 KETLAFHNMGDHYTRLDRWEPBELNEAIPNDRDITMPVAMATTLRKLLTGSELLTLASRQ 180
Db 2165 KETLAFHNMGDHYTRLDRWEPBELNEAIPNDRDITMPVAMATTLRKLLTGSELLTLASRQ 2224
QY 181 Q 181
Db 2225 Q 2225

RESULT 15
US-10-191-966-9
Sequence 9, Application US/10191966
Publication No. US20030175692A1
GENERAL INFORMATION:
APPLICANT: Pottes, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
PRIOR FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933

; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-9

Query Match 100.0%; Score 925; DB 14; Length 2307;
Best Local Similarity 100.0%; Pred. No. 4.2e-89;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKDAEDQAGRVGYIELDLSGKILSFRRPFRPPMSTFVLLCGAVLSRID 60
Db 2045 HPEITLVKVKDAEDQAGRVGYIELDLSGKILSFRRPFRPPMSTFVLLCGAVLSRID 2104
QY 61 AGOELGRIRHYSQNDLVEYSPTVEKHLTDGWTVELCSAAITMSDNTAANILLTTIGP 120
Db 2105 AGOELGRIRHYSQNDLVEYSPTVEKHLTDGWTVELCSAAITMSDNTAANILLTTIGP 2164
QY 121 KETLAFHNMGDHYTRLDRWEPBELNEAIPNDRDITMPVAMATTLRKLLTGSELLTLASRQ 180
Db 2165 KETLAFHNMGDHYTRLDRWEPBELNEAIPNDRDITMPVAMATTLRKLLTGSELLTLASRQ 2224
QY 181 Q 181
Db 2225 Q 2225

Search completed: June 10, 2005, 11:09:04
Job time : 61.6383 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:40:16 ; Search time 57.6211 Seconds
(without alignments)
1144.220 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_172

Perfect score: 885
Sequence: 1 HPEITVKKVADMDQAGARVG.....RDTTVPVAMATTIRKLNGE 172

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 1710399

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
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20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
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22: /cgn2_6/ptodata/2/pubpaa/US6_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	885	100.0	263	15 US-10-668-778-2
2	885	100.0	286	10 US-09-919-901-7
3	885	100.0	286	10 US-09-919-901-14
4	885	100.0	286	10 US-09-919-901-21
5	885	100.0	286	11 US-09-837-306-354
6	885	100.0	286	14 US-10-191-966-7
7	885	100.0	286	14 US-10-191-966-14
8	885	100.0	286	14 US-10-191-966-21
9	885	100.0	286	15 US-10-045-674-523
10	885	100.0	286	16 US-10-416-708A-73
11	885	100.0	2307	10 US-09-919-901-2

12	885	100.0	2307	10 US-09-919-901-9	Sequence 9, Appli
13	885	100.0	2307	10 US-09-919-901-16	Sequence 16, Appli
14	885	100.0	2307	14 US-10-191-966-2	Sequence 2, Appli
15	885	100.0	2307	14 US-10-191-966-9	Sequence 9, Appli
16	885	100.0	2307	14 US-10-191-966-16	Sequence 16, Appli
17	884	99.9	286	14 US-10-231-013-9	Sequence 9, Appli
18	884	99.9	286	14 US-10-842-534-9	Sequence 9, Appli
19	884	99.9	1293	14 US-10-251-385-292	Sequence 292, App
20	884	99.9	1967	16 US-10-477-044-1	Sequence 1, Appli
21	880	99.4	265	9 US-09-772-114-6	Sequence 6, Appli
22	880	99.4	265	14 US-10-280-482-2	Sequence 2, Appli
23	880	99.4	265	17 US-10-656-029-2	Sequence 2, Appli
24	880	99.4	285	9 US-09-772-114-7	Sequence 7, Appli
25	880	99.4	286	14 US-10-016-668-5	Sequence 5, Appli
26	880	99.4	286	14 US-10-280-482-4	Sequence 4, Appli
27	880	99.4	286	17 US-10-656-029-4	Sequence 4, Appli
28	880	99.4	286	17 US-10-877-952-26	Sequence 26, Appli
29	880	99.4	286	17 US-10-877-952-71	Sequence 71, Appli
30	877	99.1	264	17 US-10-877-952-18	Sequence 18, Appli
31	877	99.1	362	15 US-10-469-199-2	Sequence 2, Appli
32	877	99.1	584	17 US-10-890-675-2	Sequence 2, Appli
33	873	98.6	265	9 US-09-772-114-8	Sequence 8, Appli
34	873	98.6	265	14 US-10-280-482-6	Sequence 6, Appli
35	873	98.6	265	16 US-10-622-088-114	Sequence 114, App
36	873	98.6	265	17 US-10-656-029-6	Sequence 6, Appli
37	873	98.6	265	17 US-10-877-952-154	Sequence 154, App
38	872	98.5	264	9 US-09-772-114-9	Sequence 9, Appli
39	872	98.5	264	14 US-10-280-482-8	Sequence 8, Appli
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41	870	98.3	498	17 US-10-491-653-146	Sequence 146, App
42	865.5	97.8	262	14 US-10-177-725-3	Sequence 3, Appli
43	865.5	97.8	262	15 US-10-393-449-3	Sequence 2, Appli
44	846	95.6	284	15 US-10-062-188-2	Sequence 2, Appli
45	463	52.3	94	9 US-09-923-298-760	Sequence 760, App

ALIGNMENTS

RESULT 1
US-10-668-778-2
; Sequence 2, Application US/10668778
; Publication No. US20040038317A1
; GENERAL INFORMATION:
; APPLICANT: Balint, Robert F.
; APPLICANT: Her, Jeng-Hong
; TITLE OF INVENTION: Interaction-Activated Proteins
; FILE REFERENCE: 021167-000700US
; CURRENT APPLICATION NUMBER: US/10/668,778
; CURRENT FILING DATE: 2003-09-22
; PRIOR APPLICATION NUMBER: US/09/526,106
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: US 60/124,339
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: US 60/135,926
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: US 60/175,968
; PRIOR FILING DATE: 2000-01-13
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Escherichia coli
; FEATURE:
; OTHER INFORMATION: TEM-1 beta-lactamase
US-10-668-778-2

Query Match 100.0%; Score 885; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.3e-87;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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US-09-837-306-354
; Sequence 354, Application US/09837306
; Publication No. US20040029113A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, ROBERT C.
; APPLICANT: COHEN, EDWARD H.
; APPLICANT: NASTRI, HORACIO G.
; APPLICANT: ROOKEY, KRISTIN L.
; APPLICANT: HOET, RENE
; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC
; TITLE OF INVENTION: PACKAGES THAT COLLECTIVELY DISPLAY THE MEMBERS OF A
; FILE REFERENCE: DVAL/002
; CURRENT APPLICATION NUMBER: US/09/837,306
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/198,069
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 354
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURES:
; OTHER INFORMATION: Description of Unknown Organism: pCRES5
US-09-837-306-354
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Best Local Similarity 100.0%; Pred. No. 1.4e-87;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 24 HPEITLVKKYDABDQICARVGYIELDLNSGKILIESRPERPFPMSFTFKYLCGAYLSRID 83
QY 61 AGQEQGRIRHYSQNDLVEYSPYTERKHLTDGWTVELCSAATMTMSDNTAANLLTTIGSP 120
DB 84 AGQEQGRIRHYSQNDLVEYSPYTERKHLTDGWTVELCSAATMTMSDNTAANLLTTIGSP 143
QY 121 KELTFLHMGDHYTRLDRLWPEPELNEALPNDERTTTPVANAATTLTKLLTGE 172
DB 144 KELTFLHMGDHYTRLDRLWPEPELNEALPNDERTTTPVANAATTLTKLLTGE 195
RESULT 6
US-10-191-966-7
; Sequence 7, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patlick, Amy K.
; TITLE OF INVENTION: REFORGER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: :
US-10-191-966-7
Query Match 100.0%; Score 885; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.4e-87;

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Matches 172: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPELVVYKQADQLGARVGIETDLSNGKILSFPRPERPMMSTFKYLICGAVLSRID 60
Db 24 HPELVVYKQADQLGARVGIETDLSNGKILSFPRPERPMMSTFKYLICGAVLSRID 83

Qy 61 AGQQLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120
Db 84 AGQQLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 143

Qy 121 KETLAFILNMGDHYTRLDRWPELNEAIPNDEBDTTPVMAATILRKLLTGE 172
Db 144 KETLAFILNMGDHYTRLDRWPELNEAIPNDEBDTTPVMAATILRKLLTGE 195

RESULT 7
US-10-191-966-14
; Sequence 14, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-10-191-966-14

Query Match 100.0%; Score 885; DB 14; Length 286;
Best Local Similarity 100.0%; Pctd. No. 1,4e-87;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPELVVYKQADQLGARVGIETDLSNGKILSFPRPERPMMSTFKYLICGAVLSRID 60
Db 24 HPELVVYKQADQLGARVGIETDLSNGKILSFPRPERPMMSTFKYLICGAVLSRID 83

Qy 61 AGQQLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120
Db 84 AGQQLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 143

Qy 121 KETLAFILNMGDHYTRLDRWPELNEAIPNDEBDTTPVMAATILRKLLTGE 172
Db 144 KETLAFILNMGDHYTRLDRWPELNEAIPNDEBDTTPVMAATILRKLLTGE 195

RESULT 8
US-10-191-966-21
; Sequence 21, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
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PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 21
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-10-191-966-21

Query Match 100.0%; Score 885; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.4e-87;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 24 HPEITLVKVDADQAGAVGYIELDLSGKILSPREPERFPMSTFKYLGCGLVLSRID 83
QY 61 AGOEOLGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAAILTTTIGP 120
DB 84 AGOEOLGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAAILTTTIGP 143
QY 121 KETLFLNMGDHYTRLDRWEPELNEAIPNDERDTTMVAAATTLTKLTGE 172
DB 144 KETLFLNMGDHYTRLDRWEPELNEAIPNDERDTTMVAAATTLTKLTGE 195

RESULT 9
US-10-045-674-523
Sequence 523, Application US/10045674
Publication No. US200302333A1

GENERAL INFORMATION:
APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROONEY, KRISTIN L.
APPLICANT: HOET, RENE
APPLICANT: HOOGENDOORN, HENDRICUS R. J. M.
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: DYAX/002 CIP2
CURRENT APPLICATION NUMBER: US/10/045,674
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 60/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 523
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Vector pCRESS
US-10-045-674-523

Query Match 100.0%; Score 885; DB 15; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.4e-87;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGAVGYIELDLSGKILSPREPERFPMSTFKYLGCGLVLSRID 60
DB 24 HPEITLVKVDADQAGAVGYIELDLSGKILSPREPERFPMSTFKYLGCGLVLSRID 83
QY 61 AGOEOLGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAAILTTTIGP 120

DB 84 AGOEOLGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAAILTTTIGP 143
QY 121 KETLFLNMGDHYTRLDRWEPELNEAIPNDERDTTMVAAATTLTKLTGE 172
DB 144 KETLFLNMGDHYTRLDRWEPELNEAIPNDERDTTMVAAATTLTKLTGE 195

RESULT 10
US-10-416-708A-73
Sequence 73, Application US/10416708A
Publication No. US20040161753A1

GENERAL INFORMATION:
APPLICANT: Wise, John G.
APPLICANT: Fromknecht, Katja

TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING
TITLE OF INVENTION: SPECIFICITIES
FILE REFERENCE: 37779-0004
CURRENT APPLICATION NUMBER: US/10/416,708A
CURRENT FILING DATE: 2004-01-28
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patent In version 3.2
SEQ ID NO 73
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Construct
US-10-416-708A-73

Query Match 100.0%; Score 885; DB 16; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.4e-87;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGAVGYIELDLSGKILSPREPERFPMSTFKYLGCGLVLSRID 60
DB 24 HPEITLVKVDADQAGAVGYIELDLSGKILSPREPERFPMSTFKYLGCGLVLSRID 83
QY 61 AGOEOLGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAAILTTTIGP 120
DB 84 AGOEOLGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAAILTTTIGP 143
QY 121 KETLFLNMGDHYTRLDRWEPELNEAIPNDERDTTMVAAATTLTKLTGE 172
DB 144 KETLFLNMGDHYTRLDRWEPELNEAIPNDERDTTMVAAATTLTKLTGE 195

RESULT 11
US-09-919-901-2
Sequence 2, Application US/09919901
Publication No. US20030082518A1

GENERAL INFORMATION:
APPLICANT: Potte, Karen E.
APPLICANT: Jackson, Roberta L.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 2
LENGTH: 2307
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-09-919-901-2

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Query Match      100.0%; Score 885; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 2.6e-86;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HPEITLVKVDADQAGARVGYIELDINSKILSFPRPFRPMMSTFKVLLCGAVLSRID 60
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Db      2045 HPEITLVKVDADQAGARVGYIELDINSKILSFPRPFRPMMSTFKVLLCGAVLSRID 2104

Qy      61 AGOEOIGRRIHYSQNDLVEYSPYTEKHLTDGMTVRELCSAATMSDNTANLLTTIGGP 120
        |||
Db      2105 AGOEOIGRRIHYSQNDLVEYSPYTEKHLTDGMTVRELCSAATMSDNTANLLTTIGGP 2164

Qy      121 KELTAFIHNMGDHYTRLDRWEPBELNEAIPNDRDITMPVAMATTAKLTGE 172
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Db      2165 KELTAFIHNMGDHYTRLDRWEPBELNEAIPNDRDITMPVAMATTAKLTGE 2216

RESULT 12
US-09-919-901-9
; Sequence 9, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potter, Karen E.
; APPLICANT: Jackson, Roberta L.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-09-919-901-9

Query Match      100.0%; Score 885; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 2.6e-86;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HPEITLVKVDADQAGARVGYIELDINSKILSFPRPFRPMMSTFKVLLCGAVLSRID 60
        |||
Db      2045 HPEITLVKVDADQAGARVGYIELDINSKILSFPRPFRPMMSTFKVLLCGAVLSRID 2104

Qy      61 AGOEOIGRRIHYSQNDLVEYSPYTEKHLTDGMTVRELCSAATMSDNTANLLTTIGGP 120
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Db      2105 AGOEOIGRRIHYSQNDLVEYSPYTEKHLTDGMTVRELCSAATMSDNTANLLTTIGGP 2164

Qy      121 KELTAFIHNMGDHYTRLDRWEPBELNEAIPNDRDITMPVAMATTAKLTGE 172
        |||
Db      2165 KELTAFIHNMGDHYTRLDRWEPBELNEAIPNDRDITMPVAMATTAKLTGE 2216

RESULT 13
US-09-919-901-16
; Sequence 16, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potter, Karen E.
; APPLICANT: Jackson, Roberta L.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
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; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 16
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-09-919-901-16

Query Match      100.0%; Score 885; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 2.6e-86;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HPEITLVKVDADQAGARVGYIELDINSKILSFPRPFRPMMSTFKVLLCGAVLSRID 60
        |||
Db      2045 HPEITLVKVDADQAGARVGYIELDINSKILSFPRPFRPMMSTFKVLLCGAVLSRID 2104

Qy      61 AGOEOIGRRIHYSQNDLVEYSPYTEKHLTDGMTVRELCSAATMSDNTANLLTTIGGP 120
        |||
Db      2105 AGOEOIGRRIHYSQNDLVEYSPYTEKHLTDGMTVRELCSAATMSDNTANLLTTIGGP 2164

Qy      121 KELTAFIHNMGDHYTRLDRWEPBELNEAIPNDRDITMPVAMATTAKLTGE 172
        |||
Db      2165 KELTAFIHNMGDHYTRLDRWEPBELNEAIPNDRDITMPVAMATTAKLTGE 2216

RESULT 14
US-10-191-966-2
; Sequence 2, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potter, Karen E.
; APPLICANT: Jackson, Roberta L.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-10-191-966-2

Query Match      100.0%; Score 885; DB 14; Length 2307;
Best Local Similarity 100.0%; Pred. No. 2.6e-86;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HPEITLVKVDADQAGARVGYIELDINSKILSFPRPFRPMMSTFKVLLCGAVLSRID 60
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Db      2045 HPEITLVKVDADQAGARVGYIELDINSKILSFPRPFRPMMSTFKVLLCGAVLSRID 2104

Qy      61 AGOEOIGRRIHYSQNDLVEYSPYTEKHLTDGMTVRELCSAATMSDNTANLLTTIGGP 120
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Db      2105 AGOEOIGRRIHYSQNDLVEYSPYTEKHLTDGMTVRELCSAATMSDNTANLLTTIGGP 2164

Qy      121 KELTAFIHNMGDHYTRLDRWEPBELNEAIPNDRDITMPVAMATTAKLTGE 172
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Db 2165 KELTAFLLHMGDHYTRLDRWEPBLNEAIPNDERDTTMAPVAMATTLRKLLTGE 2216

RESULT 15

US-10-191-966-9
; Sequence 9, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patlick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-9

Query Match 100.0%; Score 885; DB 14; Length 2307;

Best Local Similarity 100.0%; Pred. No. 2.6e-86;

Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKTKDAEDQIGARVGYIELDINSKILIESFRPERPMMSTFKYLLCGAVLSRID 60
|||
DB 2045 HPEITLVKTKDAEDQIGARVGYIELDINSKILIESFRPERPMMSTFKYLLCGAVLSRID 2104
|||
QY 61 AGOEOLGRIRHYSQNDLVEYSPVTEKHLTDGWTRELSAATITMSDNTAANLLTTIGSP 120
|||
DB 2105 AGOEOLGRIRHYSQNDLVEYSPVTEKHLTDGWTRELSAATITMSDNTAANLLTTIGSP 2164
|||
QY 121 KELTAFLLHMGDHYTRLDRWEPBLNEAIPNDERDTTMAPVAMATTLRKLLTGE 172
|||
DB 2165 KELTAFLLHMGDHYTRLDRWEPBLNEAIPNDERDTTMAPVAMATTLRKLLTGE 2216
|||

Search completed: June 10, 2005, 11:09:05
Job time : 58.6231 secs

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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:40:16 ; Search time 49.9177 Seconds
(without alignments)
1144.220 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_149

Perfect score: 770
Sequence: 1 HPRTLVKKADBDQ/GARVG.....MGDHTRLDRWPELNEAIP 149

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 1710399

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10F_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	770	100.0	263	15	US-10-668-778-2
2	770	100.0	286	10	US-09-919-901-7
3	770	100.0	286	10	US-09-919-901-14
4	770	100.0	286	10	US-09-919-901-21
5	770	100.0	286	11	US-09-837-306-354
6	770	100.0	286	14	US-10-191-966-7
7	770	100.0	286	14	US-10-191-966-14
8	770	100.0	286	15	US-10-191-966-21
9	770	100.0	286	15	US-10-045-674-523
10	770	100.0	286	16	US-10-416-708A-73
11	770	100.0	2307	10	US-09-919-901-2

12	770	100.0	2307	10	US-09-919-901-9	Sequence 9, Appli
13	770	100.0	2307	10	US-09-919-901-16	Sequence 16, Appli
14	770	100.0	2307	14	US-10-191-966-2	Sequence 2, Appli
15	770	100.0	2307	14	US-10-191-966-9	Sequence 9, Appli
16	770	100.0	2307	14	US-10-191-966-16	Sequence 16, Appli
17	769	99.9	265	9	US-09-772-114-6	Sequence 6, Appli
18	769	99.9	265	14	US-10-280-482-2	Sequence 2, Appli
19	769	99.9	265	17	US-10-656-029-2	Sequence 2, Appli
20	769	99.9	285	9	US-09-772-114-7	Sequence 7, Appli
21	769	99.9	286	14	US-10-016-668-5	Sequence 5, Appli
22	769	99.9	286	14	US-10-231-013-9	Sequence 9, Appli
23	769	99.9	286	14	US-10-280-482-4	Sequence 4, Appli
24	769	99.9	286	16	US-10-842-534-9	Sequence 9, Appli
25	769	99.9	286	17	US-10-656-029-4	Sequence 4, Appli
26	769	99.9	286	17	US-10-877-952-16	Sequence 26, Appli
27	769	99.9	286	17	US-10-877-952-71	Sequence 71, Appli
28	769	99.9	1293	14	US-10-251-385-292	Sequence 292, App
29	769	99.9	1967	16	US-10-477-044-1	Sequence 1, Appli
30	762	99.0	264	17	US-10-877-952-18	Sequence 18, Appli
31	762	99.0	362	15	US-10-469-199-2	Sequence 2, Appli
32	762	99.0	584	17	US-10-890-675-2	Sequence 2, Appli
33	758	98.4	265	9	US-09-772-114-8	Sequence 8, Appli
34	758	98.4	265	14	US-10-280-482-6	Sequence 6, Appli
35	758	98.4	265	16	US-10-622-088-114	Sequence 114, App
36	758	98.4	265	17	US-10-656-029-6	Sequence 6, Appli
37	758	98.4	265	17	US-10-877-952-154	Sequence 154, App
38	757	98.3	264	9	US-09-772-114-9	Sequence 9, Appli
39	757	98.3	264	14	US-10-280-482-8	Sequence 8, Appli
40	757	98.3	264	17	US-10-656-029-8	Sequence 8, Appli
41	755	98.1	498	17	US-10-491-653-146	Sequence 146, App
42	750.5	97.5	262	14	US-10-177-725-3	Sequence 3, Appli
43	750.5	97.5	262	15	US-10-393-449-3	Sequence 2, Appli
44	750.5	97.5	284	15	US-10-062-188-2	Sequence 2, Appli
45	393	51.0	94	9	US-09-925-298-760	Sequence 760, App

ALIGNMENTS

RESULT 1

US-10-668-778-2

Sequence 2, Application US/10668778

Publication No. US20040038317A1

GENERAL INFORMATION:

APPLICANT: Balint, Robert F.

APPLICANT: Her, Jeng-Hong

TITLE OF INVENTION: Interaction-Activated Proteins

FILE REFERENCE: 021167-000700US

CURRENT APPLICATION NUMBER: US/10/668, 778

CURRENT FILING DATE: 2003-09-22

PRIOR APPLICATION NUMBER: US/09/526, 106

PRIOR FILING DATE: 2000-03-15

PRIOR APPLICATION NUMBER: US 60/124,339

PRIOR FILING DATE: 1999-03-15

PRIOR APPLICATION NUMBER: US 60/135,926

PRIOR FILING DATE: 1999-05-25

PRIOR APPLICATION NUMBER: US 60/175,968

PRIOR FILING DATE: 2000-01-13

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 263

TYPE: PRT

ORGANISM: Escherichia coli

FEATURE:

OTHER INFORMATION: TEM-1 beta-lactamase

US-10-668-778-2

Query Match 100.0%; Score 770; DB 15; Length 263;
Best Local Similarity 100.0%; Pred. No. 2.7e-77;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	HPTLVKVDABEQAFARGYIELDINSKILIESRPERPMMSTFVLLCGVLSRID	60
Qy	1	HPTLVKVDABEQAFARGYIELDINSKILIESRPERPMMSTFVLLCGVLSRID	60
Db	1	HPETLVKVDABEQAFARGYIELDINSKILIESRPERPMMSTFVLLCGVLSRID	60
Qy	61	AGEGOLGRRIRHYSQNDLVESPVTEKHLTDGNTVBECSAATMSDNTAAMLLTTIGP	120
Qy	61	AGEGOLGRRIRHYSQNDLVESPVTEKHLTDGNTVBECSAATMSDNTAAMLLTTIGP	120
Db	61	AGEGOLGRRIRHYSQNDLVESPVTEKHLTDGNTVBECSAATMSDNTAAMLLTTIGP	120
Qy	121	KELTAFLLHNGDVTRLDRWEPELNEAIP	149
Qy	121	KELTAFLLHNGDVTRLDRWEPELNEAIP	149
Db	121	KELTAFLLHNGDVTRLDRWEPELNEAIP	149

RESULT 2
US-09-919-901-7

US-09-919-901-7

	Query Match	100.0%	Score 770;	DB 10;	Length 266;
	Best Local Similarity	100.0%	Pred. No. 3e-77;		
	Matches 149;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	1	HPETLVKVDADIEDQGLGARVGIYEILDNGSKILIESFRPEREPMMSTFKVLLCGAVISRID	60		
Db	24	HPETLVKVDADIEDQGLGARVGIYEILDNGSKILIESFRPEREPMMSTFKVLLCGAVISRID	83		
QY	61	AGGEOIGRIIRIHSQNDLVESPVTEKHLTDGTTVAELCSAIIWSDNTAANLLITTTGGP	120		
Db	84	AGGEOIGRIIRIHSQNDLVESPVTEKHLTDGTTVAELCSAIIWSDNTAANLLITTTGGP	143		
QY	121	KELTAFLHNMGGHVTRLRDWEPELNEAIP	149		
Db	144	KELTAFLHNMGGHVTRLRDWEPELNEAIP	172		

RESULT 3
US-09-919-901-14'

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: PRIOR FILING DATE: 1998-08-05
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 14
: LENGTH: 286
: TYPE: PRT
: ORGANSIM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION:
US-09-919-901-14

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Query Match	100.0%	Score 770;	DB 10;	Length 286;
Best Local Similarity	100.0%;	Pred. No. 3e-77;		
Matches 149;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Qy	1	HEPTLVKVDAAEQGARVGYIELDNSGKLTLESRRPERPPMSTFVLLCGAVLSRID	60
Db	24	HPETLVKVDAAEQGARVGYIELDNSGKLTLESRRPERPPMSTFVLLCGAVLSRID	83
Qy	61	AGGEOLGRRIRHSQNDLVESPVTEKHLTDGVTVELCSAITVMSDNTAAVLLTTIGGP	120
Db	84	AGGEOLGRRIRHSQNDLVESPVTEKHLTDGVTVELCSAITVMSDNTAAVLLTTIGGP	143
Qy	121	KELTAFTAHNMGDHVTRLDRWEPELNEAIP	149
Db	144	KELTAFTAHNMGDHVTRLDRWEPELNEAIP	172

RESULT 4
US-09-919-901-21
; Sequence 21, Application US/09919901

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? Publication No. US20030082518A1
? GENERAL INFORMATION:
? APPLICANT: Potts, Karen B.
? APPLICANT: Jackson, Roberta L.
? APPLICANT: Patrick, Amy K.
? TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
? TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
? FILE REFERENCE: 0125-0005A
? CURRENT APPLICATION NUMBER: US/09/919,901
? CURRENT FILING DATE: 2001-08-02
? PRIOR APPLICATION NUMBER: 09/265,933
? PRIOR FILING DATE: 1999-02-08
? PRIOR APPLICATION NUMBER: 09/125,611
? PRIOR FILING DATE: 1998-08-05
? NUMBER OF SEQ ID NOS: 33
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 21
? LENGTH: 286
? TYPE: PR1
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION:
? US-09-919-901-21

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	Query Match	100.0%;	Score 770;	DB 10;	Length 286;
	Best Local Similarity	100.0%;	Pred. No. 3e-77;		
	Matches 149;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	1	HPETLVKVDADQADQGVGYIELDLNSGKILLESFPRPERPPMSTFKVLICGAVLSRID	60		
DB	24	HPETLVKVDADQADQGVGYIELDLNSGKILLESFPRPERPPMSTFKVLICGAVLSRID	83		
QY	61	AGQEQGLRRIRHSQNDLVESPVTEKHHLDGQTVRELCSAIIITMSDNTAANLLITTTGGP	120		
DB	84	AGQEQGLRRIRHSQNDLVESPVTEKHHLDGQTVRELCSAIIITMSDNTAANLLITTTGGP	143		
QY	121	KELTAFILHNMGDHYTRLDMQEPQLNEALP	149		
DB	144	KELTAFILHNMGDHYTRLDMQEPQLNEALP	172		

RESULT 5

US-09-837-306-354
; Sequence 354, Application US/09837306
; Publication No. US20040029113A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, ROBERT C.
; APPLICANT: COHEN, EDWARD H.
; APPLICANT: NASTRI, HORACIO G.
; APPLICANT: ROOKEY, KRISTIN L.
; APPLICANT: HOEF, RENE
; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC
; TITLE OF INVENTION: PACKAGES THAT COLLECTIVELY DISPLAY THE MEMBERS OF A
; TITLE OF INVENTION: DIVERSE FAMILY OF PEPTIDES, POLYPEPTIDES OR PROTEINS
; FILE REFERENCE: DYAX/002
; CURRENT APPLICATION NUMBER: US/09/837,306
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/198,069
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 354
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: pCES5
US-09-837-306-354
Query Match 100.0%; Score 770; DB 11; Length 286;
Best Local Similarity 100.0%; Pred. No. 3e-77;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 24 HPEITLVKKDAEDQAGAVGVIETLDNSGKILSFREPERPPMSTFVLLCGAVLSRID 83
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DB 84 AGGOLGRRHHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGCP 143
QY 121 KETLAFILNMGDHVTRLDRWEPELNEAIP 149
DB 144 KETLAFILNMGDHVTRLDRWEPELNEAIP 172
RESULT 6
US-10-191-966-7
; Sequence 7, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-7
Query Match 100.0%; Score 770; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 3e-77;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEITLVKKDAEDQAGAVGVIETLDNSGKILSFREPERPPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKKDAEDQAGAVGVIETLDNSGKILSFREPERPPMSTFVLLCGAVLSRID 83
QY 61 AGGOLGRRHHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGCP 120
DB 84 AGGOLGRRHHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGCP 143
QY 121 KETLAFILNMGDHVTRLDRWEPELNEAIP 149
DB 144 KETLAFILNMGDHVTRLDRWEPELNEAIP 172
RESULT 7
US-10-191-966-14
; Sequence 14, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-14
Query Match 100.0%; Score 770; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 3e-77;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEITLVKKDAEDQAGAVGVIETLDNSGKILSFREPERPPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKKDAEDQAGAVGVIETLDNSGKILSFREPERPPMSTFVLLCGAVLSRID 83
QY 61 AGGOLGRRHHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGCP 120
DB 84 AGGOLGRRHHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGCP 143
QY 121 KETLAFILNMGDHVTRLDRWEPELNEAIP 149
DB 144 KETLAFILNMGDHVTRLDRWEPELNEAIP 172
RESULT 8
US-10-191-966-21
; Sequence 21, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-10-191-966-21

Query Match 100.0%; Score 770; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 3e-77;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADQDQAGVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVKADQDQAGVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
QY 61 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120
DB 84 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 143
QY 121 KETLAFHNMGDHYTRLDRWEPELNEAIP 149
DB 144 KETLAFHNMGDHYTRLDRWEPELNEAIP 172

RESULT 9

US-10-045-674-523
Sequence 523, Application US/10045674
Publication No. US2003023233A1
GENERAL INFORMATION:
APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROOKEY, KRISTIN L.
APPLICANT: HOET, RENE
APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: DMAX/002 CIP2
CURRENT APPLICATION NUMBER: US/10/045,674
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 60/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 523
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Vector pCESS
US-10-045-674-523

Query Match 100.0%; Score 770; DB 15; Length 286;
Best Local Similarity 100.0%; Pred. No. 3e-77;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADQDQAGVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVKADQDQAGVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
QY 61 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120

DB 84 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 143
QY 121 KETLAFHNMGDHYTRLDRWEPELNEAIP 149
DB 144 KETLAFHNMGDHYTRLDRWEPELNEAIP 172

RESULT 10

US-10-416-708A-73
Sequence 73, Application US/10416708A
Publication No. US20040161753A1
GENERAL INFORMATION:
APPLICANT: Wise, John G.
APPLICANT: Fromknecht, Katja
TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING
TITLE OF INVENTION: SPECIFICITIES
FILE REFERENCE: 37779-0004
CURRENT APPLICATION NUMBER: US/10/416,708A
CURRENT FILING DATE: 2004-01-28
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn version 3.2
SEQ ID NO 73
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Construct
US-10-416-708A-73

Query Match 100.0%; Score 770; DB 16; Length 286;
Best Local Similarity 100.0%; Pred. No. 3e-77;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADQDQAGVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVKADQDQAGVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
QY 61 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120
DB 84 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 143
QY 121 KETLAFHNMGDHYTRLDRWEPELNEAIP 149
DB 144 KETLAFHNMGDHYTRLDRWEPELNEAIP 172

RESULT 11

US-09-919-901-2
Sequence 2, Application US/09919901
Publication No. US20030082518A1
GENERAL INFORMATION:
APPLICANT: Jackson, Robert A.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 2307
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-09-919-901-2


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Query Match      100.0%; Score 770; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 5e-76;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HPELVKVKDADQAGRVGYIELDNSGKILSFPRPFRPMMSTFKVLLCGAVLSRID 60
      |||
Db      2045 HPELVKVKDADQAGRVGYIELDNSGKILSFPRPFRPMMSTFKVLLCGAVLSRID 2104

Qy      61 AGQEQLGRRIRHYSQNDLYEVSPTVEKHLTDGMYVELCSAATMSDNTAANLLTTIGSP 120
      |||
Db      2105 AGQEQLGRRIRHYSQNDLYEVSPTVEKHLTDGMYVELCSAATMSDNTAANLLTTIGSP 2164

Qy      121 KELTAFILNMGDHVTRLDRMEPELNEAIP 149
      |||
Db      2165 KELTAFILNMGDHVTRLDRMEPELNEAIP 2193

RESULT 12
US-09-919-901-9
; Sequence 9, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-09-919-901-9

Query Match      100.0%; Score 770; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 5e-76;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HPELVKVKDADQAGRVGYIELDNSGKILSFPRPFRPMMSTFKVLLCGAVLSRID 60
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Qy      61 AGQEQLGRRIRHYSQNDLYEVSPTVEKHLTDGMYVELCSAATMSDNTAANLLTTIGSP 120
      |||
Db      2105 AGQEQLGRRIRHYSQNDLYEVSPTVEKHLTDGMYVELCSAATMSDNTAANLLTTIGSP 2164

Qy      121 KELTAFILNMGDHVTRLDRMEPELNEAIP 149
      |||
Db      2165 KELTAFILNMGDHVTRLDRMEPELNEAIP 2193

RESULT 13
US-09-919-901-16
; Sequence 16, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
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; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-09-919-901-16

Query Match      100.0%; Score 770; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 5e-76;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HPELVKVKDADQAGRVGYIELDNSGKILSFPRPFRPMMSTFKVLLCGAVLSRID 60
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Db      2045 HPELVKVKDADQAGRVGYIELDNSGKILSFPRPFRPMMSTFKVLLCGAVLSRID 2104

Qy      61 AGQEQLGRRIRHYSQNDLYEVSPTVEKHLTDGMYVELCSAATMSDNTAANLLTTIGSP 120
      |||
Db      2105 AGQEQLGRRIRHYSQNDLYEVSPTVEKHLTDGMYVELCSAATMSDNTAANLLTTIGSP 2164

Qy      121 KELTAFILNMGDHVTRLDRMEPELNEAIP 149
      |||
Db      2165 KELTAFILNMGDHVTRLDRMEPELNEAIP 2193

RESULT 14
US-10-191-966-2
; Sequence 2, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-10-191-966-2

Query Match      100.0%; Score 770; DB 14; Length 2307;
Best Local Similarity 100.0%; Pred. No. 5e-76;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HPELVKVKDADQAGRVGYIELDNSGKILSFPRPFRPMMSTFKVLLCGAVLSRID 60
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Db      2045 HPELVKVKDADQAGRVGYIELDNSGKILSFPRPFRPMMSTFKVLLCGAVLSRID 2104

Qy      61 AGQEQLGRRIRHYSQNDLYEVSPTVEKHLTDGMYVELCSAATMSDNTAANLLTTIGSP 120
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Db      2105 AGQEQLGRRIRHYSQNDLYEVSPTVEKHLTDGMYVELCSAATMSDNTAANLLTTIGSP 2164

Qy      121 KELTAFILNMGDHVTRLDRMEPELNEAIP 149
      |||
Db      2165 KELTAFILNMGDHVTRLDRMEPELNEAIP 2193
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Db 2165 KeltaFLHNMGDHVTRLDRMPEPELNEAIP 2193

RESULT 15

US-10-191-966-9
; Sequence 9, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patlick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-9

Query Match 100.0%; Score 770; DB 14; Length 2307;

Best Local Similarity 100.0%; Pred. No. 5e-76;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKTKDAEDQIGARVGYIELDINSKILIESFRPBERPMMSTFKYLICGAVLSRID 60
|||
DB 2045 HPEITLVKTKDAEDQIGARVGYIELDINSKILIESFRPBERPMMSTFKYLICGAVLSRID 2104
|||
QY 61 AGQEQIGRIHISQNDLVEYSPVTEKHLTDGWTRELCSAITMSDNTAANLLTTIGSP 120
|||
DB 2105 AGQEQIGRIHISQNDLVEYSPVTEKHLTDGWTRELCSAITMSDNTAANLLTTIGSP 2164
|||
QY 121 KeltaFLHNMGDHVTRLDRMPEPELNEAIP 149
|||
DB 2165 KeltaFLHNMGDHVTRLDRMPEPELNEAIP 2193
|||

Search completed: June 10, 2005, 11:09:04
Job time : 49.9177 secs

Spugen Ltd.

1144.220 Million cell updates/sec

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Listing first 45 e

Published Applications AA:*

22: /cgn2_6/ptodata/2/pubpraa/US60_PUBCOMB.per.*

and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	1348	100.0	263	15	US-10-666-778-2	Sequence 2, Appli
2	1348	100.0	286	10	US-09-919-901-7	Sequence 7, Appli
3	1348	100.0	286	10	US-09-919-901-14	Sequence 14, Appli
4	1348	100.0	286	10	US-09-919-901-21	Sequence 21, Appli
5	1348	100.0	286	11	US-09-837-306-354	Sequence 354, Appli
6	1348	100.0	286	14	US-10-191-966-7	Sequence 7, Appli
7	1348	100.0	286	14	US-10-191-966-14	Sequence 14, Appli
8	1348	100.0	286	14	US-10-191-966-21	Sequence 21, Appli
9	1348	100.0	286	15	US-10-045-674-523	Sequence 523, Appli
10	1348	100.0	286	16	US-10-418-708A-73	Sequence 73, Appli
11	1348	100.0	2307	10	US-09-919-901-2	Sequence 2, Appli

12	1348	100.0	2307	10	US-09-919-901-9	Sequence 9, Appl1
13	1408	100.0	2307	10	US-09-919-901-9	Sequence 16, Appl1
14	1348	100.0	2307	14	US-10-191-966-2	Sequence 2, Appl1
15	1348	100.0	2307	14	US-10-191-966-9	Sequence 9, Appl1
16	1348	100.0	2307	14	US-10-191-966-9	Sequence 16, Appl1
17	1347	99.9	286	14	US-10-331-013-9	Sequence 9, Appl1
18	1347	99.9	286	16	US-10-642-534-9	Sequence 9, Appl1
19	1347	99.9	1293	14	US-10-351-385-292	Sequence 292, App
20	1347	99.9	1967	16	US-10-477-044-1	Sequence 1, Appl1
21	1343	99.6	265	9	US-09-772-114-6	Sequence 6, Appl1
22	1343	99.6	265	14	US-10-280-482-2	Sequence 2, Appl1
23	1343	99.6	265	17	US-10-656-029-2	Sequence 2, Appl1
24	1343	99.6	285	9	US-09-772-114-7	Sequence 7, Appl1
25	1343	99.6	285	14	US-10-016-668-5	Sequence 5, Appl1
26	1343	99.6	286	14	US-10-280-482-4	Sequence 4, Appl1
27	1343	99.6	286	17	US-10-656-029-4	Sequence 4, Appl1
28	1343	99.6	286	17	US-10-877-952-26	Sequence 26, Appl
29	1343	99.6	286	17	US-10-877-952-71	Sequence 71, Appl
30	1340	99.4	264	17	US-10-877-952-18	Sequence 18, Appl
31	1340	99.4	362	15	US-10-469-199-2	Sequence 2, Appl1
32	1340	99.4	584	17	US-10-890-675-2	Sequence 2, Appl1
33	1336	99.1	265	9	US-09-772-114-8	Sequence 8, Appl1
34	1336	99.1	265	14	US-10-280-482-6	Sequence 6, Appl1
35	1336	99.1	265	16	US-10-622-088-11	Sequence 11, Appl
36	1336	99.1	265	17	US-10-656-029-6	Sequence 6, Appl1
37	1336	99.1	265	17	US-10-877-952-154	Sequence 154, App
38	1335	99.0	264	9	US-09-772-114-9	Sequence 9, Appl1
39	1335	99.0	264	14	US-10-280-482-8	Sequence 8, Appl1
40	1335	99.0	264	17	US-10-656-029-8	Sequence 8, Appl1
41	1328.5	98.6	262	14	US-10-177-725-3	Sequence 3, Appl1
42	1328.5	98.6	262	15	US-10-393-449-3	Sequence 3, Appl1
43	1320	97.9	498	17	US-10-491-653-146	Sequence 146, App
44	1329	96.4	284	15	US-10-062-188-2	Sequence 2, Appl1
45	584	43.3	118	15	US-10-062-188-3	Sequence 3, Appl1

ALIGNMENTS

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1 RESULT 1
2 US-10-668-778-2
3 Sequence 2, Application US/10668778
4 Publication No. US20040038317A1
5 GENERAL INFORMATION:
6 APPLICANT: Ballint, Robert F.
7 APPLICANT: Her, Jeng-Hong
8 APPLICANT: Kalobios, Inc.
9 TITLE OF INVENTION: Interaction-Activated Proteins
10 FILE REFERENCE: 021167-000700US
11 CURRENT APPLICATION NUMBER: US/10/668, 778
12 CURRENT FILING DATE: 2003-09-22
13 PRIOR APPLICATION NUMBER: US/09/526, 106
14 PRIOR FILING DATE: 2000-03-15
15 PRIOR APPLICATION NUMBER: US 60/124, 339
16 PRIOR FILING DATE: 1999-03-15
17 PRIOR APPLICATION NUMBER: US 60/135, 926
18 PRIOR FILING DATE: 1999-05-25
19 PRIOR APPLICATION NUMBER: US 60/175, 968
20 PRIOR FILING DATE: 2000-01-13
21 NUMBER OF SEQ ID NOS: 26
22 SOFTWARE: PatentIn Ver. 2.1
23 SEQ ID NO 2
24 LENGTH: 263
25 TYPE: PRT
26 ORGANISM: Escherichia coli
27 FEATURE:
28 OTHER INFORMATION: TEM-1 beta-lactamase
29 US-10-668-778-2

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Query Match	100.0%	Score 1348;	DB 15;	length 263;
Best Local Similarity	100.0%	Pred. No. 2.2e-125;		
Matches 263; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

Fri Jun 10 14:22:57 2005

us-10-668-778-2.rapb

Page 3

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-09-919-901-21

Query Match 100.0%; Score 1348; DB 10; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.4e-125;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGYIELDINSKILIESFRPERPMMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKVDADQAGARVGYIELDINSKILIESFRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGOBLGRRIHYSQNDLVEYSPVTEKHLTDGVTRELCSAATMSDNTANLLTTIGSP 120
DB 84 AGOBLGRRIHYSQNDLVEYSPVTEKHLTDGVTRELCSAATMSDNTANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAMATTYRKLLTGELTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAMATTYRKLLTGELTLASRQ 203
QY 181 QLIDMMEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYITTG 240
DB 204 QLIDMMEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYITTG 263
QY 241 SOATMDERNROIAEIGASLIKHW 263
DB 264 SOATMDERNROIAEIGASLIKHW 286

RESULT 5

US-09-837-306-354
Sequence 354, Application US/09837306
Publication No. US20040029113A1
GENERAL INFORMATION:
APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROOKEY, KRISTIN L.
APPLICANT: HOEF, RENE

TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC
TITLE OF INVENTION: PACKAGES THAT COLLECTIVELY DISPLAY THE MEMBERS OF A
FILE REFERENCE: DYAX/002
CURRENT APPLICATION NUMBER: US/09/837.306
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 60/198,069
PRIOR FILING DATE: 2000-04-17
NUMBER OF SEQ ID NOS: 428
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 354
LENGTH: 286
TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: PCBS5
US-09-837-306-354

Query Match 100.0%; Score 1348; DB 11; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.4e-125;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGYIELDINSKILIESFRPERPMMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKVDADQAGARVGYIELDINSKILIESFRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGOBLGRRIHYSQNDLVEYSPVTEKHLTDGVTRELCSAATMSDNTANLLTTIGSP 120
DB 84 AGOBLGRRIHYSQNDLVEYSPVTEKHLTDGVTRELCSAATMSDNTANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAMATTYRKLLTGELTLASRQ 180

DB 144 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAMATTYRKLLTGELTLASRQ 203
QY 181 QLIDMMEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYITTG 240
DB 204 QLIDMMEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYITTG 263
QY 241 SOATMDERNROIAEIGASLIKHW 263
DB 264 SOATMDERNROIAEIGASLIKHW 286

RESULT 6

US-10-191-966-7
Sequence 7, Application US/10191966
Publication No. US20030175692A1
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191.966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263.933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-10-191-966-7

Query Match 100.0%; Score 1348; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.4e-125;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGYIELDINSKILIESFRPERPMMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKVDADQAGARVGYIELDINSKILIESFRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGOBLGRRIHYSQNDLVEYSPVTEKHLTDGVTRELCSAATMSDNTANLLTTIGSP 120
DB 84 AGOBLGRRIHYSQNDLVEYSPVTEKHLTDGVTRELCSAATMSDNTANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAMATTYRKLLTGELTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAMATTYRKLLTGELTLASRQ 203
QY 181 QLIDMMEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYITTG 240
DB 204 QLIDMMEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYITTG 263
QY 241 SOATMDERNROIAEIGASLIKHW 263
DB 264 SOATMDERNROIAEIGASLIKHW 286

RESULT 7

US-10-191-966-14
Sequence 14, Application US/10191966
Publication No. US20030175692A1
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

```
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 14
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION:
US-10-191-966-14

Query Match      100.0%; Score 1348; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.4e-125;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1 HPEITLVKQDAEDQAGAVGYIELDLSNGKILSFRRPFRPMMSTFVLLCGAVLSRID 60
24 HPEITLVKQDAEDQAGAVGYIELDLSNGKILSFRRPFRPMMSTFVLLCGAVLSRID 83
61 AGQELGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGCP 120
84 AGQELGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGCP 143
121 KETLAFHNMGDHVTRLDRWEPELNEALPNDERDTMPVAMATTIRKLLTGELLTLASRQ 180
144 KETLAFHNMGDHVTRLDRWEPELNEALPNDERDTMPVAMATTIRKLLTGELLTLASRQ 203
QY QUIDMMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 240
DB QUIDMMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 263
241 SOATMDERNROIATIGASLIKHW 263
264 SOATMDERNROIATIGASLIKHW 286

RESULT 9
US-10-045-674-523
Sequence 523, Application US/10045674
Publication No. US2003023233A1
GENERAL INFORMATION:
APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROONEY, KRISTIN L.
APPLICANT: HOEY, RENE
APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
FILE REFERENCE: LIBRARIES
FILE REFERENCE: DYAX/002 CIP2
CURRENT APPLICATION NUMBER: US/10/045,674
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 60/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 523
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Vector pCESS
US-10-045-674-523

Query Match      100.0%; Score 1348; DB 15; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.4e-125;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 241 SOATMDERNROIAEIGASLIKHM 263
 DB 264 SOATMDERNROIAEIGASLIKHM 286

RESULT 10
 US-10-416-708A-73

; Sequence 73, Application US/10416708A
 ; Publication No. US20040161753A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wise, John G.
 ; APPLICANT: Fromknecht, Katja
 ; TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING
 ; FILE REFERENCE: 37779-0004
 ; CURRENT APPLICATION NUMBER: US/10/416,708A
 ; CURRENT FILING DATE: 2004-01-28
 ; NUMBER OF SEQ ID NOS: 89
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 73
 ; LENGTH: 286
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic Construct
 ; US-10-416-708A-73

Query Match 100.0%; Score 1348; DB 16; Length 286;
 Best Local Similarity 100.0%; Pred. No. 2,46-125;
 Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGAVGYIELDINSKILIESRPERPFPWMTFVKLLCGAVLSRID 60
 DB 24 HPEITLVKVDADQAGAVGYIELDINSKILIESRPERPFPWMTFVKLLCGAVLSRID 83
 QY 61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGVTVELCSAATMSDNTAANLLTTIGSP 120
 DB 84 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGVTVELCSAATMSDNTAANLLTTIGSP 143
 QY 121 KELTAFILNMGDHVRILDRWEPBELNEALPNDERTTTPVAAATTLRKLLTGELTLASRQ 180
 DB 144 KELTAFILNMGDHVRILDRWEPBELNEALPNDERTTTPVAAATTLRKLLTGELTLASRQ 203
 QY 161 QUIDMWEADKVAQPLIRGALPAGWFIADKSGAGERSGRIIAALGPDGKPSRIVIYITTG 240
 DB 204 QUIDMWEADKVAQPLIRGALPAGWFIADKSGAGERSGRIIAALGPDGKPSRIVIYITTG 263
 QY 241 SOATMDERNROIAEIGASLIKHM 263
 DB 264 SOATMDERNROIAEIGASLIKHM 286

RESULT 11
 US-09-919-901-2

; Sequence 2, Application US/09919901
 ; Publication No. US20030082518A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Potts, Karen E.
 ; APPLICANT: Jackson, Roberta L.
 ; APPLICANT: Patrick, Amy K.
 ; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
 ; FILE REFERENCE: 0125-0005A
 ; CURRENT APPLICATION NUMBER: US/09/919,901
 ; CURRENT FILING DATE: 2001-08-02
 ; PRIOR APPLICATION NUMBER: 09/263,933
 ; PRIOR FILING DATE: 1999-02-08
 ; PRIOR APPLICATION NUMBER: 09/129,611
 ; PRIOR FILING DATE: 1998-08-05
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2

; LENGTH: 2307
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION:
 ; US-09-919-901-2

Query Match 100.0%; Score 1348; DB 10; Length 2307;
 Best Local Similarity 100.0%; Pred. No. 4,66-124;
 Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGAVGYIELDINSKILIESRPERPFPWMTFVKLLCGAVLSRID 60
 DB 2045 HPEITLVKVDADQAGAVGYIELDINSKILIESRPERPFPWMTFVKLLCGAVLSRID 2104
 QY 61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGVTVELCSAATMSDNTAANLLTTIGSP 120
 DB 2105 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGVTVELCSAATMSDNTAANLLTTIGSP 2164
 QY 121 KELTAFILNMGDHVRILDRWEPBELNEALPNDERTTTPVAAATTLRKLLTGELTLASRQ 180
 DB 2165 KELTAFILNMGDHVRILDRWEPBELNEALPNDERTTTPVAAATTLRKLLTGELTLASRQ 2224
 QY 181 QUIDMWEADKVAQPLIRGALPAGWFIADKSGAGERSGRIIAALGPDGKPSRIVIYITTG 240
 DB 2225 QUIDMWEADKVAQPLIRGALPAGWFIADKSGAGERSGRIIAALGPDGKPSRIVIYITTG 2284
 QY 241 SOATMDERNROIAEIGASLIKHM 263
 DB 2285 SOATMDERNROIAEIGASLIKHM 2307

RESULT 12
 US-09-919-901-9

; Sequence 9, Application US/09919901
 ; Publication No. US20030082518A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Potts, Karen E.
 ; APPLICANT: Jackson, Roberta L.
 ; APPLICANT: Patrick, Amy K.
 ; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
 ; FILE REFERENCE: 0125-0005A
 ; CURRENT APPLICATION NUMBER: US/09/919,901
 ; CURRENT FILING DATE: 2001-08-02
 ; PRIOR APPLICATION NUMBER: 09/263,933
 ; PRIOR FILING DATE: 1999-02-08
 ; PRIOR APPLICATION NUMBER: 09/129,611
 ; PRIOR FILING DATE: 1998-08-05
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 9
 ; LENGTH: 2307
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION:
 ; US-09-919-901-9

Query Match 100.0%; Score 1348; DB 10; Length 2307;
 Best Local Similarity 100.0%; Pred. No. 4,66-124;
 Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGAVGYIELDINSKILIESRPERPFPWMTFVKLLCGAVLSRID 60
 DB 2045 HPEITLVKVDADQAGAVGYIELDINSKILIESRPERPFPWMTFVKLLCGAVLSRID 2104
 QY 61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGVTVELCSAATMSDNTAANLLTTIGSP 120
 DB 2105 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGVTVELCSAATMSDNTAANLLTTIGSP 2164
 QY 121 KELTAFILNMGDHVRILDRWEPBELNEALPNDERTTTPVAAATTLRKLLTGELTLASRQ 180

Db 2165 KETLFAFLHMGDHYTRLDRWPELNEAIPNDRDITMPVAMATTLTKLITGELLTLASRQ 2224
Qy 181 OLIDMEADKVAAGPLIRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIVITYTG 240
Db 2225 OLIDMEADKVAAGPLIRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIVITYTG 2284
Qy 241 SOATWDERNRQIAEIGASLIKHM 263
Db 2285 SOATWDERNRQIAEIGASLIKHM 2307

RESULT 13

US-09-919-901-16
; Sequence 16, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potte, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 16
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-09-919-901-16

Query Match 100.0%; Score 1348; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 4,6e-124;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPELVKVKDAEDQUGARVGYIELDINSKLTLESFRPERPMMSTFKVLLCGAVLSRID 60
Db 2045 HPELVKVKDAEDQUGARVGYIELDINSKLTLESFRPERPMMSTFKVLLCGAVLSRID 2104
Qy 61 AGOELGRRIRHYSQNDLVEYSPVTEKHLTDGVTVELCSAAITMSDNTAANLLTTIGGP 120
Db 2105 AGOELGRRIRHYSQNDLVEYSPVTEKHLTDGVTVELCSAAITMSDNTAANLLTTIGGP 2164
Qy 121 KETLFAFLHMGDHYTRLDRWPELNEAIPNDRDITMPVAMATTLTKLITGELLTLASRQ 180
Db 2165 KETLFAFLHMGDHYTRLDRWPELNEAIPNDRDITMPVAMATTLTKLITGELLTLASRQ 2224
Qy 181 OLIDMEADKVAAGPLIRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIVITYTG 240
Db 2225 OLIDMEADKVAAGPLIRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIVITYTG 2284
Qy 241 SOATWDERNRQIAEIGASLIKHM 263
Db 2285 SOATWDERNRQIAEIGASLIKHM 2307

RESULT 14

US-10-191-966-2
; Sequence 2, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potte, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-2

Query Match 100.0%; Score 1348; DB 14; Length 2307;
Best Local Similarity 100.0%; Pred. No. 4,6e-124;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPELVKVKDAEDQUGARVGYIELDINSKLTLESFRPERPMMSTFKVLLCGAVLSRID 60
Db 2045 HPELVKVKDAEDQUGARVGYIELDINSKLTLESFRPERPMMSTFKVLLCGAVLSRID 2104
Qy 61 AGOELGRRIRHYSQNDLVEYSPVTEKHLTDGVTVELCSAAITMSDNTAANLLTTIGGP 120
Db 2105 AGOELGRRIRHYSQNDLVEYSPVTEKHLTDGVTVELCSAAITMSDNTAANLLTTIGGP 2164
Qy 121 KETLFAFLHMGDHYTRLDRWPELNEAIPNDRDITMPVAMATTLTKLITGELLTLASRQ 180
Db 2165 KETLFAFLHMGDHYTRLDRWPELNEAIPNDRDITMPVAMATTLTKLITGELLTLASRQ 2224
Qy 181 OLIDMEADKVAAGPLIRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIVITYTG 240
Db 2225 OLIDMEADKVAAGPLIRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIVITYTG 2284
Qy 241 SOATWDERNRQIAEIGASLIKHM 263
Db 2285 SOATWDERNRQIAEIGASLIKHM 2307

RESULT 15

US-10-191-966-9
; Sequence 9, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potte, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-9

Query Match 100.0%; Score 1348; DB 14; Length 2307;
Best Local Similarity 100.0%; Pred. No. 4,6e-124;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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Qy      1 HPELVKVDADBDLGARVGYIELDLSGKILESFRPERPPMSTFKVLLCGAVLSRID 60
      |||
Db      2045 HPELVKVDADBDLGARVGYIELDLSGKILESFRPERPPMSTFKVLLCGAVLSRID 2104
      |||
Qy      61 AGQEOIGRRIRHSQNDLVESPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120
      |||
Db      2105 AGQEOIGRRIRHSQNDLVESPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 2164
      |||
Qy      121 KELTAFLNMGDHTVRLDRWPEELNEAIPNDERDITMPVAMATTLRKLLTGELTLASRQ 180
      |||
Db      2165 KELTAFLNMGDHTVRLDRWPEELNEAIPNDERDITMPVAMATTLRKLLTGELTLASRQ 2224
      |||
Qy      161 QLIDMWEADKVAGPILRSALPAGMFIADKSGAGERSGIIAALGPDGKPSRIWVLYTTG 240
      |||
Db      2225 QLIDMWEADKVAGPILRSALPAGMFIADKSGAGERSGIIAALGPDGKPSRIWVLYTTG 2284
      |||
Qy      241 SQATMDERNRQIAEIGASLIIKHW 263
      |||
Db      2285 SQATMDERNRQIAEIGASLIIKHW 2307
      |||

```

Search completed: June 10, 2005, 11:09:03
 Job time : 89.1097 secs

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ID ADJ67709 standard; protein; 263 AA.
 XX ADJ67709;
 AC
 DT 20-MAY-2004 (first entry)
 XX
 DE Escherichia coli TEM-1 beta-lactamase.
 XX
 KM fragment complementation system; marker protein;
 KM multiple genetic element incorporation; antibiotic resistance;
 KM beta-lactam derivative activation; anti-tumour compound;
 KM functional reassembly; protein-protein interaction; proteome interaction;
 KM immunoglobulin variable region; immune cell protein; CD40;
 KM phosphorylation-regulated cell signal transducer; TEM-1 beta-lactamase;
 KM enzyme.
 XX
 OS Escherichia coli.
 XX
 PN US2004038317-A1.
 XX
 PD 26-FEB-2004.
 XX
 PF 22-SEP-2003; 2003US-00668778.
 XX
 PR 15-MAR-1999; 99US-0124339P.
 PR 25-MAY-1999; 99US-0135926P.
 PR 13-JAN-2000; 2000US-0175968P.
 PR 15-MAR-2000; 2000US-00526106.
 XX
 PA (KALO-) KALOBIO INC.
 XX
 PI Balint RF, Her J;
 PI WPI; 2004-203222/19.
 DR N-PSDB; ADJ67708.
 DR
 XX
 PT Fragment complementation system for detecting immunoglobulin epitope, has
 PT first oligopeptide containing N-terminal fragment with C-terminal break-
 PT point, second oligopeptide containing C-terminal fragment with N-terminal
 PT break-point.
 XX
 PS Disclosure; SEQ ID NO 2; 47bp; English.
 XX
 CC The invention describes a fragment complementation system (I) comprising
 CC a first oligopeptide having an N-terminal fragment with a C-terminal
 CC break-point, and a second oligopeptide having a C-terminal fragment with
 CC a N-terminal break-point, where the N-terminal fragment and the C-
 CC terminal fragment each are derived from a marker protein and reassemble
 CC to form a functionally reconstituted marker protein. (I) is useful for
 CC selecting simultaneous incorporation of multiple genetic elements into a
 CC host cell, and activating a beta-lactam derivative of an anti-tumour
 CC compound in a host. The method described is useful for identifying a
 CC second oligopeptide to which a first oligopeptide binds, involving co-
 CC expressing the first and second oligopeptides. Binding of the first
 CC oligopeptide to the second oligopeptide results in the functional
 CC reassembly of the marker protein. The method is also useful for
 CC monitoring the occurrence of protein-protein interactions in a sample;
 CC identifying oligopeptide interactions between two different proteomes;
 CC and identifying epitopes that bind to an immunoglobulin variable region.
 CC (I) or an expression cassette (II), encoding a selectable N or C-terminal
 CC peptide, is useful for identifying interactions between an extra cellular
 CC domain of a transmembrane protein and a polypeptide, where the
 CC transmembrane protein is an immune cell protein, preferably CD40. (I) or
 CC (II) is useful for high-throughput identification of compound that
 CC inhibit phosphorylation-regulated cell signal transducers. (I)
 CC efficiently detects multiple interaction between extracellular and
 CC intracellular protein with high throughput format. This is the amino acid
 CC sequence of antibiotic resistance enzyme TEM-1 beta-lactamase that can be
 CC used as a selectable gene in the fragment complementation system of the
 CC invention.
 CC
 CC Sequence 263 AA;

Query Match 100.0%; Score 770; DB 8; Length 263;
 Best Local Similarity 100.0%; Pred. No. 7.9e-80;
 Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDDGARVGYIELDLSGKILLESFRRPEPPPMSTFVLLCGAVLSRID 60
 DB 1 HPETLVKVKDAEDDGARVGYIELDLSGKILLESFRRPEPPPMSTFVLLCGAVLSRID 60
 QY 61 AGQELGRIRIRYSQNDLYEYSPVTRKHLTDGMTVRELCSAAITMGSDNTAAAILTTIGSP 120
 DB 61 AGQELGRIRIRYSQNDLYEYSPVTRKHLTDGMTVRELCSAAITMGSDNTAAAILTTIGSP 120
 QY 121 KELTAFILNMGDHVTPLDRMEPELNEAIP 149
 DB 121 KELTAFILNMGDHVTPLDRMEPELNEAIP 149

RESULT 4
 AAM16634
 ID AAM16634 standard; protein; 264 AA.
 XX
 AC AAM16634;
 XX
 DT 09-AUG-1997 (first entry)
 XX
 DE Beta-lactamase (including signal peptide).

XX Gene directed enzyme prodnrg therapy; GDEPT;
 XX virus directed enzyme prodnrg therapy; VDEPT; beta-lactamase; cancer;
 KM HIV; inflammation.
 XX
 OS Escherichia coli.

XX
 FH Key Location/Qualifiers
 FT Peptide 1..23
 FT /label= Sig_peptide

XX MO9719180-A2.

XX 29-MAY-1997.

XX 19-NOV-1996; 96WO-GB002845.

XX 20-NOV-1995; 95GB-00023703.

XX (GLAX) GLAXO GROUP LTD.

XX Dev I, Moore JT, Ohmstede C;

XX WPI; 1997-298117/27.

XX N-PSDB; AAT66736.

XX Molecular chimera for gene or virus directed enzyme prodnrg therapy -
 XX useful for treatment of cancer, viral infection or inflammation.

XX Example; Page 28; 38pp; English.

XX Escherichia coli beta-lactamase (AAM16634), including the signal peptide,
 CC is the expression product of a molecular chimera, designated pCMV-BL
 CC (AAT66737), in which the beta-lactamase gene is under control of the CMV
 CC intermediate/early promoter. Vectors consisting of a transcriptional
 CC regulatory DNA sequence linked to a beta-lactamase gene can be used for
 CC enzyme prodnrg therapy. Expression of the beta-lactamase in a targeted
 CC cell allows conversion of a prodnrg into an agent toxic to the cell for
 CC treatment of cancer, viral (e.g. HIV) infection or inflammation.
 CC Secretion of the enzyme has the advantage of increasing neighbouring cell
 CC kill
 CC
 CC Sequence 264 AA;

Query Match 100.0%; Score 770; DB 2; Length 264;
 Best Local Similarity 100.0%; Pred. No. 7.9e-80;
 Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 144 KELTAFILNMGDHVTRLDRWPEPELNEAIP 172

RESULT 7
AAR97619
ID AAR97619 standard; protein; 286 AA.
XX AAR97619;
AC
XX
XX 20-AUG-1996 (first entry)
DT
XX
DE Secretory beta-lactamase.
XX
KM Gene therapy; gene directed enzyme prodnug therapy; GDEPT;
KM virus directed enzyme prodnug therapy; VDEPT; prodnug activation;
KM cytotoxic; cytostatic; cancer; tumour; retrovirus; vector;
KM beta-lactamase; cephalosporin.
XX
OS Synthetic.
XX
XX MO9616179-A1.
PN
XX 30-MAY-1996.
PD
XX 20-NOV-1995; 95WO-GB002716.
PF
XX 18-NOV-1994; 94GB-00023367.
PR
XX (WBLI) WBLICOME FOUND LTD.
PA
XX
XX Dev IK, Moore JT, Ohmsted C;
PI
XX WPI; 1996-268615/27.
DR N-PSDB; AAT29220.
XX
PT Molecular chimaera for use in enzyme gene therapy - is activated in a
PT target cell to express a secretible enzyme which cleaves a prodnug
PT outside the cell into a cytotoxic or cytostatic agent.
XX
XX Example 3; Page 57-58; 73pp; English.
PS
XX A secretory beta-lactamase (AAR97619) is expressed from DNA construct
CC PCMV-BL (AAT29220), in which the beta-lactamase coding sequence is under
CC the control of the intermediate/early cytomegalovirus promoter. Beta-
CC lactamase delivery to mammalian cells confers sensitivity to
CC cephalosporin prodnugs. Liposomal DNA/5-fluorouracil prodnug combinations
CC resulted in 8.c. tumour regression in mice bearing A549 tumours. Survival
CC of mice bearing human large cell lung H460 intrathoracic (i.e.) tumours
CC was increased upon i.t. injection of the secretory beta-lactamase DNA
CC construct
XX
SQ Sequence 286 AA;
Query Match 100.0%; Score 770; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 8.8e-80;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKXVDADQAGARVGYIELDLSNGKILSRPBERPMMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKXVDADQAGARVGYIELDLSNGKILSRPBERPMMSTFKVLLCGAVLSRID 83
QY 61 AGQEBOLGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGCP 120
DB 84 AGQEBOLGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGCP 143
QY 121 KELTAFILNMGDHVTRLDRWPEPELNEAIP 149
DB 144 KELTAFILNMGDHVTRLDRWPEPELNEAIP 172

RESULT 8
AAR96423
ID AAR96423 standard; protein; 286 AA.

XX AAR96423;
AC
XX 25-MAR-2003 (revised)
DT
XX 25-NOV-1996 (first entry)
DT
XX
DE Cytochrome P450 (CYP1A1 construct).
XX
KM cytochrome; P450; metallothionein; mouse; human; cytotoxicity; assay;
KM metabolism.
XX
OS Homo sapiens.
XX
XX US5525482-A.
PN
XX 11-JUN-1996.
PD
XX 15-NOV-1994; 94US-00339658.
PF
XX 27-JUN-1991; 91US-00721775.
PR 09-DEC-1992; 92US-00990295.
XX
XX (UYWA-) UNIV WAYNE STATE.
XX
XX Hines RN, Novak RF, States JC;
PI
XX WPI; 1996-286397/29.
DR N-PSDB; AAT30354.
XX
XX Testing chemicals for cytotoxicity to human by detecting gene damage -
PT using recombinant fibroblasts transformed with cytochrome P450 gene under
PT control of inducible promoter.
XX
XX Disclosure; Col 17-24; 26pp; English.
PS
XX
XX The present sequence is encoded by a chimeric mouse metallothionein-
CC cytochrome P450Ia1 (CYP1A1) expression construct. Two clones, pRNM127 and
CC pRNM15, were isolated by different methods and which both had the same
CC sequence. The CYP1A1 construct is used in assays to test for cytotoxicity
CC of humans to a chemical. The method comprises exposing human fibroblast
CC cells normally not including any cytochrome P450 activity to potentially
CC toxic chemicals. The cells having been transformed to express cytochrome
CC P450, under the control of a controllable promoter through the CYP1A1
CC gene, upon exposure to the chemical in vitro. The chemical is metabolised
CC intracellularly into a cytochrome metabolite by oxidation within the
CC fibroblasts through the intracellular cytochrome P450 mixed function
CC oxidase enzymes expressed by the cells. Gene damage in the test cells is
CC detected as an indication of cytotoxicity of the chemical. (Updated on 25
CC -MAR-2003 to correct PF field.)
XX
SQ Sequence 286 AA;
Query Match 100.0%; Score 770; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 8.8e-80;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKXVDADQAGARVGYIELDLSNGKILSRPBERPMMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKXVDADQAGARVGYIELDLSNGKILSRPBERPMMSTFKVLLCGAVLSRID 83
QY 61 AGQEBOLGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGCP 120
DB 84 AGQEBOLGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGCP 143
QY 121 KELTAFILNMGDHVTRLDRWPEPELNEAIP 149
DB 144 KELTAFILNMGDHVTRLDRWPEPELNEAIP 172

RESULT 9
AAW16635
ID AAW16635 standard; protein; 286 AA.
XX

```

AC AAW16635;
XX
XX 09-AUG-1997 (first entry)
XX
XX Beta-lactamase (no signal peptide).
XX
XX Gene directed enzyme prodnrg therapy; GDEPT;
XX virus directed enzyme prodnrg therapy; VDEPT; beta-lactamase; cancer;
XX HIV; inflammation.
XX
XX Escherichia coli.
XX
XX WO9719180-A2.
XX
XX 29-MAY-1997.
XX
XX 19-NOV-1996; 96WO-GB002845.
XX
XX 20-NOV-1995; 95GB-00023703.
XX
XX (GLAX ) GLAXO GROUP LTD.
XX
XX Dev I, Moore JT, Ohmstede C;
XX
XX WPI; 1997-298117/27.
XX
XX N-PSDB; AAT66737.
XX
XX Molecular chimera for gene or virus directed enzyme prodnrg therapy -
XX useful for treatment of cancer, viral infection or inflammation.
XX
XX Example; Page 26; 38pp; English.
XX
XX Escherichia coli beta-lactamase (AAW16635), lacking the signal peptide,
XX is the expression product of a molecular chimera, designated PCMV-delBL
XX (AAT66738), in which the beta-lactamase gene is under control of the CMV
XX intermediate/early promoter. Vectors consisting of a transcriptional
XX regulatory DNA sequence linked to a beta-lactamase gene can be used for
XX enzyme prodnrg therapy. Intracellular expression of the beta-lactamase in
XX CC targeted cell allows conversion of a prodnrg into an agent toxic to
XX the cell for treatment of cancer, viral (e.g. HIV) infection or
XX inflammation.
XX
XX Sequence 286 AA;
XX
XX SQ
XX
XX Query Match 100.0%; Score 770; DB 2; Length 286;
XX Best Local Similarity 100.0%; Pred. No. 8.8e-80;
XX Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 HPEITLVKVKADBDQAGARVGYIEIDLNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
XX |||||||
XX DB 24 HPEITLVKVKADBDQAGARVGYIEIDLNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
XX |||||||
XX QY 61 AGGQQLGRRHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITWSDNTAANLLTTIGCP 120
XX |||||||
XX DB 84 AGGQQLGRRHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITWSDNTAANLLTTIGCP 143
XX |||||||
XX QY 121 KETLTAFLNMGDHYTRLDRWPELNEAIP 149
XX |||||||
XX DB 144 KETLTAFLNMGDHYTRLDRWPELNEAIP 172
XX |||||||
XX
XX RESULT 10
XX AAW18679
XX ID AAW18679 standard; protein; 286 AA.
XX
XX AC AAW18679;
XX
XX XX 13-AUG-1997 (first entry)
XX
XX XX Secretory beta-lactamase.
XX
XX DE Secretory beta-lactamase.
XX
XX XX Prodnrg therapy; gene directed enzyme prodnrg therapy; GDEPT;
XX virus directed enzyme prodnrg therapy; VDEPT; lung cancer;
XX

```

```

KW beta-lactamase; PCMV-BL.
XX
XX Escherichia coli.
XX
XX Key Location/Qualifiers
XX Peptide 1..23
XX Protein /label= sig_peptide
XX /label= Mat_protein
XX
XX WO9719183-A2.
XX
XX 29-MAY-1997.
XX
XX 19-NOV-1996; 96WO-GB002846.
XX
XX 20-NOV-1995; 95GB-00023703.
XX
XX (GLAX ) GLAXO GROUP LTD.
XX
XX Dev I, Moore JT, Sethna PB;
XX
XX WPI; 1997-298118/27.
XX
XX N-PSDB; AAT70309.
XX
XX DNA construct for gene-directed enzyme prodnrg therapy of lung cancer -
XX comprises lung- or neuroendocrine-specific promoter controlling
XX expression of prodnrg-converting enzyme.
XX
XX Example 81; Page 26-27; 53pp; English.
XX
XX The secreted form (AAW18679) of TEM beta-lactamase is expressed by PCMV-
XX BL (AAT70309) in which a PCR-amplified beta-lactamase coding sequence is
XX placed under control of the intermediate/early promoter of
XX cytomagalavirus. Secretory beta-lactamase constructs, placed under
XX control of promoter/enhancer elements of lung- associated protein or
XX neuroendocrine marker protein genes, can be used in novel chimeric
XX molecules for use in prodnrg therapy of lung cancer
XX
XX Sequence 286 AA;
XX
XX SQ
XX
XX Query Match 100.0%; Score 770; DB 2; Length 286;
XX Best Local Similarity 100.0%; Pred. No. 8.8e-80;
XX Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 HPEITLVKVKADBDQAGARVGYIEIDLNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
XX |||||||
XX DB 24 HPEITLVKVKADBDQAGARVGYIEIDLNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
XX |||||||
XX QY 61 AGGQQLGRRHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITWSDNTAANLLTTIGCP 120
XX |||||||
XX DB 84 AGGQQLGRRHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITWSDNTAANLLTTIGCP 143
XX |||||||
XX QY 121 KETLTAFLNMGDHYTRLDRWPELNEAIP 149
XX |||||||
XX DB 144 KETLTAFLNMGDHYTRLDRWPELNEAIP 172
XX |||||||
XX
XX RESULT 11
XX AAY08529
XX ID AAY08529 standard; protein; 286 AA.
XX
XX AC AAY08529;
XX
XX XX 03-AUG-1999 (first entry)
XX
XX XX Vector pASK75 beta-la protein.
XX
XX DE Firefly; luciferase; tetracycline; transcriptional control; Tetr; TetA;
XX tetracycline repressor; tetracycline promoter; luxCDABE;
XX insect; Tn10; medicine; dosage; cheese production; antibiotic; foodstuff;
XX allergy.
XX

```



```
OS Synthetic.
XX
XX MO9925866-A1.
XX
XX 27-MAY-1999.
XX
XX 11-NOV-1998; 98MO-F1000873.
XX
XX 14-NOV-1997; 97FI-00004235.
XX
XX (KORP/) KORPELA M.
XX (KARP/) KARP M.
XX (KURIT/) KURITU J.
XX
XX Korpele M, Karp M, Kuritu J;
XX
XX WPI; 1999-338015/28.
XX DR N-PSDB; AAV72418.
XX
XX Assaying for tetracycline using recombinant prokaryotic cells.
XX
XX Disclosure; Page 47-48; 67pp; English.
XX
XX This invention describes a novel tetracycline assay that uses recombinant
CC prokaryotic cells comprising a luciferase gene under the transcriptional
CC control of a tetracycline repressor and tetracycline promoter and
CC involves the detection of luminescence emitted from the cells. The assay
CC can be used to distinguish tetracycline form other microbial agents. The
CC invention also describes a novel plasmid comprising either the luxDABG
CC genes, a tetracycline repressor (Tetr) and a tetracycline promoter (TetA)
CC from Tn10, or the insect luciferase gene, a tetracycline repressor (Tetr)
CC and a tetracycline promoter (TetA) from Tn10. The tetracycline assay
CC method can be used for the determination of tetracycline in a sample,
CC e.g. to study the dosage and penetration of the medicine. The method can
CC also be used to test cheese production, as cheese making bacteria are not
CC able to work in the presence of tetracycline. The method can also be used
CC to determine the presence or concentration of antibiotics in foodstuffs,
CC e.g. for allergic people. The present assay method does not rely on the
CC growth of microbes as do conventional tests, and so is much more rapid.
CC The present assay is also more sensitive, as even a small amount of
CC luminescence can be detected
XX
XX Sequence 286 AA;
SQ
Query Match 100.0%; Score 770; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 8.8e-80;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPETLVKTKDADDDQAGAVGYIELDLSGKILSFRRPRRPPMSTFVLLCGAVLSRID 60
DB 24 HPETLVKTKDADDDQAGAVGYIELDLSGKILSFRRPRRPPMSTFVLLCGAVLSRID 83
QY 61 AGOELGRIRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGSP 120
DB 84 AGOELGRIRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGSP 143
QY 121 KETLAFILNMGDHVTIRLDREPELNEAIP 149
DB 144 KETLAFILNMGDHVTIRLDREPELNEAIP 172
RESULT 12
AAB10442
ID AAB10442 standard; protein; 286 AA.
XX
XX AAB10442;
XX
XX 01-DEC-2000 (first entry)
XX
XX Expression vector pSEX15G2 bla protein.
XX
XX Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
XX B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.
```

```
XX
XX Synthetic.
XX
XX DE19900635-A1.
XX
XX 13-JUL-2000.
XX
XX 11-JAN-1999; 99DE-01000635.
XX
XX 11-JAN-1999; 99DE-01000635.
XX
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
XX Breittling F, Poustka A, Moldenhauer G;
XX
XX WPI; 2000-499832/45.
XX DR N-PSDB; AAA71430.
XX
XX Selecting monoclonal antibodies, by expressing them on the surface of
XX hybridomas attached to antibody-binding protein, then reaction with
XX antibody library.
XX
XX Claim 16; Fig 3; 22pp; German.
XX
XX This invention describes a novel method for the selection of monoclonal
CC antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma
CC cells to produce antibody-producing hybridomas such that the antibodies
CC are presented at the surface of the hybridomas by an antibody-binding
CC protein (i); and (ii) binding the antibody to antigens (Ag). The
CC invention also describes antibody-binding proteins (i) that comprise a
CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa
CC chain or a murine MHC (major histocompatibility complex) Class I K(Ik)
CC molecule; an antibody-binding site of proteins A, G, L or Ig, and the
CC transmembrane domain of PDGFR (platelet-derived growth factor receptor)
CC or CD52. The method is used to select Mab with specificity for particular
CC antigens. Mab can be selected without separate culture of hybridomas, and
CC selection can be made against many antigens in a library, optionally on
CC the basis of strength of affinity for a particular antigen. Complex
CC mixtures of hybridomas can be used for selection, reducing the time and
CC cost involved in Mab selection. This sequence represents the bla protein
CC protein contained in the expression vector pSEX15G2 which contains the
CC bla protein, Neo-R and protein G described in the method of the invention
XX
XX Sequence 286 AA;
SQ
Query Match 100.0%; Score 770; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 8.8e-80;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPETLVKTKDADDDQAGAVGYIELDLSGKILSFRRPRRPPMSTFVLLCGAVLSRID 60
DB 24 HPETLVKTKDADDDQAGAVGYIELDLSGKILSFRRPRRPPMSTFVLLCGAVLSRID 83
QY 61 AGOELGRIRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGSP 120
DB 84 AGOELGRIRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGSP 143
QY 121 KETLAFILNMGDHVTIRLDREPELNEAIP 149
DB 144 KETLAFILNMGDHVTIRLDREPELNEAIP 172
RESULT 13
AAB10438
ID AAB10438 standard; protein; 286 AA.
XX
XX AAB10438;
XX
XX 01-DEC-2000 (first entry)
XX
XX Expression vector pSEX11L4 bla protein.
XX
XX Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
```


XX bla resistance marker; recombinant host cell; saccharification;
KW fermentation; polysaccharase; oligosaccharide degradation; celz gene;
KW glucanase; integration vector; pLOI2306.
XX unidentified.
OS
PN WO200071729-A2.
XX
XX 30-NOV-2000.
PD
XX 26-MAY-2000; 2000WO-US014773.
PF
XX 26-MAY-1999; 99US-0136376P.
PR
XX (UYFL) UNIV FLORIDA RES FOUND.
PA
XX Ingram LO, Zhou S;
PI
XX
XX MPI; 2001-032043/04.
DR
DR N-PSDB; AAC91455.
XX
XX Recombinant host cells useful for producing polysaccharase for degrading
PT oligosaccharides, comprises a first heterologous polynucleotide encoding
PT polysaccharase under control of surrogate promoter.
XX
XX Disclosure; Page 82-83; 87pp; English.
PS
XX The present sequence is given in a specification relating to a
CC recombinant host cell suitable for simultaneous saccharification and
CC fermentation. The host cell contains at least one heterologous
CC polynucleotide encoding a polysaccharase under the transcriptional
CC control of a surrogate promoter capable of increasing expression of the
CC polysaccharase. The host cell also contains a second heterologous
CC polynucleotide encoding a secretory polypeptide to facilitate the
CC secretion of the expressed polysaccharase. The recombinant host cell is
CC useful for producing polysaccharase which is useful for enzymatically
CC degrading oligosaccharides such as lignocellulose, hemicellulose,
CC cellulose, pectin or their combinations, and fermenting the product to
CC ethanol, by simultaneous saccharification and fermentation processes. The
CC present sequence is encoded by an integration vector which was introduced
CC into cells to generate recombinant host cells. The vector contains a
CC surrogate promoter from *Zymomonas mobilis*, the celz gene from *Erwinia*
CC *chrysanthemi*, resistance markers bla and tet, and *Klebsiella oxytoca*
CC target sequence
CC
SQ Sequence 286 AA;

Query Match 100.0%; Score 770; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 8.8e-80;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKDAEDQAGRVGYIELDINSKILIESFRPERFPMMSTFKVLCGAVLSRID 60
DB 24 HPELVKVKDAEDQAGRVGYIELDINSKILIESFRPERFPMMSTFKVLCGAVLSRID 83

QY 61 AGQSGQLGRRIHNSQNDLYEYSPVTEKHLTDGWTRELCSAATYMSDNTANILLTTIGSP 120
DB 84 AGQSGQLGRRIHNSQNDLYEYSPVTEKHLTDGWTRELCSAATYMSDNTANILLTTIGSP 143

QY 121 KEITAFLEHNMGGDHVTRLDKWEPELNEAIP 149
DB 144 KEITAFLEHNMGGDHVTRLDKWEPELNEAIP 172

Search completed: June 10, 2005, 10:49:11
Job time : 58.7711 secs

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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:23:36 ; Search time 88.1097 Seconds
(without alignments)
1528.512 Million cell updates/sec

Title: US-10-668-778-2
Perfect score: 1348
Sequence: 1 HPELVKVKVADQAGARVG.....TMDERNRQIAETGASLIKHW 263

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1348	100.0	286	2	Q38058 bacterioph
2	1348	100.0	286	2	Q00626 staphylococ
3	1348	100.0	286	2	Q79CL6 methylobac
4	1348	100.0	286	2	Q79DR3 escherichia
5	1343	99.6	286	1	BLAT_ECOLI
6	1343	99.6	286	1	BLAT_SALUTI
7	1343	99.6	286	2	Q6A253
8	1343	99.6	286	2	Q6LBN9
9	1343	99.6	286	2	Q6LTV6
10	1343	99.6	286	2	Q6TMM1
11	1343	99.6	286	2	Q6WRX2
12	1343	99.6	286	2	Q6WRX2
13	1343	99.6	286	2	Q6WZD4
14	1343	99.6	286	2	Q7B3X5
15	1343	99.6	286	2	Q7B899
16	1343	99.6	286	2	Q7B875
17	1343	99.6	286	2	Q7BR75
18	1343	99.6	286	2	Q7DFY3
19	1343	99.6	286	2	Q7DHD3
20	1343	99.6	286	2	Q799Y1
21	1343	99.6	286	2	Q7BVP8
22	1340	99.4	286	2	Q8KSD2
23	1339	99.3	286	2	Q3J372
24	1339	99.3	286	2	Q8KSD3
25	1339	99.3	286	2	Q9J2Y6
26	1339	99.3	286	2	Q9J3A80
27	1339	99.3	286	2	Q6QCR1
28	1339	99.3	286	2	Q6SQJ9
29	1339	99.3	286	2	Q6URK84
30	1339	99.3	286	2	Q6UVM7
31	1339	99.3	286	2	Q6W7J4

32	1339	99.3	286	2	Q7B0V0	O7B0V0 xanthomonas
33	1339	99.3	286	2	Q9RM52	Q9RM52 escherichia
34	1339	99.3	286	2	Q9RM48	Q9RM48 escherichia
35	1338	99.3	286	2	Q8KRH0	Q8KRH0 klebsiella
36	1338	99.3	286	2	Q9J3A77	Q9J3A77 escherichia
37	1338	99.3	286	2	Q9R745	Q9R745 escherichia
38	1337	99.2	285	2	Q6K67	Q6K67 hordium vul
39	1337	99.2	286	2	Q8YP43	Q8YP43 klebsiella
40	1337	99.2	286	2	Q48406	Q48406 klebsiella
41	1337	99.2	286	2	Q6ZYM6	Q6ZYM6 salmoneila
42	1337	99.2	286	2	Q844X1	Q844X1 klebsiella
43	1337	99.2	286	2	Q8G485	Q8G485 escherichia
44	1337	99.2	286	2	Q96678	Q96678 klebsiella
45	1336	99.1	286	2	P78144	P78144 escherichia

ALIGNMENTS

RESULT 1
ID Q38058 PRELIMINARY; PRT; 286 AA.
AC Q38058;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Beta lactamase.
GN Name=bla;
OS Bacteriophage phi-X174.
OC Viruses; ssDNA viruses; Microviridae; Microvirus.
OX NCBI_TaxID=10847;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95172401; Pubmed=7867948; DOI=10.1016/0378-1119(94)00839-K;
RA Hendrich B., Schmidtberger B.;
RT "A variant of phix174 gene E-based positive selection vectors with
enhanced lytic potential.";
RL Gene 154:51-54 (1995)
DR EMBL; Z55638; CAA84692.1; -.
DR PIR; S47061; S47061.
DR HSSP; Q9R435; 1HT2.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASE.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
SQ SEQUENCE 286 AA; 31557 MW; 5BB2F22753375FA9 CRC64;

Query Match 100.0%; Score 1348; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.1e-96;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	HPELVKVKVADQAGARVGYLELDLNSGKILSFRRPFRPMSFPKVLGAVLSRID	60
DB	24	HPELVKVKVADQAGARVGYLELDLNSGKILSFRRPFRPMSFPKVLGAVLSRID	83
QY	61	AGQELGRIRHSQNDLYEYSPVTEKHLLDTGTTVAELCSAATMMDNPAANLLTTIGP	120
DB	84	AGQELGRIRHSQNDLYEYSPVTEKHLLDTGTTVAELCSAATMMDNPAANLLTTIGP	143
QY	121	KELTAFILNMGDHVTRLRWBPBLNEALPNDERDTTMPAMATTTLKLTGLTLTAASQ	180
DB	144	KELTAFILNMGDHVTRLRWBPBLNEALPNDERDTTMPAMATTTLKLTGLTLTAASQ	203
QY	181	QLIDWMDKVAQPLRLSALPAWPIADKSGAGERSGIIIALGPDGKPSRIIVITYTG	240
DB	204	QLIDWMDKVAQPLRLSALPAWPIADKSGAGERSGIIIALGPDGKPSRIIVITYTG	263
QY	241	SOATMDERNRQIAETGASLIKHW 263	
DB	264	SOATMDERNRQIAETGASLIKHW 286	

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RESULT 2
ID 000626 PRELIMINARY: PRT: 286 AA.
AC 000626: 008022; 008102; 009393; 009396; 009397; 009398; 009399;
AC 009400; 009401; 009402; 009403; 009404; 009405; 009406; 009407;
AC 009408; 009481; 009482; 009483; 009490; 057339;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Beta-lactamase.
OS Staphylococcus aureus.
OC Plasmid J3356/POX7/3, and Plasmid J3356/POX7/1.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCB1_TaxID=1280;
RN NCB1
RP SEQUENCE FROM N.A.
RC PLASMID=J3356/POX7/3, and J3356/POX7/1;
RX MEDLINE=9642275; PubMed=8825372; DOI=10.1006/plas.1995.0005;
RA Needham C., Noble W.C., Dyke K.G.;
RT "The staphylococcal insertion sequence IS257 is active.";
RL Plasmid 34:198-205(1995).
DR EMBL: U36912; AAB39957.1; -.
DR EMBL: U36911; AAB39956.1; -.
DR InterPro: IPR001466; Beta_lactamase.
DR Pfam: PF00144; Beta_lactamase_A.
DR PRINTS: PR00118; BLACTAMASE.
DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
KW Plasmid.
SQ SEQUENCE 286 AA; 31557 MW; 5EB2F2275375FA9 CRC64;

Query Match 100.0%; Score 1348; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 2,le-96;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKDADQAGVGYIELDLSGKTIIESRPERPMMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVKDADQAGVGYIELDLSGKTIIESRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGOELGRRIHYSQNDLVEYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGP 120
DB 84 AGOELGRRIHYSQNDLVEYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGP 143
QY 121 KELTAFILNMGDHYRLDRWPEBELNEALPNDERDTMPVANAATLRKLLTGBLLTASRQ 180
DB 144 KELTAFILNMGDHYRLDRWPEBELNEALPNDERDTMPVANAATLRKLLTGBLLTASRQ 203
QY 181 OLIDMEADKVAGPLLRGALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYITGG 240
DB 204 OLIDMEADKVAGPLLRGALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYITGG 263
QY 241 SOATMDERNROIABIGASLIKHM 263
DB 264 SOATMDERNROIABIGASLIKHM 286

RESULT 3
QY99CL6 PRELIMINARY: PRT: 286 AA.
AC QY99CL6:
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Beta-lactamase.
OS Methylobacillus flagellatum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Methylobactiales;
OC Methylobacteriaceae; Methylobacillus.
OX NCB1_TaxID=405;
RN NCB1
RP SEQUENCE FROM N.A.
RX MEDLINE=97074643; PubMed=8917070; DOI=10.1016/0378-1119(96)00114-X;
RA Seberljski I.G., Vasssin V.M., Tsygankov Y.D.;

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RT "Two new members of the BioB superfamily: cloning, sequencing and
RT expression of bioB genes of Methylobacillus flagellatum and
RT Corynebacterium glutamicum.";
RL Gene 175:15-22(1996).
RN NCB1
RP SEQUENCE FROM N.A.
RA Seberljski I., Vasssin V., Tsygankov Y.;
RT Submitted (JUL-1995) to the EMBL/Genbank/DBJ databases.
DR EMBL: U31280; AAC44581.1; -.
DR HSSP: P00807; IALO.
DR InterPro: IPR001466; Beta_lactamase.
DR Pfam: PF00144; Beta_lactamase_A.
DR PRINTS: PR00118; BLACTAMASE.
DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
SQ SEQUENCE 286 AA; 31557 MW; 5EB2F2275375FA9 CRC64;

Query Match 100.0%; Score 1348; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 2,le-96;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKDADQAGVGYIELDLSGKTIIESRPERPMMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVKDADQAGVGYIELDLSGKTIIESRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGOELGRRIHYSQNDLVEYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGP 120
DB 84 AGOELGRRIHYSQNDLVEYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGP 143
QY 121 KELTAFILNMGDHYRLDRWPEBELNEALPNDERDTMPVANAATLRKLLTGBLLTASRQ 180
DB 144 KELTAFILNMGDHYRLDRWPEBELNEALPNDERDTMPVANAATLRKLLTGBLLTASRQ 203
QY 181 OLIDMEADKVAGPLLRGALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYITGG 240
DB 204 OLIDMEADKVAGPLLRGALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYITGG 263
QY 241 SOATMDERNROIABIGASLIKHM 263
DB 264 SOATMDERNROIABIGASLIKHM 286

RESULT 4
QY99DR3 PRELIMINARY: PRT: 286 AA.
AC QY99DR3:
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Mutant extended-spectrum beta-lactamase precursor (EC 3.5.2.6).
GN Name=bla; Synonyms=blaTEM-116;
OS Escherichia coli.
OC Plasmid pRP4, and plasmid pCAPs.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCB1_TaxID=562;
RN NCB1
RP SEQUENCE FROM N.A.
RC STRAIN=K-12;
RA Maneewannakul K., Maneevannakul S., Ippen-Ihler K.;
RL Submitted (AUG-1991) to the EMBL/Genbank/DBJ databases.
RN NCB1
RP SEQUENCE FROM N.A.
RC STRAIN=K12; PLASMID=pRP4;
RA Rondot S., Anthony K., Dubel S., Ida N., Beyreuther K., Frost L.,
RL Little M., Breitling F.; the EMBL/Genbank/DBJ databases.
RN NCB1
RP SEQUENCE FROM N.A.
RC PLASMID=pCAPs;
RX MEDLINE=98189310; PubMed=9514792; DOI=10.1006/abio.1997.2558;
RA Schlieper D., Von Wilcken-Bergmann B., Schmidt M., Sobek H.,
RA Mueller-Hill B.;

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RT "A positive selection vector for cloning of long polymerase chain
 RT reaction fragments based on a lethal mutant of the *cip* gene
 RT *Escherichia coli*.";
 RL Anal. Biochem. 257:203-209 (1998).
 RN (4)
 RP SEQUENCE FROM N.A.
 RX PubMed=15243036;
 RA Jeong S.H., Bae I.K., Lee J.H., Sohn S.G., Kang G.H., Jeon G.J.,
 RA Kim Y.H., Jeong B.C., Lee S.H.;
 RT "Molecular Characterization of Extended-Spectrum Beta-lactamases
 RT Produced by Clinical Isolates of *Klebsiella pneumoniae* and *Escherichia*
 RT *coli* from a Korean Nationwide Survey.";
 RL J. Clin. Microbiol. 42:2902-2906 (2004).
 DR EMBL; M74750; AAA24057.1; -;
 DR EMBL; Y12694; CAA73226.1; -;
 DR EMBL; AJ001614; CA04868.1; -;
 DR EMBL; AY425988; AA095605.1; -;
 DR HSSP; P00807; 1ALQ.
 DR GO; GO:0008800; F:beta-lactamase activity; IEA.
 DR GO; GO:0016787; F:hydrolyase activity; IEA.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 KW Hydrolyase; Plasmid; Signal.
 FT SIGNAL 1 23
 SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;
 Query Match 100.0%; Score 1348; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 2; 1e-96;
 Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HETLVKVDADQAGRVGYELDINSKTIIESPPEEPFPMSTFKYLCAVLSRID 60
 DB 24 HETLVKVDADQAGRVGYELDINSKTIIESPPEEPFPMSTFKYLCAVLSRID 83
 QY 61 AGQBLGRIRHSQNDLVYSPVTEKRLDGMVRELCSAATMTSNTANLLTTIGSP 120
 DB 84 AGQBLGRIRHSQNDLVYSPVTEKRLDGMVRELCSAATMTSNTANLLTTIGSP 143
 QY 121 KELTAFILHMGDHYRLDRMEPELNEAIPNDRSDTTMPVAMATTLLKLTGELLTLASRQ 180
 DB 144 KELTAFILHMGDHYRLDRMEPELNEAIPNDRSDTTMPVAMATTLLKLTGELLTLASRQ 203
 QY 191 QIIDMMEADKVAQPLIRSAIPAGWPIADKSGAGGERSGIIAALGPDGPRSVIYYTTG 240
 DB 204 QIIDMMEADKVAQPLIRSAIPAGWPIADKSGAGGERSGIIAALGPDGPRSVIYYTTG 263
 QY 241 SQATMDERROTAETGASLIKIM 263
 DB 264 SQATMDERROTAETGASLIKIM 286

RESULT 5
 BLAT_ECOLI STANDARD; PRT; 286 AA.
 AC P62593; P00810; Q47313;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Beta-lactamase TEM precursor (RC 3.5.2.6) (TEM-1) (TEM-2) (TEM-3)
 DE (TEM-4) (TEM-5) (TEM-6) (TEM-8/CAZ-2) (TEM-16/CAZ-7) (TEM-24/CAZ-6)
 DE (IRT-4) (Penicillinase).
 GN Name=bla;
 GN Name=bla;
 GN Name=blaT-3;
 GN Name=blaT-4;
 GN Name=blaT-5;
 GN Name=blaT-6;
 GN Name=blaT-6;

OS *Escherichia coli*.
 OG Plasmid R1 (R7268), Plasmid IncFII R100, Plasmid R6K, Plasmid pUD16,
 OG Plasmid pCFP04, and Plasmid pCFP14.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; *Escherichia*.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A. (TEM-1).
 RC PLASMID-R1 (R7268); TRANSPOSON-Tn3;
 RX MEDLINE=79012484; PubMed=358200;
 RA Sutcliffe J.G.;
 RT "Nucleotide sequence of the ampicillin resistance gene of *Escherichia*
 RT *coli* plasmid pBR322.";
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3737-3741 (1978).
 RN [2]
 RP SEQUENCE FROM N.A. (TEM-1).
 RC PLASMID-R1 (R7268); TRANSPOSON-Tn3;
 RX MEDLINE=8002802; PubMed=383387;
 RA Sutcliffe J.G.;
 RT "Complete nucleotide sequence of the *Escherichia coli* plasmid
 RT pBR322.";
 RL Cold Spring Harb. Symp. Quant. Biol. 43:77-90 (1979).
 RN [3]
 RP SEQUENCE FROM N.A. (TEM-1).
 RC PLASMID-IncFII R100;
 RX MEDLINE=86319522; PubMed=3019092; DOI=10.1016/0065-227X(86)90018-3;
 RA Ohtsubo H., Ryder T.B., Maeda Y., Armstrong K., Ohtsubo E.;
 RT "DNA replication of the resistance plasmid R100 and its control.";
 RL Adv. Biophys. 21:115-133 (1986).
 RN [4]
 RP SEQUENCE OF 24-286 (TEM-2).
 RC PLASMID-R6K; TRANSPOSON-Tn1;
 RX MEDLINE=79012483; PubMed=358199;
 RA Ambler R.P., Scott G.K.;
 RT "Partial amino acid sequence of penicillinase coded by *Escherichia*
 RT *coli* plasmid R6K.";
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3732-3736 (1978).
 RN [5]
 RP SEQUENCE FROM N.A. (TEM-3).
 RA Sougakoff W., Goussard S., Courvalin P.;
 RT "The TEM-3 beta-lactamase, which hydrolyzes broad-spectrum
 RT cephalosporins, is derived from the TEM-2 penicillinase by two amino
 RT acid substitutions.";
 RL FEMS Microbiol. Lett. 56:343-348 (1988).
 RN [6]
 RP SEQUENCE FROM N.A. (TEM-3).
 RC PLASMID-pCFP04;
 RX MEDLINE=93062798; PubMed=1331747;
 RA Mabilat C., Lourencao-Vital J., Goussard S., Courvalin P.;
 RT "A new example of physical linkage between *Tn1* and *Tn21*: the
 RT antibiotic multiple-resistance region of plasmid pCFP04 encoding
 RT extended-spectrum beta-lactamase TEM-3.";
 RL Mol. Gen. Genet. 235:113-121 (1992).
 RN [7]
 RP SEQUENCE FROM N.A. (TEM-4 AND TEM-5).
 RC STRAIN-CH6134; PLASMID-pCFP04, and pUD16;
 RX MEDLINE=89378760; PubMed=2550326; DOI=10.1016/0378-1119(89)90236-9;
 RA Sougakoff W., Petit A., Goussard S., Sirot D., Bure A., Courvalin P.;
 RT "Characterization of the plasmid genes *blaT-4* and *blaT-5* which encode
 RT the broad-spectrum beta-lactamases TEM-4 and TEM-5 in
 RT enterobacteriaceae.";
 RL Gene 78:339-348 (1989).
 RN [8]
 RP SEQUENCE FROM N.A. (TEM-6).
 RC STRAIN-HB251;
 RX MEDLINE=9216702; PubMed=165171;
 RA Goussard S., Sougakoff W., Mabilat C., Bauernfeind A., Courvalin P.;
 RT "An ISI-like element is responsible for high-level synthesis of
 RT extended-spectrum beta-lactamase TEM-6 in Enterobacteriaceae.";
 RL J. Gen. Microbiol. 137:2681-2687 (1991).
 RN [9]
 RP SEQUENCE FROM N.A. (TEM-8; TEM-16 AND TEM-24).
 RX MEDLINE=93037315; PubMed=1416873;

RA Chanal C., Poupart M.C., Sirot D., Labia R., Sirot J., Cluzel R.;
 RT "Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase
 RL genes.";
 RN Antimicrob. Agents Chemother. 36:1817-1820 (1992).
 CC (10)
 RP SEQUENCE OF 24-286 (IRT-4).
 RC STRAIN=PEY;
 RX MEDLINE=94333751; PubMed=8056282; DOI=10.1016/0378-1097(94)00186-3;
 RA Brun T., Peduzzi J., Canica M.M., Paul G., Nevot P., Barchelemy M.,
 Labia R.;
 RT "Characterization and amino acid sequence of IRT-4, a novel TEM-type
 RT enzyme with a decreased susceptibility to beta-lactamase inhibitors.";
 RL FEMS Microbiol. Lett. 120:111-117 (1994).
 CC (11)
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF TEM-1.
 RX MEDLINE=92183921; PubMed=15444485; DOI=10.1016/0014-5793(92)80232-6;
 RA Jelsch C., Lefant P., Masson J.-M., Samama J.-P.;
 RT "Beta-lactamase TEM1 of E. coli. Crystal structure determination at
 RT 2.5-A resolution.";
 RL FEBS Lett. 299:135-142 (1992).
 CC (12)
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF TEM-1.
 RX MEDLINE=93361453; PubMed=8356032;
 RA Jelsch C., Mourey L., Masson J.-M., Samama J.-P.;
 RT "Crystal structure of Escherichia coli TEM1 beta-lactamase at 1.8-A
 RT resolution.";
 RL Proteins 16:364-383 (1993).
 CC (13)
 RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF TEM-1 COMPLEXED WITH BLIP.
 RX MEDLINE=96186252; PubMed=8605632;
 RA Struyacka N.C.J., Jensen S.E., Alzari P.M., James M.N.G.;
 RT "A potent new mode of beta-lactamase inhibition revealed by the 1.7 A
 RT X-ray crystallographic structure of the TEM-1-BLIP complex.";
 RL Nat. Struct. Biol. 3:290-297 (1996).
 CC (14)
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF TEM-1.
 RX MEDLINE=98153145; PubMed=9485412; DOI=10.1021/b1972501b;
 RA Maveyraud L., Pratt R.F., Samama J.-P.;
 RT "Crystal structure of an acylation transition-state analog of the TEM-
 RT 1 beta-lactamase. Mechanistic implications for class A beta-
 RL lactamases.";
 RL Biochemistry 37:2622-2628 (1998).
 CC (15)
 RP X-RAY CRYSTALLOGRAPHY (2.28 ANGSTROMS) OF TEM-1.
 RX MEDLINE=99352177; PubMed=10423234; DOI=10.1021/bi990758z;
 RA Swaren P., Golemi D., Cabanous S., Bulchev A., Maveyraud L.,
 Mobashery S., Samama J.-P.;
 RT "X-ray structure of the Asn276asp variant of the Escherichia coli TEM-
 RT 1 beta-lactamase: direct observation of electrostatic modulation in
 RT resistance to inactivation by clavulanic acid.";
 RL Biochemistry 38:9570-9576 (1999).
 CC -I- FUNCTION: TEM-type are the most prevalent beta-lactamases in
 CC enterobacteria; they hydrolyze the beta-lactam bond in susceptible
 CC beta-lactam antibiotics, thus conferring resistance to penicillins
 CC and cephalosporins. TEM-3 and TEM-5 are capable of hydrolyzing
 CC cefotaxime and ceftazidime. TEM-5 is capable of hydrolyzing
 CC ceftazidime. TEM-6 is capable of hydrolyzing ceftazidime and
 CC aztreonam. TEM-8/CAZ-2, TEM-16/CAZ-7 and TEM-24/CAZ-6 are markedly
 CC active against ceftazidime. IRT-4 shows resistance to beta-
 CC lactamase inhibitors.
 CC -I- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
 CC amino acid.
 CC -I- BIOTECHNOLOGY: This protein is used as a marker in many commonly
 CC used cloning vectors, such as pBR322 and the pUC series.
 CC -I- MISCELLANEOUS: The beta-lactamase present on pBR322 was cloned
 CC from plasmid R1 (R7268).
 CC -I- SIMILARITY: Belongs to the class-A beta-lactamase family.
 CC -----
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 CC -----
 CC DR EMBL J01749; AA59737.1; -
 CC DR EMBL V00613; CA23886.1; -
 CC DR EMBL X64523; CAA45828.1; -
 CC DR EMBL X57972; CAA41038.1; -
 CC DR EMBL X65252; CAA46344.1; -
 CC DR EMBL X65253; CAA46345.1; -
 CC DR EMBL X65254; CAA46346.1; -
 CC DR EMBL U89928; AAB64386.1; -
 CC DR EMBL U66885; AAC48875.1; -
 CC DR PIR A93821; PNECP.
 CC DR PIR S30113; S30113.
 CC DR PDB 1AXB; X-ray; -
 CC DR PDB 1BRT5; X-ray; -
 CC DR PDB 1BTL; X-ray; -
 CC DR PDB 1CK3; X-ray; -
 CC DR PDB 1BRM; X-ray; -
 CC DR PDB 1ERO; X-ray; -
 CC DR PDB 1ERO; X-ray; -
 CC DR PDB 1RSQ; X-ray; -
 CC DR PDB 1PQG; X-ray; -
 CC DR PDB 1JTD; X-ray; -
 CC DR PDB 1JTG; X-ray; -
 CC DR PDB 1JUV; X-ray; -
 CC DR PDB 1JVP; X-ray; -
 CC DR PDB 1JWV; X-ray; -
 CC DR PDB 1JWZ; X-ray; -
 CC DR PDB 1LHY; X-ray; -
 CC DR PDB 1L10; X-ray; -
 CC DR PDB 1L19; X-ray; -
 CC DR PDB 1NXY; X-ray; -
 CC DR PDB 1NVO; X-ray; -
 CC DR PDB 1NYY; X-ray; -
 CC DR PDB 1TEM; X-ray; -
 CC DR PDB 1XPB; X-ray; -
 CC -----
 CC Query Match 99.6%; Score 1343; DB 1; Length 286;
 CC Best Local Similarity 99.2%; Pred. No. 5; 1e-96;
 CC Matches 261; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 CC -----
 CC QY 1 HPELVKVKADBDQGAHVGYIELDNSGKILBSFPERPPEPMSSTFVLLCGAVLSRID 60
 CC DB 24 HPELVKVKADBDQGAHVGYIELDNSGKILBSFPERPPEPMSSTFVLLCGAVLSRID 83
 CC QY 61 AGQELGRIRYSONDLVEYSPVTEKHLTDGMTVRELCSAITMSDNTAAVLLTTIGSP 120
 CC DB 84 AGQELGRIRYSONDLVEYSPVTEKHLTDGMTVRELCSAITMSDNTAAVLLTTIGSP 143
 CC QY 121 KELTAFLEHMGDHYTRLDREPELENEALPNDERDTTPVMAATTLRKLLTGELLTLASRQ 180
 CC DB 144 KELTAFLEHMGDHYTRLDREPELENEALPNDERDTTPVMAATTLRKLLTGELLTLASRQ 203
 CC QY 191 QLIDMEADKVAAPLRLSALPAWGFADKSGAGERSGIIAALGDPGKPSRIVIYTTG 240
 CC DB 204 QLIDMEADKVAAPLRLSALPAWGFADKSGAGERSGIIAALGDPGKPSRIVIYTTG 263
 CC QY 241 SQATDERNRQIAETGASLIRHW 263
 CC DB 264 SQATDERNRQIAETGASLIRHW 286
 CC -----
 CC RESULT 6
 CC BLAT_SALT
 CC ID BLAT_SALT STANDARD; PRT; 286 AA.
 CC AC P62594; P00810; Q47313;
 CC DT 21-JUL-1986 (Rel. 01, Created)
 CC DT 21-JUL-1986 (Rel. 01, Last sequence update)
 CC DT 25-JAN-2005 (Rel. 46, Last annotation update)
 CC DE Beta-lactamase TEM precursor (EC 3.5.2.6) (Penicillinase).
 CC GN Name=bla; OrderedLocNames=Hcm1.216;
 CC OS Salmonella typhi.

OG Plasmid pHCMI.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Salmonella.
 OK NCBI_TaxID=601;
 RN SEQUENCE FROM N.A.
 RC STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
 RA Parthill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,
 RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebatina M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Croxall A., Davis P., Davies R.M., Dow L., White N., Farrar J.,
 RA Felwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jorgels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M.A., Rutterell K.M., Simmonds W., Skellon J., Stevens K.,
 RA Whitehead S., Barrett B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 RT enterica serovar Typh CT18.";
 RL Nature 413:848-852(2001).
 CC -1- FUNCTION: TEM-type are the most prevalent beta-lactamases in
 CC enterobacteria; they hydrolyze the beta-lactam bond in susceptible
 CC beta-lactam antibiotics, thus conferring resistance to penicillins
 CC and cephalosporins (By similarity).
 CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2O) = a substituted beta-
 CC amino acid.
 CC -1- SIMILARITY: Belongs to the class-A beta-lactamase family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AL513383; CAD09800.1; -
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 KW Antibioc resistance; Complete proteome; Hydrolase; Plasmid; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 286
 FT ACT_SITE 68 68
 FT ACT_SITE 166 166
 FT SITE 232 234
 FT DISULFID 75 121
 SO SEQUENCE 286 AA; 31515 MW; BB678943BB18934B CRC64;
 Query Match 99.6%; Score 1343; DB 1; Length 286;
 Best Local Similarity 99.2%; Pred. No. 5,1e-96;
 Matches 261; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 HPETLVKVDADQAGAVGYIELDLSGKILLESFRPERPPMSTFVLLCGAVLSRD 60
 DB HPEITLVKVDADQAGAVGYIELDLSGKILLESFRPERPPMSTFVLLCGAVLSRD 83
 QY 61 AGQELGRIRIHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
 DB AGQELGRIRIHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143
 QY 121 KELTAFLLNMGDVTLRDWEPELNEAIPNDRDITMPVAAATTIRKLLTGELTLASRQ 180
 DB KELTAFLLNMGDVTLRDWEPELNEAIPNDRDITMPVAAATTIRKLLTGELTLASRQ 203
 QY 144 KELTAFLLNMGDVTLRDWEPELNEAIPNDRDITMPVAAATTIRKLLTGELTLASRQ 203
 DB OLIDMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 240
 QY 204 OLIDMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 263
 DB SOATWDERNRQIAEIGASLIKIM 263
 QY 241 SOATWDERNRQIAEIGASLIKIM 263
 DB SOATWDERNRQIAEIGASLIKIM 286

RESULT 7
 ID 06A253 PRELIMINARY; PRT; 286 AA.
 AC 06A253;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DE Beta-lactamase TEM precursor (EC 3.5.2.6).
 GN Name=blatEM12; ORFNames=pl056.57c;
 OS Haemophilus influenzae.
 OG Plasmid ICBH1056.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 CC Pasteurellaceae; Haemophilus.
 OK NCBI_TaxID=727;
 RN SEQUENCE FROM N.A.
 RP MOHd-Zain Z.;
 RA "Molecular biology of plasmid encoded resistance in Haemophilus
 RT influenzae.";
 RT Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.
 RL Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RA Crook D.W.;
 RL Submitted (Feb-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ627386; CAF29065.1; -
 DR GO; GO:0008800; F:beta-lactamase activity; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 KW Hydrolase; Plasmid; Signal.
 FT SIGNAL 1 24
 FT CHAIN 24 286
 SO SEQUENCE 286 AA; 31515 MW; BB678943BB18934B CRC64;
 Query Match 99.6%; Score 1343; DB 2; Length 286;
 Best Local Similarity 99.2%; Pred. No. 5,1e-96;
 Matches 261; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 HPETLVKVDADQAGAVGYIELDLSGKILLESFRPERPPMSTFVLLCGAVLSRD 60
 DB HPEITLVKVDADQAGAVGYIELDLSGKILLESFRPERPPMSTFVLLCGAVLSRD 83
 QY 61 AGQELGRIRIHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
 DB AGQELGRIRIHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143
 QY 121 KELTAFLLNMGDVTLRDWEPELNEAIPNDRDITMPVAAATTIRKLLTGELTLASRQ 180
 DB KELTAFLLNMGDVTLRDWEPELNEAIPNDRDITMPVAAATTIRKLLTGELTLASRQ 203
 QY 144 KELTAFLLNMGDVTLRDWEPELNEAIPNDRDITMPVAAATTIRKLLTGELTLASRQ 203
 DB OLIDMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 240
 QY 204 OLIDMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 263
 DB SOATWDERNRQIAEIGASLIKIM 263
 QY 241 SOATWDERNRQIAEIGASLIKIM 286
 DB SOATWDERNRQIAEIGASLIKIM 286
 RESULT 8
 ID 06LEN9 PRELIMINARY; PRT; 286 AA.
 AC 06LEN9;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 25-OCT-2004 (TREMBlrel. 27, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Penicillinase TEM-1.
 GN Name=bla(tem-1A); Synonyms=bla(tem-1B);

OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 CX NCBI_TaxID=287;
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91323733; PubMed=1650734; DOI=10.1016/0378-1119(91)90540-R;
 RA Goussard S., Courvalin P.;
 RT "Sequence of the genes blaT-1B and blaT-2."
 RL Gene 102:71-73(1981).
 DR EMBL; X54604; CAA38428.1; -.
 DR EMBL; X54607; CAA38430.1; -.
 DR HSSP; P00807; IALO.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 SQ SEQUENCE 286 AA; 31515 MW; BB678943BB18934B CRC64;

Query Match 99.6%; Score 1343; DB 2; Length 286;
 Best Local Similarity 99.2%; Pred. No. 5.1e-96;
 Matches 261; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPELVKXKADQDQAGVGYIEIDLNSGKILSFRRPFRPMMSTFFVLLCGAVLSRID 60
 DB 24 HPELVKXKADQDQAGVGYIEIDLNSGKILSFRRPFRPMMSTFFVLLCGAVLSRID 83
 QY 61 AGQEQGRRHYSONDLVEYSPVTEKHLTDGMYRELCSAATMSDNTAANLLTTGGP 120
 DB 84 AGQEQGRRHYSONDLVEYSPVTEKHLTDGMYRELCSAATMSDNTAANLLTTGGP 143
 QY 121 KEITAFILNMGDHYTRLDRWPELNEAI PNDERDTMPVAMATTLRKLLTGELLTLASRQ 180
 DB 144 KEITAFILNMGDHYTRLDRWPELNEAI PNDERDTMPVAMATTLRKLLTGELLTLASRQ 203
 QY 181 QLIDMEADKYAGPLRLSALPAGWFIADKSGAGRGSGRTIAALGPDGKPSRIIVYITTG 240
 DB 204 QLIDMEADKYAGPLRLSALPAGWFIADKSGAGRGSGRTIAALGPDGKPSRIIVYITTG 263
 QY 241 SOATMDERNROIARIGASLIRKW 263
 DB 264 SOATMDERNROIARIGASLIRKW 286

RESULT 9

ID Q6LCV6 PRELIMINARY; PRT; 286 AA.
 AC Q6LCV6;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Beta-lactamase.
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 CX NCBI_TaxID=485;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=GCJ-182;
 RX MEDLINE=99225589; PubMed=10208798; DOI=10.1006/mcpr.1998.0216;
 RA Dillon J.R., Li H., Yeung K.-H., Aman T.A.;
 RT "A PCR assay for discriminating Neisseria gonorrhoeae beta-lactamase-producing plasmids."
 RL Mol. Cell. Probes 13:89-92(1999).
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=GCJ-182;
 RX MEDLINE=20079289; PubMed=10610817; DOI=10.1006/plas.1999.1431;
 RA Pagotto F., Aman A.T., Ng L.K., Yeung K.H., Bretz M., Dillon J.A.;
 RT "Sequence analysis of the family of penicillinase-producing plasmids of Neisseria gonorrhoeae.";

RL Plasmid 43:24-34(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GCJ-182;
 RX MEDLINE=20156387; PubMed=10689182; DOI=10.1016/S0378-1119(99)00557-0;
 RA Pagotto F.J., Salimnia H., Totten P.A., Dillon J.R.;
 RT "Stable shuttle vectors for Neisseria gonorrhoeae, Hemophilus spp. and other bacteria based on a single origin of replication."
 RL Gene 244:13-19(2000).
 DR EMBL; U20374; AAB40517.1; -.
 DR HSSP; P00807; IALO.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 KM Plasmid.
 SQ SEQUENCE 286 AA; 31515 MW; BB678943BB18934B CRC64;

Query Match 99.6%; Score 1343; DB 2; Length 286;
 Best Local Similarity 99.2%; Pred. No. 5.1e-96;
 Matches 261; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPELVKXKADQDQAGVGYIEIDLNSGKILSFRRPFRPMMSTFFVLLCGAVLSRID 60
 DB 24 HPELVKXKADQDQAGVGYIEIDLNSGKILSFRRPFRPMMSTFFVLLCGAVLSRID 83
 QY 61 AGQEQGRRHYSONDLVEYSPVTEKHLTDGMYRELCSAATMSDNTAANLLTTGGP 120
 DB 84 AGQEQGRRHYSONDLVEYSPVTEKHLTDGMYRELCSAATMSDNTAANLLTTGGP 143
 QY 121 KEITAFILNMGDHYTRLDRWPELNEAI PNDERDTMPVAMATTLRKLLTGELLTLASRQ 180
 DB 144 KEITAFILNMGDHYTRLDRWPELNEAI PNDERDTMPVAMATTLRKLLTGELLTLASRQ 203
 QY 181 QLIDMEADKYAGPLRLSALPAGWFIADKSGAGRGSGRTIAALGPDGKPSRIIVYITTG 240
 DB 204 QLIDMEADKYAGPLRLSALPAGWFIADKSGAGRGSGRTIAALGPDGKPSRIIVYITTG 263
 QY 241 SOATMDERNROIARIGASLIRKW 263
 DB 264 SOATMDERNROIARIGASLIRKW 286

RESULT 10

ID Q6TMH1 PRELIMINARY; PRT; 286 AA.
 AC Q6TMH1;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Name=blatEM-1;
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 CX NCBI_TaxID=1313;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=SR001;
 RX Ding Y., Huang Z.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY392531; AAC94057.1; -.
 DR HSSP; P00807; IALO.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 SQ SEQUENCE 286 AA; 31515 MW; BB678943BB18934B CRC64;

Query Match 99.6%; Score 1343; DB 2; Length 286;
 Best Local Similarity 99.2%; Pred. No. 5.1e-96;

Matches 261; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 HPEITLVKVDADQAGARVGYIELDLSGKILSFRRPFRPMSTPKVLLCGAVLSRD 60
DB 24 HPEITLVKVDADQAGARVGYIELDLSGKILSFRRPFRPMSTPKVLLCGAVLSRD 83
QY 61 AGOBLGRIRIHSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGOBLGRIRIHSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDRTTMAPAAATTIRKLLTGELTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDRTTMAPAAATTIRKLLTGELTLASRQ 203
QY 181 OLIDWMEADKVAGPLIRSLPAGWFIADKSGAGERSGRII AALGPDGKPSRIVIYTTG 240
DB 204 OLIDWMEADKVAGPLIRSLPAGWFIADKSGAGERSGRII AALGPDGKPSRIVIYTTG 263
QY 241 SOATWDERNRQIAETIGASLIRKM 263
DB 264 SOATWDERNRQIAETIGASLIRKM 286

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RESULT 11

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ID 06W9J1 PRELIMINARY; PRT; 286 AA.
AC 06W9J1.
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE TEM-1 beta-lactamase.
GN Name=blatEM-1;
OS Enterobacter cloacae
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Enterobacter.
OX NCBI_TaxID=550;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=212;
RA Cagno J., Katz S.E.;
RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY302260; AAQ73497.1; -.
DR HSSP; P00807; IALQ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
SQ SEQUENCE 286 AA; 31515 MW; BB678943BB18934B CRC64;

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Query Match 99.6%; Score 1343; DB 2; Length 286;
 Best Local Similarity 99.2%; Pred. No. 5.1e-96;
 Matches 261; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 HPEITLVKVDADQAGARVGYIELDLSGKILSFRRPFRPMSTPKVLLCGAVLSRD 60
DB 24 HPEITLVKVDADQAGARVGYIELDLSGKILSFRRPFRPMSTPKVLLCGAVLSRD 83
QY 61 AGOBLGRIRIHSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGOBLGRIRIHSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDRTTMAPAAATTIRKLLTGELTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDRTTMAPAAATTIRKLLTGELTLASRQ 203
QY 181 OLIDWMEADKVAGPLIRSLPAGWFIADKSGAGERSGRII AALGPDGKPSRIVIYTTG 240
DB 204 OLIDWMEADKVAGPLIRSLPAGWFIADKSGAGERSGRII AALGPDGKPSRIVIYTTG 263
QY 241 SOATWDERNRQIAETIGASLIRKM 263
DB 264 SOATWDERNRQIAETIGASLIRKM 286

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RESULT 12

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ID 06WRX2 PRELIMINARY; PRT; 286 AA.
AC 06WRX2.
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Beta-lactamase TEM-1.
GN Name=blatEM-1;
OS Zymomonas mobilis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Zymomonas.
OX NCBI_TaxID=542;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CP4;
RA Cagno J., Katz S.E.;
RL Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY271827; AAQ02307.1; -.
DR HSSP; P00807; IALQ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
SQ SEQUENCE 286 AA; 31515 MW; BB678943BB18934B CRC64;

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Query Match 99.6%; Score 1343; DB 2; Length 286;
 Best Local Similarity 99.2%; Pred. No. 5.1e-96;
 Matches 261; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 HPEITLVKVDADQAGARVGYIELDLSGKILSFRRPFRPMSTPKVLLCGAVLSRD 60
DB 24 HPEITLVKVDADQAGARVGYIELDLSGKILSFRRPFRPMSTPKVLLCGAVLSRD 83
QY 61 AGOBLGRIRIHSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGOBLGRIRIHSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDRTTMAPAAATTIRKLLTGELTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDRTTMAPAAATTIRKLLTGELTLASRQ 203
QY 181 OLIDWMEADKVAGPLIRSLPAGWFIADKSGAGERSGRII AALGPDGKPSRIVIYTTG 240
DB 204 OLIDWMEADKVAGPLIRSLPAGWFIADKSGAGERSGRII AALGPDGKPSRIVIYTTG 263
QY 241 SOATWDERNRQIAETIGASLIRKM 263
DB 264 SOATWDERNRQIAETIGASLIRKM 286

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RESULT 13

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ID 06WZD4 PRELIMINARY; PRT; 286 AA.
AC 06WZD4.
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Beta-lactamase TEM-1.
GN Name=blatEM-1;
OS Acinetobacter baumannii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=470;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H240;
RA Huang Z., Chen Y., Mao P., Wu J., Wu L., Shan H., Shen J.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
[2]

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RP SEQUENCE FROM N.A.
 RC STRAIN-1-43;
 RA Huang C.-C., Chen C.-H., Wu M.-H., Chu W.-C., Huang C.-W.;
 RL Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY263331; AAP0891.1; -;
 DR EMBL; AY560328; AAS68104.1; -;
 DR HSSP; P00807; 1ALQ.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASE.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 SQ SEQUENCE 286 AA; 31515 MW; BB678943BB18934B CRC64;

Query Match 99.6%; Score 1343; DB 2; Length 286;
 Best Local Similarity 99.2%; Pred. No. 5, 1e-96;
 Matches 261; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPELVKVKDAEDQAGRVGYIELDLSNGKILSFPRPERPMMSTFKVLLCGAVLSRID 60
 DB 24 HPELVKVKDAEDQAGRVGYIELDLSNGKILSFPRPERPMMSTFKVLLCGAVLSRID 83
 QY 61 AGGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGCP 120
 DB 84 AGGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGCP 143
 QY 121 KEITAFILNMGDHVTRLDRWEPELNEAIPNDRDPTMPVAMATTLRKLLTGELTLASRQ 180
 DB 144 KEITAFILNMGDHVTRLDRWEPELNEAIPNDRDPTMPVAMATTLRKLLTGELTLASRQ 203
 QY 181 QLIIDMEADKVAAGPLLSALPAGWFIADKSGAGSGRSGIITIALGPDGKPSRIVIYTTG 240
 DB 204 QLIIDMEADKVAAGPLLSALPAGWFIADKSGAGSGRSGIITIALGPDGKPSRIVIYTTG 263
 QY 241 SOATMDERNROIARIGASLIRKM 263
 DB 264 SOATMDERNROIARIGASLIRKM 286

RESULT 14
 ID Q7B3X5 PRELIMINARY; PRT; 286 AA.
 AC Q7B3X5;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE BLATEM1.
 GN Name=blATEM1;
 OS Citrobacter freundii.
 OG Plasmid pCTX-M3.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Citrobacter.
 CX NCBI_TaxID=546;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gojebiewski M., Zienkiewicz M., Adamczyk M., Kern-Zdanowicz I.,
 RA Ceglowski P.;
 RL Submitted (OCT-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF550415; AAN87698.1; -;
 DR HSSP; P00807; 1ALQ.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASE.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 KW Plasmid.
 SQ SEQUENCE 286 AA; 31515 MW; BB678943BB18934B CRC64;

Query Match 99.6%; Score 1343; DB 2; Length 286;
 Best Local Similarity 99.2%; Pred. No. 5, 1e-96;
 Matches 261; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 HPELVKVKDAEDQAGRVGYIELDLSNGKILSFPRPERPMMSTFKVLLCGAVLSRID 60

DB 24 HPELVKVKDAEDQAGRVGYIELDLSNGKILSFPRPERPMMSTFKVLLCGAVLSRID 83
 QY 61 AGGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGCP 120
 DB 84 AGGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGCP 143
 QY 121 KEITAFILNMGDHVTRLDRWEPELNEAIPNDRDPTMPVAMATTLRKLLTGELTLASRQ 180
 DB 144 KEITAFILNMGDHVTRLDRWEPELNEAIPNDRDPTMPVAMATTLRKLLTGELTLASRQ 203
 QY 181 QLIIDMEADKVAAGPLLSALPAGWFIADKSGAGSGRSGIITIALGPDGKPSRIVIYTTG 240
 DB 204 QLIIDMEADKVAAGPLLSALPAGWFIADKSGAGSGRSGIITIALGPDGKPSRIVIYTTG 263
 QY 241 SOATMDERNROIARIGASLIRKM 263
 DB 264 SOATMDERNROIARIGASLIRKM 286

RESULT 15
 ID Q7B899 PRELIMINARY; PRT; 286 AA.
 AC Q7B899;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE TEM beta-lactamase TEM-1H.
 DE (Beta-lactamase TEM-1H).
 GN Name=bla; Synonyms=blATEM-1b, blATEM1H;
 OS Klebsiella pneumoniae.
 OG Plasmid pJHCW1, Plasmid pRM760, Plasmid E3, and Plasmid pKpn99-1029.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Klebsiella.
 CX NCBI_TaxID=573;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC PLASMID=pJHCW1;
 RX MEDLINE=22270945; PubMed=12384346;
 RA Sarno R., McGillicuddy G., Sherratt D.J., Actis L.A., Tolmashy M.E.;
 RT "Complete nucleotide sequence of Klebsiella pneumoniae multiresistance
 RT plasmid pJHCW1.";
 RL Antimicrob. Agents Chemother. 46:3422-3427(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC PLASMID=pJHCW1;
 RA Tolmashy M.E.;
 RL Submitted (NOV-2002) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC PLASMID=pRM760;
 RA Partridge S.R., Hall R.M.;
 RL Submitted (JAN-2004) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC PLASMID=E3;
 RA Chen Y., Zhou W., Yu Y.;
 RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=kpn99-1029; PLASMID=pKpn99-1029;
 RA Xiong Z., Zhu D., Wang F., Zhang Y.;
 RT "Study on the encoding gene of extended-spectrum beta-lactamases in a
 RT Klebsiella pneumoniae isolate.";
 RL Zhongguo Kang Sheng Su Za Zhi 28:96-100(2003).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX PubMed=14613957;
 RA Nelson B.C., Segal H., Elieha B.G.;
 RT "Outer membrane protein alterations and blATEM-1 variants: their role
 RT in beta-lactam resistance in Klebsiella pneumoniae.";
 RL J. Antimicrob. Chemother. 52:999-903(2003).
 DR EMBL; AF479774; AAL93144.1; -;

DR EMBL: AY123253; AAR91458.1; -;
 DR EMBL: AF309824; AAG4772.1; -;
 DR EMBL: AY293072; AAP43782.1; -;
 DR EMBL: AY394610; AAQ96920.1; -;
 DR HSSP: P00807; IALQ.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR000871; Beta_lactamase_A.
 DR Pfam: PF00144; Beta_lactamase; 1.
 DR PRINTS: PRO0118; BACTAMASEA.
 DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
 KW Plasmaid.
 SQ SEQUENCE 286 AA; 31515 MW; BB678943BB18934B CRC64;

Query Match 99.6%; Score 1343; DB 2; Length 286;
 Best local similarity 99.2%; Pred. No. 5.1e-96;

Matches 261; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	1	HPE	T	V	K	V	K	D	A	E	D	O	L	G	A	R	V	G	T	E	L	D	N	S	G	K	I	L	S	F	R	P	E	R	F	P	M	S	T	F	K	V	L	C	G	A	V	L	S	R	I	D	60					
DB	24	HPE	T	V	K	V	K	D	A	E	D	O	L	G	A	R	V	G	T	E	L	D	N	S	G	K	I	L	S	F	R	P	E	R	F	P	M	S	T	F	K	V	L	C	G	A	V	L	S	R	I	D	83					
QY	61	A	G	E	O	L	G	R	R	I	H	S	Q	N	D	L	V	E	S	P	T	E	K	H	L	D	G	M	T	V	R	E	L	C	S	A	I	T	M	S	D	N	T	A	N	I	L	L	T	T	I	G	P	120				
DB	84	A	G	E	O	L	G	R	R	I	H	S	Q	N	D	L	V	E	S	P	T	E	K	H	L	D	G	M	T	V	R	E	L	C	S	A	I	T	M	S	D	N	T	A	N	I	L	L	T	T	I	G	P	143				
QY	121	K	E	L	T	A	F	L	N	M	G	H	V	T	R	L	D	R	M	E	P	E	L	N	E	A	I	P	N	D	E	R	D	T	T	M	P	V	A	M	A	T	T	L	R	K	L	T	G	E	L	L	T	L	A	S	R	180
DB	144	K	E	L	T	A	F	L	N	M	G	H	V	T	R	L	D	R	M	E	P	E	L	N	E	A	I	P	N	D	E	R	D	T	T	M	P	V	A	M	A	T	T	L	R	K	L	T	G	E	L	L	T	L	A	S	R	203
QY	181	Q	L	I	D	M	E	A	D	K	V	A	G	P	L	L	R	S	N	L	P	A	G	M	F	I	A	D	K	S	G	A	G	E	R	G	S	R	G	I	I	A	L	G	P	D	G	K	S	R	I	V	I	Y	T	T	G	240
DB	204	Q	L	I	D	M	E	A	D	K	V	A	G	P	L	L	R	S	N	L	P	A	G	M	F	I	A	D	K	S	G	A	G	E	R	G	S	R	G	I	I	A	L	G	P	D	G	K	S	R	I	V	I	Y	T	T	G	263
QY	241	S	O	A	T	M	D	E	R	N	R	O	I	A	E	I	G	A	S	L	I	K	M	263																																		
DB	264	S	O	A	T	M	D	E	R	N	R	O	I	A	E	I	G	A	S	L	I	K	M	286																																		

Search completed: June 10, 2005, 10:56:59
 Job time : 90.1097 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:35:06 ; Search time 19.1791 Seconds
(without alignments)
1319.408 Million cell updates/sec

Title: US-10-668-778-2

Perfect score: 1348

Sequence: 1 HPETLVKVKDAEDQLGARVQ.....TMDERNRQIAETGASLIKHW 263

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1348	100.0	286	2 TS1301	beta-lactamase (EC
2	1348	100.0	286	2 S47061	beta-lactamase (EC
3	1348	100.0	286	4 S41975	beta-lactamase (EC
4	1343	99.6	286	1 PNECP	beta-lactamase (EC
5	1343	99.6	286	4 I40905	beta-lactamase (EC
6	1330	98.7	286	2 S60312	extended spectrum
7	1329	98.6	286	2 S30113	beta-lactamase (EC
8	1323	98.1	286	2 S60310	extended spectrum
9	1321	98.0	286	2 S60311	beta-lactamase (EC
10	1317	97.7	286	2 J01546	Bla protein - Salm
11	936	69.4	265	2 S00464	beta-lactamase (EC
12	934	69.3	286	2 S16146	beta-lactamase (EC
13	934	69.3	286	2 A60679	beta-lactamase (EC
14	930	69.0	265	2 S02434	beta-lactamase (EC
15	930	69.0	286	1 A44958	beta-lactamase (EC
16	927	68.8	286	2 A37200	beta-lactamase (EC
17	926	68.7	286	2 A60632	beta-lactamase (EC
18	923	68.5	265	2 A60448	beta-lactamase (EC
19	901.5	66.9	287	1 A44996	beta-lactamase (EC
20	891	66.1	279	1 A24469	beta-lactamase (EC
21	866	64.2	286	1 A44958	beta-lactamase (EC
22	665	49.3	298	2 A41381	beta-lactamase (EC
23	527.5	39.1	304	2 J01136	beta-lactamase (EC
24	527.5	39.1	304	2 A35001	beta-lactamase (EC
25	524	38.9	105	2 JCS566	Bla protein - pseu
26	523.5	38.8	304	2 A49789	beta-lactamase (EC
27	517.5	38.4	288	2 J50755	beta-lactamase (EC
28	516.5	38.3	281	2 D95395	probable Beta lact
29	509.5	37.8	293	2 S04649	beta-lactamase (EC

30	509	37.8	276	2 JH0268	beta-lactamase (EC
31	503.5	37.4	263	2 A54543	beta-lactamase (EC
32	502.5	37.3	291	2 S42075	beta-lactamase (EC
33	493.5	36.6	302	2 S36188	beta-lactamase (EC
34	492.5	36.5	294	2 S16553	beta-lactamase (EC
35	492.5	36.5	306	1 B45822	beta-lactamase (EC
36	489.5	36.3	306	2 G69674	beta-lactamase (EC
37	488.5	36.2	306	2 S47330	penicillinase - Ba
38	482	35.8	291	2 JH0074	beta-lactamase (EC
39	480.5	35.6	305	2 A61156	beta-lactamase (EC
40	480.5	35.6	305	2 A57002	beta-lactamase (EC
41	480.5	35.6	305	2 A60680	beta-lactamase (EC
42	478	35.5	314	2 S06967	beta-lactamase (EC
43	472	35.0	263	2 S23929	beta-lactamase (EC
44	468.5	34.8	294	2 S19006	beta-lactamase (EC
45	464.5	34.5	306	2 S03167	beta-lactamase (EC

ALIGNMENTS

RESULT 1

TS1301 beta-lactamase (EC 3.5.2.6) - fission yeast (Schizosaccharomyces pombe)

C/Species: Schizosaccharomyces pombe

C/Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000

C/Accession: TS1301

R/MACH, A.; BRACHAT, A.; ALBERTSSEUT, C.; REBISCHUNG, C.; PHILIPSEN, P.

Yeast 13, 1065-1075, 1997

A/Title: Heterologous His3 marker and GFP reporter modules for PCR-targeting in Saccharom

A/Reference number: Z09587

A/Accession: TS1301

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-286 <MAC>

A/Cross-references: EMBL:AJ002683; PIDN:CAA05686.1

C/Genetics:

A/Gene: bla

C/Superfamily: beta-lactamase I

C/Keywords: hydrolase

Query Match 100.0%; Score 1348; DB 2; Length 286;
Best local similarity 100.0%; Pred. No. 1.2e-105;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	HPETLVKVDADQLGARVGYIELDNSGKIIESTRPERFPMSTFKYLLGAVLSRID	60
DB	24	HPETLVKVDADQLGARVGYIELDNSGKIIESTRPERFPMSTFKYLLGAVLSRID	83
QY	61	AGQDQGRRIHYSQNDIVKSPYTEKHLTDGNTVELCSAATMTSDNTNANLLTTIGSP	120
DB	84	AGQDQGRRIHYSQNDIVKSPYTEKHLTDGNTVELCSAATMTSDNTNANLLTTIGSP	143
QY	121	KEITAFIHNMGDHYTRLRWBEPELNEAIPNDRDITMPVAMATTIRKLLTGELTLASRQ	180
DB	144	KEITAFIHNMGDHYTRLRWBEPELNEAIPNDRDITMPVAMATTIRKLLTGELTLASRQ	203
QY	181	QIIDWMEADKVAQPLRSALPAGWFIADKSGAGERGSGIIALGPDGKPSRIIVITYTG	240
DB	204	QIIDWMEADKVAQPLRSALPAGWFIADKSGAGERGSGIIALGPDGKPSRIIVITYTG	263
QY	241	SOATMDERNRQIAETGASLIKHW 263	
DB	264	SOATMDERNRQIAETGASLIKHW 286	

RESULT 2

S47061 beta-lactamase (EC 3.5.2.6) - phage phi-X174

C/Species: phage phi-X174

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C/Accession: S47061

R/Henrich, B.; Schmidtberger, B.

submitted to the EMBL Data Library, July 1994

A:Description: A variant of phix174 gene B-based positive selection vectors with enhance

A:Reference number: S47060

A:Accession: S47061

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-286 <HEN>

A:Cross-references: UNIPROT:Q38058; EMBL:Z35638; NID:g520996; PIDN:CAA84692.1; PID:g5209

C:Superfamily: beta-lactamase I

C:Keywords: hydrolase

Query Match 100.0%; Score 1348; DB 2; Length 286;

Best Local Similarity 100.0%; Pred. No. 1.2e-105;

Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 HETLVKVDADDOUGARVGYIELDLSNGKILIESRPERPFPMSTFKYLICGAVLSRD 60
 24 HETLVKVDADDOUGARVGYIELDLSNGKILIESRPERPFPMSTFKYLICGAVLSRD 83
 61 AGOEOLGRIHYSQNDLVESPVTEKHLTDGVTRELCSAATMSDNTANLLTTIGSP 120
 84 AGOEOLGRIHYSQNDLVESPVTEKHLTDGVTRELCSAATMSDNTANLLTTIGSP 143
 121 KELTAFILNMGDHVTRLDWEPELNEAIPNDRDITTPVAMATTIRKLLTGEILTLASRQ 180
 144 KELTAFILNMGDHVTRLDWEPELNEAIPNDRDITTPVAMATTIRKLLTGEILTLASRQ 203
 181 QLIDWMEADKAVGPIRLSALPAGWFIADKSGAGERSRGIITIALGPDGKPSRIIVITTTG 240
 204 QLIDWMEADKAVGPIRLSALPAGWFIADKSGAGERSRGIITIALGPDGKPSRIIVITTTG 263
 241 SOATMDERRROIAEIGASLIKHM 263
 264 SOATMDERRROIAEIGASLIKHM 286

RESULT 3

S41975 beta-lactamase (EC 3.5.2.6) precursor - synthetic

C:Species: synthetic

C:Date: 25-Dec-1994 #sequence_revision 22-Aug-1996 #text_change 20-Oct-2000

C:Accession: S41975

R:Kaestner, K.H.; Montolín, L.; Kern, H.; Thulke, M.; Schutz, G.

Gene 148, 67-70, 1994

A:Title: Universal beta-galactosidase cloning vectors for promoter analysis and gene tar

A:Reference number: A57991; MUID:95011660; PMID:7926839

A:Accession: S41975

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-286 <KAB>

A:Cross-references: EMBL:X76682; NID:g453622; PIDN:CAA54104.1; PID:g453623

A:Note: submitted to the EMBL Data Library, December 1993

C:Keywords: hydrolase

Query Match 100.0%; Score 1348; DB 4; Length 286;

Best Local Similarity 100.0%; Pred. No. 1.2e-105;

Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 HETLVKVDADDOUGARVGYIELDLSNGKILIESRPERPFPMSTFKYLICGAVLSRD 60
 24 HETLVKVDADDOUGARVGYIELDLSNGKILIESRPERPFPMSTFKYLICGAVLSRD 83
 61 AGOEOLGRIHYSQNDLVESPVTEKHLTDGVTRELCSAATMSDNTANLLTTIGSP 120
 84 AGOEOLGRIHYSQNDLVESPVTEKHLTDGVTRELCSAATMSDNTANLLTTIGSP 143
 121 KELTAFILNMGDHVTRLDWEPELNEAIPNDRDITTPVAMATTIRKLLTGEILTLASRQ 180
 144 KELTAFILNMGDHVTRLDWEPELNEAIPNDRDITTPVAMATTIRKLLTGEILTLASRQ 203
 181 QLIDWMEADKAVGPIRLSALPAGWFIADKSGAGERSRGIITIALGPDGKPSRIIVITTTG 240
 204 QLIDWMEADKAVGPIRLSALPAGWFIADKSGAGERSRGIITIALGPDGKPSRIIVITTTG 263

241 SOATMDERRROIAEIGASLIKHM 263
 264 SOATMDERRROIAEIGASLIKHM 286

RESULT 4

PNEC

beta-lactamase (EC 3.5.2.6) precursor - Escherichia coli plasmid

N:Alternate names: beta-lactamase TEM-6 (for bla-6 DNA); penicillinase

C:Species: Escherichia coli

C:Date: 30-Nov-1980 #sequence_revision 01-Sep-1981 #text_change 16-Aug-2004

C:Accession: A93821; A93820; A35387; S24415; A01005

R:Suciliffe, J.G.

Proc. Natl. Acad. Sci. U.S.A. 75, 3737-3741, 1978

A:Title: Nucleotide sequence of the ampicillin resistance gene of Escherichia coli plasmid

A:Reference number: A93821; MUID:79012484; PMID:358200

A:Accession: A93821

A:Molecule type: DNA

A:Residues: 1-286 <STU>

A:Cross-references: UNIPROT:P00810; GB:V00613; GB:J01832; NID:g43710; PIDN:CAA23886.1; P

A:Experimental source: plasmid pBR322

R:Ambler, R.P.; Scott, G.K.

Proc. Natl. Acad. Sci. U.S.A. 75, 3732-3736, 1978

A:Title: Partial amino acid sequence of penicillinase coded by Escherichia coli plasmid

A:Reference number: A93820; MUID:79012483; PMID:358199

A:Accession: A93820

A:Molecule type: protein

A:Residues: 24-36, 'K', 38-286 <AMB>

A:Experimental source: plasmid R6K

J. Kornacki, J.A.; Burlage, R.S.; Figurek, D.H.

J. Bacteriol. 172, 3040-3050, 1990

A:Title: The kil-kor region of broad-host-range plasmid RK2: nucleotide sequence, polype

A:Reference number: A35387; MUID:90264294; PMID:2160936

A:Accession: A35387

A:Molecule type: DNA

A:Residues: 182-286 <KOR>

A:Cross-references: GB:M32794; NID:g152521; PIDN:AAA26408.1; PID:g152522

A:Experimental source: PK2

R:Goussard, S.; Sougkoff, W.; Mabilat, C.; Bauernfeind, A.; Courvalin, P.

J. Gen. Microbiol. 137, 2681-2687, 1991

A:Title: An ISI-like element is responsible for high-level synthesis of extended-spectrum

A:Reference number: S24415; MUID:92166702; PMID:1665171

A:Accession: S24415

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-101, 'K', 103-161, 'H', 163-286 <GOU>

A:Cross-references: EMBL:X57972; NID:g41816; PIDN:CAA41038.1; PID:g41817

A:Experimental source: ISI-like bla-6 DNA

R:Suciliffe, J.G.

Cold Spring Harb. Symp. Quant. Biol. 43, 77-90, 1979

A:Title: Complete nucleotide sequence of the Escherichia coli plasmid pBR322.

A:Reference number: A90923; MUID:80002802; PMID:383387

A:Accession: A90923

A:Status: annotation

A:Contents: annotation

C:Comment: Like most penicillinases from gram-negative bacteria, this enzyme, coded by a

C:Genetics:

A:Superfamily: Beta-lactamase I

C:Keywords: antibiotic resistance; hydrolase; membrane protein

F1-23/Domains: signal sequence #status predicted <SIG>

F124-286/Product: beta-lactamase #status experimental <MAT>

F168/Active site: Ser #status predicted

F175-121/Disulfide bonds: #status predicted

Query Match 99.6%; Score 1343; DB 1; Length 286;

Best Local Similarity 99.2%; Pred. No. 3.1e-105;

Matches 261; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 HETLVKVDADDOUGARVGYIELDLSNGKILIESRPERPFPMSTFKYLICGAVLSRD 60

24 HETLVKVDADDOUGARVGYIELDLSNGKILIESRPERPFPMSTFKYLICGAVLSRD 83

61 AGOEOLGRIHYSQNDLVESPVTEKHLTDGVTRELCSAATMSDNTANLLTTIGSP 120


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Db      84 AGOEOLGRRIRHYSQNDLVYSPVTEKHLTDGNTVRELCSAAITMSDNTANILLTTIGSP 143
      121 KELTSFLLHNMGDHVTRLDRWPEBELNEAIPNDRDRTTMPVAMATTYLRKLLTGELLTLASRQ 180
      144 KELTSFLLHNMGDHVTRLDRWPEBELNEAIPNDRDRTTMPVAMATTYLRKLLTGELLTLASRQ 203
Qy      181 QUIDMWEADKVAQPLLRSLPAGWFIADKSGAGERSRGIITAAIGPDGKPSRIIVYITTTG 240
      204 QUIDMWEADKVAQPLLRSLPAGWFIADKSGAGERSRGIITAAIGPDGKPSRIIVYITTTG 263
Db      241 SOATMDERNRQIAETIGASLTIKHM 263
      264 SOATMDERNRQIAETIGASLTIKHM 286
Qy      241 SOATMDERNRQIAETIGASLTIKHM 263
      264 SOATMDERNRQIAETIGASLTIKHM 286

RESULT 5
140905
beta-lactamase (EC 3.5.2.6) - synthetic
C:Species: synthetic
A>Note: Cloning vector pCG1408 engineered and expressed in Clavibacter xyli subsp. cynod
C>Date: 15-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Oct-2000
C:Accession: 140905
R:Taylor, J.; Stearman, R.S.; Uratani, B.B.
plasmid 29, 241-244, 1993
A>Title: Development of a native plasmid as a cloning vector in Clavibacter xyli subsp.
A:Reference number: 140904; MUID:93361581; PMID:7689234
A:Accession: 140905
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-286 <RBS>
A:Cross-references: EMBL:U21228; NID:g885956; PIND:AAA70411.1; PID:g885958
C:Keywords: hydrolase

Query Match      99.6%; Score 1343; DB 4; Length 286;
Best Local Similarity 99.2%; Pred. No. 3.1e-105;
Matches 261; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 HPEITLVKVDADQAGARVGYELDLNSGKILSPRPBRPFPMSTFKVLLCGAVLSRD 60
      24 HPEITLVKVDADQAGARVGYELDLNSGKILSPRPBRPFPMSTFKVLLCGAVLSRD 83
Db      61 AGOEOLGRRIRHYSQNDLVYSPVTEKHLTDGNTVRELCSAAITMSDNTANILLTTIGSP 120
      84 AGOEOLGRRIRHYSQNDLVYSPVTEKHLTDGNTVRELCSAAITMSDNTANILLTTIGSP 143
Qy      121 KELTSFLLHNMGDHVTRLDRWPEBELNEAIPNDRDRTTMPVAMATTYLRKLLTGELLTLASRQ 180
      144 KELTSFLLHNMGDHVTRLDRWPEBELNEAIPNDRDRTTMPVAMATTYLRKLLTGELLTLASRQ 203
Db      181 QUIDMWEADKVAQPLLRSLPAGWFIADKSGAGERSRGIITAAIGPDGKPSRIIVYITTTG 240
      204 QUIDMWEADKVAQPLLRSLPAGWFIADKSGAGERSRGIITAAIGPDGKPSRIIVYITTTG 263
Qy      241 SOATMDERNRQIAETIGASLTIKHM 263
      264 SOATMDERNRQIAETIGASLTIKHM 286

RESULT 6
560312
extended spectrum beta-lactamase CAZ-7 - Klebsiella pneumoniae
C:Species: Klebsiella pneumoniae
C>Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 22-Jun-1999
C:Accession: 560312
R:Chanal, C.; Poupert, M.C.; Siroc, D.; Labia, R.; Siroc, J.; Cluzel, R.
Antimicrob. Agents Chemother. 36, 1817-1820, 1992
A>Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.
A:Reference number: 560310; MUID:93037315; PMID:1416873
A:Accession: 560312
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <CHA>
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A:Cross-references: EMBL:X65254; NID:g296955; PIND:CAA46346.1; PID:g296956
C:Superfamily: beta-lactamase I

Query Match      98.7%; Score 1330; DB 2; Length 286;
Best Local Similarity 98.1%; Pred. No. 3.8e-104;
Matches 258; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      1 HPEITLVKVDADQAGARVGYELDLNSGKILSPRPBRPFPMSTFKVLLCGAVLSRD 60
      24 HPEITLVKVDADQAGARVGYELDLNSGKILSPRPBRPFPMSTFKVLLCGAVLSRD 83
Db      61 AGOEOLGRRIRHYSQNDLVYSPVTEKHLTDGNTVRELCSAAITMSDNTANILLTTIGSP 120
      84 AGOEOLGRRIRHYSQNDLVYSPVTEKHLTDGNTVRELCSAAITMSDNTANILLTTIGSP 143
Qy      121 KELTSFLLHNMGDHVTRLDRWPEBELNEAIPNDRDRTTMPVAMATTYLRKLLTGELLTLASRQ 180
      144 KELTSFLLHNMGDHVTRLDRWPEBELNEAIPNDRDRTTMPVAMATTYLRKLLTGELLTLASRQ 203
Db      181 QUIDMWEADKVAQPLLRSLPAGWFIADKSGAGERSRGIITAAIGPDGKPSRIIVYITTTG 240
      204 QUIDMWEADKVAQPLLRSLPAGWFIADKSGAGERSRGIITAAIGPDGKPSRIIVYITTTG 263
Qy      241 SOATMDERNRQIAETIGASLTIKHM 263
      264 SOATMDERNRQIAETIGASLTIKHM 286
```

```
RESULT 7
530113
beta-lactamase (EC 3.5.2.6) TEM-3 - Klebsiella pneumoniae plasmid pCFP04
C:Species: Klebsiella pneumoniae
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: 530113
R:Mabliat, C.; Lourenco-Vital, J.; Gousard, S.; Courvalin, P.
Mol. Gen. Genet. 235, 113-121, 1992
A>Title: A new example of physical linkage between Tnl and Tn21: the antibiotic multiple.
A:Reference number: 530112; MUID:93062798; PMID:1331747
A:Accession: 530113
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <MAB>
A:Cross-references: UNIPROT:P00810; EMBL:X64523; NID:g43797; PIND:CAA45828.1; PID:g43798
C:Genetics:
A:Gene: bla(TEM-3)
A:Genome: plasmid
C:Superfamily: beta-lactamase I
C:Keywords: antibiotic resistance; hydrolase

Query Match      98.6%; Score 1329; DB 2; Length 286;
Best Local Similarity 98.1%; Pred. No. 4.6e-104;
Matches 258; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      1 HPEITLVKVDADQAGARVGYELDLNSGKILSPRPBRPFPMSTFKVLLCGAVLSRD 60
      24 HPEITLVKVDADQAGARVGYELDLNSGKILSPRPBRPFPMSTFKVLLCGAVLSRD 83
Db      61 AGOEOLGRRIRHYSQNDLVYSPVTEKHLTDGNTVRELCSAAITMSDNTANILLTTIGSP 120
      84 AGOEOLGRRIRHYSQNDLVYSPVTEKHLTDGNTVRELCSAAITMSDNTANILLTTIGSP 143
Qy      121 KELTSFLLHNMGDHVTRLDRWPEBELNEAIPNDRDRTTMPVAMATTYLRKLLTGELLTLASRQ 180
      144 KELTSFLLHNMGDHVTRLDRWPEBELNEAIPNDRDRTTMPVAMATTYLRKLLTGELLTLASRQ 203
Db      181 QUIDMWEADKVAQPLLRSLPAGWFIADKSGAGERSRGIITAAIGPDGKPSRIIVYITTTG 240
      204 QUIDMWEADKVAQPLLRSLPAGWFIADKSGAGERSRGIITAAIGPDGKPSRIIVYITTTG 263
Qy      241 SOATMDERNRQIAETIGASLTIKHM 263
      264 SOATMDERNRQIAETIGASLTIKHM 286
```

RESULT 8

extended spectrum beta-lactamase CAZ-2 - Klebsiella pneumoniae

C:Species: Klebsiella pneumoniae

C:Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 22-Jun-1999

C:Accession: S60310

R:Chanal, C.; Poupart, M.C.; Strot, D.; Labia, R.; Strot, J.; Cluzel, R.

Antimicrob. Agents Chemother. 36, 1817-1820, 1992

A:Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.

A:Reference number: S60310; MUID:93037315; PMID:1416873

A:Accession: S60310

A:Status: preliminary; translation not shown

A:Molecule type: DNA

A:Residues: 1-286 <CH>

A:Cross-references: EMBL:X65252; NID:g2296951; PIDD:CAA46344.1; PID:g2296952

C:Superfamily: beta-lactamase I

Query Match 98.1%; Score 1323; DB 2; Length 286;

Best Local Similarity 97.7%; Pred. No. 1.5e-103;

Matches 257; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 HPEITVKKYKADADQAGRVGTYIELDNSGKILSFPRPFRPMSTFKVLLCGAVLSRID 60
 DB 24 HPEITVKKYKADADQAGRVGTYIELDNSGKILSFPRPFRPMSTFKVLLCGAVLSRID 83
 QY 61 AGOEOLGRRIHYSQNDLVESPVTEKHLTDGVTVELCSAATITMSDNTAANLLTTIGSP 120
 DB 84 AGOEOLGRRIHYSQNDLVESPVTEKHLTDGVTVELCSAATITMSDNTAANLLTTIGSP 143
 QY 121 KELTAFILNMGDHYTRLDRWEPBELNEAIPNDRDITMPVAAATTIRKLLTGELLTLASRQ 180
 DB 144 KELTAFILNMGDHYTRLDRWEPBELNEAIPNDRDITMPVAAATTIRKLLTGELLTLASRQ 203
 QY 181 OLIDMEADKVAAGPLLRALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 240
 DB 204 OLIDMEADKVAAGPLLRALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 263
 QY 241 SOATMDERNROIAEIGASLIRKM 263
 DB 264 SOATMDERNROIAEIGASLIRKM 286

RESULT 9

beta-lactamase (EC 3.5.2.6) TEM-1 - Klebsiella pneumoniae transposon Tn1331

C:Species: Klebsiella pneumoniae

C:Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004

C:Accession: S60311; F37392; PQ0498

R:Chanal, C.; Poupart, M.C.; Strot, D.; Labia, R.; Strot, J.; Cluzel, R.

Antimicrob. Agents Chemother. 36, 1817-1820, 1992

A:Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.

A:Reference number: S60310; MUID:93037315; PMID:1416873

A:Accession: S60311

A:Status: preliminary; translation not shown

A:Molecule type: DNA

A:Residues: 1-286 <CH>

A:Cross-references: UNIPROT:Q99224; EMBL:X65253; NID:g2296953; PIDD:CAA46345.1; PID:g2296954

R:Toimasty, M.E.

A:Title: Sequencing and expression of aadA, bla, and tnpR from the multiresistance trans

A:Reference number: A37392; MUID:91172904; PMID:1963948

A:Accession: F37392

A:Molecule type: DNA

A:Residues: 1-32 <TOL>

A:Cross-references: GB:M55547; NID:g155010; PIDD:AAA98408.1; PID:g155016

C:Gene: TEM-bla

C:Superfamily: beta-lactamase I

C:Keywords: antibiotic resistance; hydrolase

Query Match 98.0%; Score 1321; DB 2; Length 286;

Best Local Similarity 97.3%; Pred. No. 2.2e-103;

Matches 257; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 HPEITVKKYKADADQAGRVGTYIELDNSGKILSFPRPFRPMSTFKVLLCGAVLSRID 60
 DB 24 HPEITVKKYKADADQAGRVGTYIELDNSGKILSFPRPFRPMSTFKVLLCGAVLSRID 83
 QY 61 AGOEOLGRRIHYSQNDLVESPVTEKHLTDGVTVELCSAATITMSDNTAANLLTTIGSP 120
 DB 84 AGOEOLGRRIHYSQNDLVESPVTEKHLTDGVTVELCSAATITMSDNTAANLLTTIGSP 143
 QY 121 KELTAFILNMGDHYTRLDRWEPBELNEAIPNDRDITMPVAAATTIRKLLTGELLTLASRQ 180
 DB 144 KELTAFILNMGDHYTRLDRWEPBELNEAIPNDRDITMPVAAATTIRKLLTGELLTLASRQ 203
 QY 181 OLIDMEADKVAAGPLLRALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 240
 DB 204 OLIDMEADKVAAGPLLRALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 263
 QY 241 SOATMDERNROIAEIGASLIRKM 263
 DB 264 SOATMDERNROIAEIGASLIRKM 286

Matches 256; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 HPEITVKKYKADADQAGRVGTYIELDNSGKILSFPRPFRPMSTFKVLLCGAVLSRID 60
 DB 24 HPEITVKKYKADADQAGRVGTYIELDNSGKILSFPRPFRPMSTFKVLLCGAVLSRID 83
 QY 61 AGOEOLGRRIHYSQNDLVESPVTEKHLTDGVTVELCSAATITMSDNTAANLLTTIGSP 120
 DB 84 AGOEOLGRRIHYSQNDLVESPVTEKHLTDGVTVELCSAATITMSDNTAANLLTTIGSP 143
 QY 121 KELTAFILNMGDHYTRLDRWEPBELNEAIPNDRDITMPVAAATTIRKLLTGELLTLASRQ 180
 DB 144 KELTAFILNMGDHYTRLDRWEPBELNEAIPNDRDITMPVAAATTIRKLLTGELLTLASRQ 203
 QY 181 OLIDMEADKVAAGPLLRALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 240
 DB 204 OLIDMEADKVAAGPLLRALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 263
 QY 241 SOATMDERNROIAEIGASLIRKM 263
 DB 264 SOATMDERNROIAEIGASLIRKM 286

RESULT 10

Bla protein - Salmonella typhimurium plasmid NTP16

N:Alternate names: beta lactamase homolog

C:Species: Salmonella typhimurium

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C:Accession: J01546

R:Canonon, P.M.; Strike, P.

Plasmid 27, 220-230, 1992

A:Title: Complete nucleotide sequence and gene organization of plasmid NTP16.

A:Reference number: J01546; MUID:92383313; PMID:1325061

A:Accession: J01546

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-286 <CAN>

A:Cross-references: UNIPROT:Q8L2F9

C:Genetics:

A:Genome: plasmid

C:Superfamily: beta-lactamase I

Query Match 97.7%; Score 1317; DB 2; Length 286;

Best Local Similarity 97.7%; Pred. No. 4.7e-103;

Matches 257; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 HPEITVKKYKADADQAGRVGTYIELDNSGKILSFPRPFRPMSTFKVLLCGAVLSRID 60
 DB 24 HPEITVKKYKADADQAGRVGTYIELDNSGKILSFPRPFRPMSTFKVLLCGAVLSRID 83
 QY 61 AGOEOLGRRIHYSQNDLVESPVTEKHLTDGVTVELCSAATITMSDNTAANLLTTIGSP 120
 DB 84 AGOEOLGRRIHYSQNDLVESPVTEKHLTDGVTVELCSAATITMSDNTAANLLTTIGSP 143
 QY 121 KELTAFILNMGDHYTRLDRWEPBELNEAIPNDRDITMPVAAATTIRKLLTGELLTLASRQ 180
 DB 144 KELTAFILNMGDHYTRLDRWEPBELNEAIPNDRDITMPVAAATTIRKLLTGELLTLASRQ 203
 QY 181 OLIDMEADKVAAGPLLRALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 240
 DB 204 OLIDMEADKVAAGPLLRALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 263
 QY 241 SOATMDERNROIAEIGASLIRKM 263
 DB 264 SOATMDERNROIAEIGASLIRKM 286

RESULT 11

beta-lactamase (EC 3.5.2.6) class A - Escherichia coli plasmid p453

N:Alternate names: beta-lactamase PRT-2; beta-lactamase SHV-1

C:Species: Escherichia coli

C>Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993

C/Accession: S02434

R/Batch: Lemay, M.; Peduzzi, J.; Yaghlane, H.B.; Labie, R.

FEBS Lett. 231, 217-220, 1988

A/Title: Single amino acid substitution between SHV-1 beta-lactamase and cefotaxime-hyd

A/Reference number: S02434; MUID:88196385; PMID:3129309

A/Accession: S02434

A/Molecule type: protein

A/Residues: 1-265 <BAR>

C/Superfamily: beta-lactamase I

C/Keywords: antibiotic resistance; hydrolase

Query Match 69.0%; Score 930; DB 2; Length 265;

Best Local Similarity 67.6%; Pred. No. 1.3e-70;

Matches 177; Conservative 38; Mismatches 47; Indels 0; Gaps 0;

QY 2 PETLVKVDADQDQGVYIELDINSKILSFPEERFPMSTFKVLLCGAVLSRIDA 61

DB 2 PQLPQIKLSQSGRGVGMIEMLASGRITLWADRSFPMSTFKVLLCGAVLARVDA 61

QY 62 GQQLGRRIHYSQNDIVYSPVTEKHLTDGNTVRELCSAATMSDNTANLLTTIGPK 121

DB 62 GDEQLERKIHQQDLVDYSPVSEKHLADGNTVRELCSAATMSDNTANLLTTAVGSPA 121

QY 122 ELTAFLHMGDHTVRLDRWPELNEAIPNDERDTMPVAMATTLRKLTGELLTLASRQ 181

DB 122 GLTAFRLQIGDNTVRLDRWPELNEALPGDARDTTTPASMAATLRKLTLSQRLSARSGRQ 181

QY 182 LIDWMEADKVAQPLIRSLPAGWFIADKSGAGERSGRTIALGPDGKPSRIIVYITGGS 241

DB 182 LLQWVDDRVAGPLIRSVLPAGWFIADKSGAGERSGRTIALGPNNAERIVVIYLRDT 241

QY 242 QATMDERRROIAEIGASLIKHM 263

DB 242 PASMAERNQQLAGIGALLIEHW 263

RESULT 15

A44998 beta-lactamase (EC 3.5.2.6) SHV-2 - Klebsiella ozaenae plasmid pBB60

C/Species: Klebsiella ozaenae

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004

C/Accession: A44998; S12703

R/Huletaky, A.; Couture, F.; Levesque, R.C.

Antimicrob. Agents Chemother. 34, 1725-1732, 1990

A/Title: Nucleotide sequence and phylogeny of SHV-2 beta-lactamase.

A/Reference number: A44998; MUID:91136192; PMID:2285285

A/Accession: A44998

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-286 <HUU>

A/Cross-references: UNIPROT:P14558; GB:M95179; NID:G150486; PIDN:AAA5526.1; PID:G150486

R/Podbielski, A.; Melzer, B.

Nucleic Acids Res. 18, 4916, 1990

A/Title: Nucleotide sequence of the gene encoding the SHV-2 beta-lactamase (bla(SHV-2))

A/Reference number: S12703; MUID:90370479; PMID:2395654

A/Accession: S12703

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-286 <POD>

A/Cross-references: EMBL:X53433; NID:G43789; PIDN:CAA37524.1; PID:G43790

C/Genetics:

A/Genome: plasmid

C/Superfamily: Beta-lactamase I

C/Keywords: antibiotic resistance; hydrolase

Query Match 69.0%; Score 930; DB 1; Length 286;

Best Local Similarity 67.6%; Pred. No. 1.5e-70;

Matches 177; Conservative 38; Mismatches 47; Indels 0; Gaps 0;

QY 2 PETLVKVDADQDQGVYIELDINSKILSFPEERFPMSTFKVLLCGAVLSRIDA 61

DB 23 PQLPQIKLSQSGRGVGMIEMLASGRITLWADRSFPMSTFKVLLCGAVLARVDA 82

QY 62 GQQLGRRIHYSQNDIVYSPVTEKHLTDGNTVRELCSAATMSDNTANLLTTIGPK 121

DB 83 GDEQLERKIHQQDLVDYSPVSEKHLADGNTVRELCSAATMSDNTANLLTTAVGSPA 142

QY 122 ELTAFLHMGDHTVRLDRWPELNEAIPNDERDTMPVAMATTLRKLTGELLTLASRQ 181

DB 143 GLTAFRLQIGDNTVRLDRWPELNEALPGDARDTTTPASMAATLRKLTLSQRLSARSGRQ 202

QY 182 LIDWMEADKVAQPLIRSLPAGWFIADKSGAGERSGRTIALGPDGKPSRIIVYITGGS 241

DB 203 LLQWVDDRVAGPLIRSVLPAGWFIADKSGAGERSGRTIALGPNNAERIVVIYLRDT 262

QY 242 QATMDERRROIAEIGASLIKHM 263

DB 263 PASMAERNQQLAGIGALLIEHW 284

Search completed: June 10, 2005, 10:58:44
Job time : 20.1791 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:22:36 ; Search time 101.972 Seconds
(without alignments)
997.510 Million cell updates/sec

Title: US-10-668-778-2

1348

Perfect score: 1 HPELVVKNKADQLGARVG.....TMDERNQIAIGASLIKHW 263

Sequence: 1 HPELVVKNKADQLGARVG.....TMDERNQIAIGASLIKHW 263

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp19908:.*
2: geneseqp19908:.*
3: geneseqp20008:.*
4: geneseqp20018:.*
5: geneseqp20028:.*
6: geneseqp20038:.*
7: geneseqp20038:.*
8: geneseqp20048:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1348	100.0	263 4 AAB05544	AAB05544 B. coli m
2	1348	100.0	263 4 AAB36692	AAB36692 Escherich
3	1348	100.0	263 4 ADJ67709	ADJ67709 Escherich
4	1348	100.0	264 2 AAM16634	AAM16634 Beta-lact
5	1348	100.0	264 2 AAM18680	AAM18680 Intracell
6	1348	100.0	264 2 AAR31575	AAR31575 Ampicilli
7	1348	100.0	286 2 AAR97619	AAR97619 Secretory
8	1348	100.0	286 2 AAR96423	AAR96423 Cytochrom
9	1348	100.0	286 2 AAM16635	AAM16635 Beta-lact
10	1348	100.0	286 2 AAM18679	AAM18679 Secretory
11	1348	100.0	286 2 AAY08529	AAY08529 Vector pA
12	1348	100.0	286 2 AAB10442	AAB10442 Expressio
13	1348	100.0	286 3 AAB10438	AAB10438 Expressio
14	1348	100.0	286 3 AAB10440	AAB10440 Expressio
15	1348	100.0	286 4 AAB50898	AAB50898 Protein e
16	1348	100.0	286 4 AAB31173	AAB31173 Amino aci
17	1348	100.0	286 5 AAY75551	AAY75551 cel2 inte
18	1348	100.0	286 5 AAB55474	AAB55474 Vector pC
19	1348	100.0	286 6 ABR43622	ABR43622 Cloning v
20	1348	100.0	286 8 ADR70422	ADR70422 Vector pA
21	1348	100.0	286 8 ADR70410	ADR70410 Vector pA
22	1348	100.0	286 8 ADR70404	ADR70404 Vector pA
23	1348	100.0	286 8 ADR70416	ADR70416 Vector pA
24	1348	100.0	286 8 ADR70428	ADR70428 Vector pA
25	1348	100.0	290 4 AAU23219	AAU23219 Novel hum

26	1348	100.0	290 4 AAM84362	AAM84362 Human imm
27	1348	100.0	327 2 AAW16536	AAW16536 Beta-lact
28	1348	100.0	327 2 AAM18681	AAM18681 Membrane-
29	1348	100.0	408 6 ABR55981	ABR55981 hCG beta-
30	1348	100.0	585 6 ADA67747	ADA67747 Beta-lact
31	1348	100.0	1031 5 ADI46109	ADI46109 Single st
32	1348	100.0	1088 2 AAR88636	AAR88636 Plasmid p
33	1348	100.0	1277 2 AAR52701	AAR52701 Plasmid p
34	1348	100.0	2307 3 AAY70064	AAY70064 Recombina
35	1348	100.0	2307 3 AAY70066	AAY70066 Recombina
36	1347	99.9	286 2 AAY06551	AAY06551 Escherich
37	1347	99.9	872 7 ADK65686	ADK65686 E coli c1
38	1347	99.9	1293 7 ADC22811	ADC22811 Human G p
39	1347	99.9	1293 7 ADH14284	ADH14284 Vector pC
40	1347	99.9	1967 6 ABB82793	ABB82793 Amino aci
41	1343	99.6	265 2 AAY08234	AAY08234 E. coli R
42	1343	99.6	265 2 AAY08232	AAY08232 E. coli R
43	1343	99.6	265 2 AAW48613	AAW48613 Escherich
44	1343	99.6	265 2 AAY49892	AAY49892 RTM with
45	1343	99.6	265 2 AAY49890	AAY49890 Escherich

ALIGNMENTS

RESULT 1	
AAE05544	AAE05544 standard; protein, 263 AA.
XX	
AC	AAE05544;
XX	
DT	24-SEP-2001 (first entry)
XX	
DE	B. coli mature TEM-1 beta-lactamase.
XX	
KW	Interaction-dependent enzyme association; IdeA system; biosensor;
KW	circularly permuted interaction-activated protein; marker protein;
KW	type A beta-lactamase; TEM-1 beta-lactamase; protein-protein interaction;
KW	therapeutic; drug screening; thiodoxin; ampicillin resistance.
XX	
OS	Escherichia coli.
XX	
PH	Key
FT	Cleavage-site
FT	Location/Qualifiers
FT	/note= "Break-point between alpha and omega fragments"
FT	36. .40
FT	/note= "Inter-sub-domain loop"
FT	38. .39
FT	/note= "Break-point between alpha and omega fragments"
FT	45
FT	/note= "Break-point between alpha and omega fragments"
FT	74. .75
FT	/note= "Break-point between alpha and omega fragments"
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FT	/note= "Break-point between alpha and omega fragments"
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FT	/note= "Break-point between alpha and omega fragments"
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FT	/note= "Inter-sub-domain loop"
FT	190. .191
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FT	202. .203
FT	/note= "Break-point between alpha and omega fragments"
FT	228. .229
FT	/note= "Break-point between alpha and omega fragments"
FT	
XX	
PN	WO200151629-A2.
XX	
PD	19-JUL-2001.
XX	
PF	16-JAN-2001; 2001WO-US001651.
XX	
PR	13-JAN-2000; 2000US-0175968P.
PR	15-MAR-2000; 2000US-00526106.

QY 121 KETLAFPHNMGDHTRLDREWEPELNEAI PNDERDTMPVAMATTLRKLTGELLTLASRQ 180
 DB 121 KETLAFPHNMGDHTRLDREWEPELNEAI PNDERDTMPVAMATTLRKLTGELLTLASRQ 180
 QY 181 QLTIMWEADKVAGPLNSALPAGWFIADKSGAGRGSGRIITAAALGPDGKPSRIVITYTTG 240
 DB 181 QLTIMWEADKVAGPLNSALPAGWFIADKSGAGRGSGRIITAAALGPDGKPSRIVITYTTG 240
 QY 241 SQATMDERNROIARIIGASLIRGW 263
 DB 241 SQATMDERNROIARIIGASLIRGW 263

RESULT 3
 ADJ67709 standard; protein, 263 AA.
 XX ADJ67709;
 AC ADJ67709;
 XX 20-MAY-2004 (first entry)
 DT
 XX Escherichia coli TEM-1 beta-lactamase.
 DE
 XX fragment complementation system; marker protein;
 KW multiple genetic element incorporation; antibiotic resistance;
 KW beta-lactam derivative activation; anti-tumour compound;
 KW functional reassembly; protein-protein interaction; proteome interaction;
 KW immunoglobulin variable region; immune cell protein; CD40;
 KW phosphorylation-regulated cell signal transducer; TEM-1 beta-lactamase;
 KM enzyme.
 XX Escherichia coli.
 OS
 XX US2004038317-A1.
 PN
 XX 26-FEB-2004.
 PD
 XX 22-SEP-2003; 2003US-00668778.
 PF
 XX 15-MAR-1999; 99US-0124339P.
 PR 25-MAY-1999; 99US-0135926P.
 PR 13-JAN-2000; 2000US-0175968P.
 PR 13-MAR-2000; 2000US-00526106.
 XX
 XX (KALO-) KALOBIOIS INC.
 PA
 XX Balint RF, Her J;
 PI
 XX WPI, 2004-203222/19.
 DR
 XX N-PSDB; ADJ67708.
 DR
 XX Fragment complementation system for detecting immunoglobulin epitope, has
 PT first oligopeptide containing N-terminal fragment with C-terminal break-
 PT point, second oligopeptide containing C-terminal fragment with N-terminal
 PT break-point.
 XX
 XX Disclosure; SEQ ID NO 2; 47pp; English.
 PS
 XX The invention describes a fragment complementation system (I) comprising
 CC a first oligopeptide having an N-terminal fragment with a C-terminal
 CC break-point, and a second oligopeptide having a C-terminal fragment with
 CC a N-terminal break-point, where the N-terminal fragment and the C-
 CC terminal fragment each are derived from a marker protein and the C-
 CC terminal fragment is functionally reconstituted marker protein. (I) is useful for
 CC to form a functionally reconstituted marker protein. (I) is useful for
 CC selecting simultaneously incorporation of multiple genetic elements into a
 CC host cell, and activating a beta-lactam derivative of an anti-tumour
 CC compound in a host. The method described is useful for identifying a
 CC second oligopeptide to which a first oligopeptide binds, involving co-
 CC expressing the first and second oligopeptides. Binding of the first
 CC oligopeptide to the second oligopeptide results in the functional
 CC reassembly of the marker protein. The method is also useful for
 CC monitoring the occurrence of protein-protein interactions in a sample;

CC identifying oligopeptide interactions between two different proteomes;
 CC and identifying epitopes that bind to an immunoglobulin variable region.
 CC (I) or an expression cassette (II), encoding a selectable N or C-terminal
 CC peptide, is useful for identifying interactions between an extra cellular
 CC domain of a transmembrane protein and a polypeptide, where the
 CC transmembrane protein is an immune cell protein, preferably CD40. (I) or
 CC (II) is useful for high-throughput identification of compound that
 CC inhibit phosphorylation-regulated cell signal transducers. (I)
 CC efficiently detects multiple interaction between extracellular and
 CC intracellular protein with high throughput format. This is the amino acid
 CC sequence of antibiotic resistance enzyme TEM-1 beta-lactamase that can be
 CC used as a selectable gene in the fragment complementation system of the
 CC invention.
 XX
 XX SQ Sequence 263 AA;
 XX
 XX Query Match 100.0%; Score 1348; DB 8; Length 263;
 XX Best Local Similarity 100.0%; Pred. No. 1.8e-132;
 XX Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVAEDOLGARVGYIEIDLNSGKILSFRRPBERPPMNSTFKVLLCGAVLSRID 60
 DB 1 HPEITLVKVAEDOLGARVGYIEIDLNSGKILSFRRPBERPPMNSTFKVLLCGAVLSRID 60
 QY 61 AGGOLGRRIHYSONDIVESPVTEKHLTDGMTVREICSAITMSDNTAAVLLTTIGSP 120
 DB 61 AGGOLGRRIHYSONDIVESPVTEKHLTDGMTVREICSAITMSDNTAAVLLTTIGSP 120
 QY 121 KETLAFPHNMGDHTRLDREWEPELNEAI PNDERDTMPVAMATTLRKLTGELLTLASRQ 180
 DB 121 KETLAFPHNMGDHTRLDREWEPELNEAI PNDERDTMPVAMATTLRKLTGELLTLASRQ 180
 QY 181 QLTIMWEADKVAGPLNSALPAGWFIADKSGAGRGSGRIITAAALGPDGKPSRIVITYTTG 240
 DB 181 QLTIMWEADKVAGPLNSALPAGWFIADKSGAGRGSGRIITAAALGPDGKPSRIVITYTTG 240
 QY 241 SQATMDERNROIARIIGASLIRGW 263
 DB 241 SQATMDERNROIARIIGASLIRGW 263

RESULT 4
 AAM16634 standard; protein, 264 AA.
 ID AAM16634;
 XX AAM16634;
 AC AAM16634;
 XX 09-AUG-1997 (first entry)
 DT
 XX Beta-lactamase (including signal peptide).
 DE
 XX Gene directed enzyme prodng therapy; GDEPT;
 KW virus directed enzyme prodng therapy; VDEPT; beta-lactamase; cancer;
 KW HIV, inflammation.
 KM
 XX Escherichia coli.
 OS
 XX
 XX Key Location/Qualifiers
 FH 1.23
 FT Peptide /label= Sig_peptide
 PT
 XX WO9719180-A2.
 XX 29-MAY-1997.
 PD
 XX 19-NOV-1996; 96WO-GB002845.
 PF
 XX 20-NOV-1995; 95GB-00023703.
 PR
 XX (GLAX) GLAXO GROUP LTD.
 PA
 XX Dev I, Moore JT, Ohmstede C;
 PI
 XX

DR WPI; 1997-298117/27.
 DR N-PSDB; AAT66736.
 XX Molecular chimera for gene or virus directed enzyme prodng therapy -
 PT useful for treatment of cancer, viral infection or inflammation.
 XX
 PS Example; Page 28; 38pp; English.
 CC Escherichia coli beta-lactamase (AAW16634), including the signal peptide,
 CC is the expression product of a molecular chimera, designated PCMV-BL
 CC (AAT66737), in which the beta-lactamase gene is under control of the CMV
 CC intermediate/early promoter. Vectors consisting of a transcriptional
 CC regulatory DNA sequence linked to a beta-lactamase gene can be used for
 CC enzyme prodng therapy. Expression of the beta-lactamase in a targeted
 CC cell allows conversion of a prodng into an agent toxic to the cell for
 CC treatment of cancer. viral (e.g. HIV) infection or inflammation.
 CC Secretion of the enzyme has the advantage of increasing neighbouring cell
 CC kill
 CC
 SQ Sequence 264 AA;

Query Match 100.0%; Score 1348; DB 2; Length 264;
 Best Local Similarity 100.0%; Pred. No. 1.8e-132; Mismatches 0; Indels 0; Gaps 0;
 Matches 263; Conservative 0;

QY 1 HPEITLVKKAEDQAGARVGYIEIDLSGKILSFREPERPPMSTFVLLCGAVLSRID 60
 DB 2 HPEITLVKKAEDQAGARVGYIEIDLSGKILSFREPERPPMSTFVLLCGAVLSRID 61
 QY 61 AGGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTGGP 120
 DB 62 AGGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTGGP 121
 QY 121 KELTAPFLNMGDHYTRLDRWEPELNEALPNDERDTMPVAAATTLRKLLTSELTLASRQ 180
 DB 122 KELTAPFLNMGDHYTRLDRWEPELNEALPNDERDTMPVAAATTLRKLLTSELTLASRQ 181
 QY 181 QLIIDMEADKVAGPLRLSALPAGWFIADKSGAGRGSGRGIITAAIGPDGKPSRIIVITYTTG 240
 DB 182 QLIIDMEADKVAGPLRLSALPAGWFIADKSGAGRGSGRGIITAAIGPDGKPSRIIVITYTTG 241
 QY 241 SQATMDERNROIATIGASLIKHW 263
 DB 242 SQATMDERNROIATIGASLIKHW 264

RESULT 5

AAW16680
 ID AAW16680 standard; protein; 264 AA.

XX AAW16680;
 AC
 XX 13-AUG-1997 (first entry)
 DT
 XX Intracellularly-expressed beta-lactamase.
 DB
 XX Prodng therapy; gene directed enzyme prodng therapy; GDEPT;
 KW virus directed enzyme prodng therapy; VDEPT; lung cancer;
 KW beta-lactamase; PCMV-delBL.
 XX
 OS Escherichia coli.
 XX
 PN M09719183-A2.
 PD 29-MAY-1997.
 XX 19-NOV-1996; 96MO-GB002846.
 PF 20-NOV-1995; 95GB-00023703.
 PR (GLAXO) GLAXO GROUP LTD.
 XX
 PA Dev I, Moore JT, Sethna PB;
 XX
 PI

XX WPI; 1997-298118/27.
 DR N-PSDB; AAT70311.
 XX DNA construct for gene-directed enzyme prodng therapy of lung cancer -
 PT comprises lung- or neuroendocrine-specific promoter controlling
 PT expression of prodng-converting enzyme.
 XX
 PS Example 811; Page 32-34; 53pp; English.
 CC The intracellular form (AAW16680) of TEM beta-lactamase is expressed by
 CC PCMV-delBL (AAT70311) in which a PCR-amplified beta-lactamase coding
 CC sequence, minus the signal sequence, is placed under control of the
 CC intermediate/early promoter of cytomegalovirus. Intracellular beta-
 CC lactamase constructs, placed under control of promoter/enhancer elements
 CC of lung-associated protein or neuroendocrine marker protein genes, can be
 CC used in novel chimeraic molecules for use in prodng therapy of lung
 CC cancer
 CC
 SQ Sequence 264 AA;

Query Match 100.0%; Score 1348; DB 2; Length 264;
 Best Local Similarity 100.0%; Pred. No. 1.8e-132; Mismatches 0; Indels 0; Gaps 0;
 Matches 263; Conservative 0;

QY 1 HPEITLVKKAEDQAGARVGYIEIDLSGKILSFREPERPPMSTFVLLCGAVLSRID 60
 DB 2 HPEITLVKKAEDQAGARVGYIEIDLSGKILSFREPERPPMSTFVLLCGAVLSRID 61
 QY 61 AGGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTGGP 120
 DB 62 AGGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTGGP 121
 QY 121 KELTAPFLNMGDHYTRLDRWEPELNEALPNDERDTMPVAAATTLRKLLTSELTLASRQ 180
 DB 122 KELTAPFLNMGDHYTRLDRWEPELNEALPNDERDTMPVAAATTLRKLLTSELTLASRQ 181
 QY 181 QLIIDMEADKVAGPLRLSALPAGWFIADKSGAGRGSGRGIITAAIGPDGKPSRIIVITYTTG 240
 DB 182 QLIIDMEADKVAGPLRLSALPAGWFIADKSGAGRGSGRGIITAAIGPDGKPSRIIVITYTTG 241
 QY 241 SQATMDERNROIATIGASLIKHW 263
 DB 242 SQATMDERNROIATIGASLIKHW 264

RESULT 6

AAR31575
 ID AAR31575 standard; protein; 286 AA.

XX AAR31575;
 AC
 XX 10-MAR-2003 (revised)
 DT 04-JUN-1993 (first entry)
 XX Ampicillin resistance protein.
 DE
 KW CYP1A1; PRNH127; PRNH155; xeroderma pigmentosum group A; XPA;
 KW xenobiotics; circular; chimeric cytochrome P4501A1.
 XX
 OS Homo sapiens.
 XX
 PN US5180666-A.
 PD 19-JAN-1993.
 XX 27-JUN-1991; 91US-00721775.
 PF 27-JUN-1991; 91US-00721775.
 PR (UYMA-) UNIV WAYNE STATE.
 XX
 PA States JC, Hines RN, Novak RF;
 XX
 PI


```

XX  WPI; 1993-052845/06.
DR  N-PSDB; AA036498.
XX
XX  In vitro method for testing mutagenicity of a chemical - by metabolising
PT  chemical cell line consisting of transformed fibroblasts having
PT  detectable cytochrome P450 mixed function oxidase activity and detecting
PT  gene damage.
XX
XX  Disclosure; Col 21-24; 24pp; English.
XX
XX  The expression constructs PRNH127 and PRNH155 contain identical sequences
CC  but were constructed using different strategies (see AA036498). The
CC  constructs comprise exons 2-7 of human CYP1A1 gene under the control of
CC  the inducible mouse metallothionein (MT-1) promoter. The constructs also
CC  contain an open reading frame in the opposite orientation to the
CC  cytochrome P450 exons. This ORF encodes ampicillin resistance. The
CC  constructs are suitable for transformation of human fibroblasts derived
CC  from the xeroderma pigmentosum group A. Cultures of the transformed
CC  fibroblasts can be used to test substances for mutagenicity. The presence
CC  of the inducible cytochrome P450 gene allows metabolism of the substance
CC  to mutagenic metabolites. (Updated on 10-MAR-2003 to add missing OS
CC  field.)
XX
SQ  Sequence 286 AA:

Query Match      100.0%; Score 1348; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 2e-132;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 HPEITLVKTKDABDQGARVGYIELDLSGKILSFRRPFRPMMSTFVYLCGAVLSRID 60
   |||||
DB  24 HPEITLVKTKDABDQGARVGYIELDLSGKILSFRRPFRPMMSTFVYLCGAVLSRID 83
QY  61 AGOBLGRRIHYSQNDLVEYSPTVEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
   |||||
DB  84 AGOBLGRRIHYSQNDLVEYSPTVEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143
QY  121 KELTAFILNMGDHVTRLDRWEPBELNEAIPNDRDITTMVAMATTLRKLLTGELTLASRQ 180
   |||||
DB  144 KELTAFILNMGDHVTRLDRWEPBELNEAIPNDRDITTMVAMATTLRKLLTGELTLASRQ 203
QY  181 OLIDMEADKVAAGPLIRGALPAGWFIADKSGAGERSGIIIALGPDGKPSRIVIYTTG 240
   |||||
DB  204 OLIDMEADKVAAGPLIRGALPAGWFIADKSGAGERSGIIIALGPDGKPSRIVIYTTG 263
QY  241 SOATMDERNROIABIGASLIRKM 263
   |||||
DB  264 SOATMDERNROIABIGASLIRKM 286
   |||||

RESULT 7
ID  AAR97619 standard; protein; 286 AA.
XX
AC  AAR97619;
XX
DT  20-AUG-1996 (first entry)
XX
DE  Secretory beta-lactamase.
XX
KW  Gene therapy; gene directed enzyme prodnug therapy; GDBPT;
KM  virus directed enzyme prodnug therapy; VDBPT; prodnug activation;
KW  cytotoxic; cyclostatic; cancer; tumour; retrovirus; vector;
KW  beta-lactamase; cephalosporin.
XX
OS  Synthetic.
XX
PM  WO9616179-A1.
XX
PD  30-MAY-1996.
XX
PF  20-NOV-1995; 95WO-GB002716.

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XX  18-NOV-1994; 94GB-00023367.
PR  (WELL ) WELLCOME FOUND LTD.
XX
XX  Dev IX, Moore JT, Ohmsted C;
PI  WPI; 1996-268615/27.
XX
XX  N-PSDB; AAT29220.
DR
XX
XX  Molecular chimera for use in enzyme gene therapy - is activated in a
PT  target cell to express a secretable enzyme which cleaves a prodng
PT  outside the cell into a cytotoxic or cyclostatic agent.
XX
XX  Example 3; Page 57-58; 73pp; English.
XX
XX  A secretory beta-lactamase (AAR97619) is expressed from DNA construct
CC  PCMW-BL (AAT29220), in which the beta-lactamase coding sequence is under
CC  the control of the intermediate/early cytomegalovirus promoter. Beta-
CC  lactamase delivery to mammalian cells confers sensitivity to
CC  cephalosporin prodngs. Liposomal DNA/5-fluorouracil prodng combinations
CC  resulted in s.c. tumour regression in mice bearing A549 tumours. Survival
CC  of mice bearing human large cell lung H460 intrathoracic (i.t.) tumours
CC  was increased upon i.t. injection of the secretory beta-lactamase DNA
CC  construct
XX
SQ  Sequence 286 AA:

Query Match      100.0%; Score 1348; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 2e-132;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 HPEITLVKTKDABDQGARVGYIELDLSGKILSFRRPFRPMMSTFVYLCGAVLSRID 60
   |||||
DB  24 HPEITLVKTKDABDQGARVGYIELDLSGKILSFRRPFRPMMSTFVYLCGAVLSRID 83
QY  61 AGOBLGRRIHYSQNDLVEYSPTVEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
   |||||
DB  84 AGOBLGRRIHYSQNDLVEYSPTVEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143
QY  121 KELTAFILNMGDHVTRLDRWEPBELNEAIPNDRDITTMVAMATTLRKLLTGELTLASRQ 180
   |||||
DB  144 KELTAFILNMGDHVTRLDRWEPBELNEAIPNDRDITTMVAMATTLRKLLTGELTLASRQ 203
QY  181 OLIDMEADKVAAGPLIRGALPAGWFIADKSGAGERSGIIIALGPDGKPSRIVIYTTG 240
   |||||
DB  204 OLIDMEADKVAAGPLIRGALPAGWFIADKSGAGERSGIIIALGPDGKPSRIVIYTTG 263
QY  241 SOATMDERNROIABIGASLIRKM 263
   |||||
DB  264 SOATMDERNROIABIGASLIRKM 286
   |||||

RESULT 8
ID  AAR96423 standard; protein; 286 AA.
XX
AC  AAR96423;
XX
DT  25-MAR-2003 (revised)
DT  25-NOV-1996 (first entry)
XX
DE  Cytochrome P450 (CYP1A1 construct).
XX
KW  cytochrome; P450; metallothionein; mouse; human; cytotoxicity; assay;
KW  metabolism.
XX
OS  Homo sapiens.
XX
PM  US5525482-A.
XX
PD  11-JUN-1996.
XX

```

PF 15-NOV-1994; 94US-00339658.
 XX
 PR 27-JUN-1991; 91US-00721775.
 PR 09-DEC-1992; 92US-00990295.
 XX
 PA (UTWA-) UNIV WAYNE STATE.
 XX
 PI Hines RN, Novak RF, States JC;
 XX WPI: 1996-286397/29.
 DR N-PSDB; AAT30354.
 XX
 PT Testing chemicals for cytotoxicity to human by detecting gene damage -
 PT using recombinant fibroblasts transformed with cytochrome P450 gene under
 PT control of inducible promoter.
 XX
 PS Disclosure; Col 17-24; 26pp; English.
 XX
 CC The present sequence is encoded by a chimeric mouse metallothionein-
 CC cytochrome P450Ia1 (CYP1A1) expression construct. Two clones, PRNH127 and
 CC PRNH15, were isolated by different methods and which both had the same
 CC sequence. The CYP1A1 construct is used in assays to test for cytotoxicity
 CC of humans to a chemical. The method comprises exposing human fibroblast
 CC cells normally not including any cytochrome P450 activity to potentially
 CC toxic chemicals. The cells having been transformed to express cytochrome
 CC P450, under the control of a controllable promoter through the CYP1A1
 CC gene, upon exposure to the chemical in vitro. The chemical is metabolised
 CC intracellularly into a cytochrome metabolite by oxidation within the
 CC fibroblasts through the intracellular cytochrome P450 mixed function
 CC oxidase enzymes expressed by the cells. Gene damage in the test cells is
 CC detected as an indication of cytotoxicity of the chemical. (Updated on 25
 CC -MAR-2003 to correct PF field.)
 XX
 SQ Sequence 286 AA;

Query Match 100.0%; Score 1348; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 2e-132;
 Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKQKDEPDGARGVYIELDINSKLTLESFPRPERPMMSTFVLLCGAVLSRID 60
 DB 24 HPEITLVKQKDEPDGARGVYIELDINSKLTLESFPRPERPMMSTFVLLCGAVLSRID 83
 QY 61 AGOGLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGCP 120
 DB 84 AGOGLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGCP 143
 QY 121 KeltaFLHNMGDHYTRLDRWEPELNEAIPNDEBDTTPVMAATTLRKLLTSELTLASRQ 180
 DB 144 KeltaFLHNMGDHYTRLDRWEPELNEAIPNDEBDTTPVMAATTLRKLLTSELTLASRQ 203
 QY 181 QLIIMMEADKYAGPLRLSALPAGWFIADKSGAGRSRGITIALGPDGKPSRIVITYTGG 240
 DB 204 QLIIMMEADKYAGPLRLSALPAGWFIADKSGAGRSRGITIALGPDGKPSRIVITYTGG 263
 QY 241 SQATMDERNROIAGISLIGKM 263
 DB 264 SQATMDERNROIAGISLIGKM 286

RESULT 9
 AAM16635
 ID AAM16635 standard; protein; 286 AA.
 XX
 AC AAM16635;
 XX
 DT 09-AUG-1997 (first entry)
 XX
 DE Beta-lactamase (no signal peptide).
 XX
 KW Gene directed enzyme prodng therapy; GDEPT;
 KW virus directed enzyme prodng therapy; VDEPT; beta-lactamase; cancer;
 KW HIV; inflammation.

XX
 OS Escherichia coli.
 XX
 PN W09719180-A2.
 XX
 PD 29-MAY-1997.
 XX
 PF 19-NOV-1996; 96WO-GB002845.
 XX
 PR 20-NOV-1995; 95GB-00023703.
 XX
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Dev I, Moore JT, Ohmstede C;
 XX WPI: 1997-298117/27.
 DR N-PSDB; AAT66737.
 XX
 PT Molecular chimera for gene or virus directed enzyme prodng therapy -
 PT useful for treatment of cancer, viral infection or inflammation.
 XX
 PS Example; Page 26; 38pp; English.
 XX
 CC Escherichia coli beta-lactamase (AAM16635), lacking the signal peptide,
 CC is the expression product of a molecular chimera, designated PCMV-delBL
 CC (AAT66738), in which the beta-lactamase gene is under control of the CMV
 CC intermediate/early promoter. Vectors consisting of a transcriptional
 CC regulatory DNA sequence linked to a beta-lactamase gene can be used for
 CC enzyme prodng therapy. Intracellular expression of the beta-lactamase in
 CC a targeted cell allows conversion of a prodng into an agent toxic to
 CC the cell for treatment of cancer, viral (e.g. HIV) infection or
 CC inflammation
 XX
 SQ Sequence 286 AA;

Query Match 100.0%; Score 1348; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 2e-132;
 Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKQKDEPDGARGVYIELDINSKLTLESFPRPERPMMSTFVLLCGAVLSRID 60
 DB 24 HPEITLVKQKDEPDGARGVYIELDINSKLTLESFPRPERPMMSTFVLLCGAVLSRID 83
 QY 61 AGOGLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGCP 120
 DB 84 AGOGLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGCP 143
 QY 121 KeltaFLHNMGDHYTRLDRWEPELNEAIPNDEBDTTPVMAATTLRKLLTSELTLASRQ 180
 DB 144 KeltaFLHNMGDHYTRLDRWEPELNEAIPNDEBDTTPVMAATTLRKLLTSELTLASRQ 203
 QY 181 QLIIMMEADKYAGPLRLSALPAGWFIADKSGAGRSRGITIALGPDGKPSRIVITYTGG 240
 DB 204 QLIIMMEADKYAGPLRLSALPAGWFIADKSGAGRSRGITIALGPDGKPSRIVITYTGG 263
 QY 241 SQATMDERNROIAGISLIGKM 263
 DB 264 SQATMDERNROIAGISLIGKM 286

RESULT 10
 AAM18679
 ID AAM18679 standard; protein; 286 AA.
 XX
 AC AAM18679;
 XX
 DT 13-AUG-1997 (first entry)
 XX
 DE Secretory beta-lactamase.
 XX
 KW Prodng therapy; gene directed enzyme prodng therapy; GDEPT;
 KW virus directed enzyme prodng therapy; VDEPT; lung cancer;
 KW beta-lactamase; PCMV-BL.

```
XX Escherichia coli.
OS
XX
XX Key Location/Qualifiers
XX Peptide 1..23
XX FT /label= Sig_peptide
XX FT 24..286
XX Protein /label= Mat_protein
XX
XX WO9719183-A2.
XX
XX 29-MAY-1997.
XX
XX 19-NOV-1996; 96WO-GB002846.
XX
XX 20-NOV-1995; 95GB-00023703.
XX
XX (GLAXO ) GLAXO GROUP LTD.
XX
XX Dev I, Moore JT, Sethna PB;
XX
XX WPI; 1997-298118/27.
XX
XX N-PSDB; AAT70309.
XX
XX DNA construct for gene-directed enzyme prodnrg therapy of lung cancer -
XX comprises lung- or neuroendocrine-specific promoter controlling
XX expression of prodnrg-converting enzyme.
XX
XX Example 811; Page 26-27; 53pp; English.
XX
XX The secreted form (AA018679) of TEM beta-lactamase is expressed by PCMV-
XX BL (AA070309) in which a PCR-amplified beta-lactamase coding sequence is
XX placed under control of the intermediate/early promoter of
XX Cytomegalovirus. Secretory beta-lactamase constructs, placed under
XX control of promoter/enhancer elements of lung- associated protein or
XX neuroendocrine marker protein genes, can be used in novel chimeric
XX molecules for use in prodnrg therapy of lung cancer
XX
XX Sequence 286 AA:
XX
XX Query Match 100.0%; Score 1348; DB 2; Length 286;
XX Best Local Similarity 100.0%; Pred. No. 2e-132;
XX Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 HPEITLVKTKDABDQGAAGVGYIELDLSGKIIIESRPERPRPMSSTFVLLCGAVLSRID 60
XX 24 HPEITLVKTKDABDQGAAGVGYIELDLSGKIIIESRPERPRPMSSTFVLLCGAVLSRID 83
XX
XX 61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP 120
XX 84 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP 143
XX
XX 121 KELTAFILNMGDHYTRLDRWEPBELNEAIPNDRDITMVAATTLRKLLTGELLTLASRQ 180
XX 144 KELTAFILNMGDHYTRLDRWEPBELNEAIPNDRDITMVAATTLRKLLTGELLTLASRQ 203
XX
XX 181 QLIDMMEADKVAAGPLIRGALPAGWFIADKSGAGERSGIIIAALGPDGKPSRIIVITYTG 240
XX 204 QLIDMMEADKVAAGPLIRGALPAGWFIADKSGAGERSGIIIAALGPDGKPSRIIVITYTG 263
XX
XX 241 SOATWDERNRQIAEIGASLIKHW 263
XX 264 SOATWDERNRQIAEIGASLIKHW 266
XX
XX RESULT 11
XX ID AAY08529 standard; protein; 286 AA.
XX AC AAY08529;
XX AC AAY08529;
XX DT 03-AUG-1999 (first entry)
XX
```

```
DE Vector pASK75 beta-1a protein.
XX
XX Firefly; luciferase; tetracycline; transcriptional control; TetR; TetA;
XX tetracycline repressor; tetracycline promoter; luminescence; luxCDABE;
XX insect; Tn10; medicine; dosage; cheese production; antibiotic; foodstuff;
XX allergy.
XX
XX Synthetic.
XX
XX WO9925866-A1.
XX
XX 27-MAY-1999.
XX
XX 11-NOV-1998; 98WO-FI000873.
XX
XX 14-NOV-1997; 97FI-00004235.
XX
XX (KORP/) Korpela M.
XX (KARP/) Karp M.
XX (KURIT/) Kurittu J.
XX
XX Korpela M, Karp M, Kurittu J;
XX
XX WPI; 1999-338015/28.
XX
XX N-PSDB; AAV72418.
XX
XX Assaying for tetracycline using recombinant prokaryotic cells.
XX
XX Disclosure; Page 47-48; 67pp; English.
XX
XX This invention describes a novel tetracycline assay that uses recombinant
XX prokaryotic cells comprising a luciferase gene under the transcriptional
XX control of a tetracycline repressor and tetracycline promoter and
XX involves the detection of luminescence emitted from the cells. The assay
XX can be used to distinguish tetracycline form other microbial agents. The
XX invention also describes a novel plasmid comprising either the luxCDABE
XX genes, a tetracycline repressor (TetR) and a tetracycline promoter (TetA)
XX from Tn10, or the insect luciferase gene, a tetracycline repressor (TetR)
XX and a tetracycline promoter (TetA) from Tn10. The tetracycline assay
XX method can be used for the determination of tetracycline in a sample,
XX e.g. to study the dosage and penetration of the medicine. The method can
XX also be used to test cheese production, as cheese making bacteria are not
XX able to work in the presence of tetracycline. The method can also be used
XX to determine the presence or concentration of antibiotics in foodstuffs,
XX e.g. for allergic people. The present assay method does not rely on the
XX growth of microbes as do conventional tests, and so is much more rapid.
XX The present assay is also more sensitive, as even a small amount of
XX luminescence can be detected
XX
XX Sequence 286 AA:
XX
XX Query Match 100.0%; Score 1348; DB 2; Length 286;
XX Best Local Similarity 100.0%; Pred. No. 2e-132;
XX Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 HPEITLVKTKDABDQGAAGVGYIELDLSGKIIIESRPERPRPMSSTFVLLCGAVLSRID 60
XX 24 HPEITLVKTKDABDQGAAGVGYIELDLSGKIIIESRPERPRPMSSTFVLLCGAVLSRID 83
XX
XX 61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP 120
XX 84 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP 143
XX
XX 121 KELTAFILNMGDHYTRLDRWEPBELNEAIPNDRDITMVAATTLRKLLTGELLTLASRQ 180
XX 144 KELTAFILNMGDHYTRLDRWEPBELNEAIPNDRDITMVAATTLRKLLTGELLTLASRQ 203
XX
XX 181 QLIDMMEADKVAAGPLIRGALPAGWFIADKSGAGERSGIIIAALGPDGKPSRIIVITYTG 240
XX 204 QLIDMMEADKVAAGPLIRGALPAGWFIADKSGAGERSGIIIAALGPDGKPSRIIVITYTG 263
XX
XX 241 SOATWDERNRQIAEIGASLIKHW 263
XX
```

Db 264 SOATMDERNROIAEIGASLICKW 286

RESULT 12
AAB10442
ID AAB10442 standard; protein; 286 AA.
XX
AC AAB10442;
XX
DT 01-DEC-2000 (first entry)
XX
DE Expression vector pSEX15G2 bla protein.
XX
KM Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
KM B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.
XX
OS Synthetic.
XX
PD DE1900635-A1.
XX
PD 13-JUL-2000.
XX
PF 11-JAN-1999; 99DE-01000635.
XX
PR 11-JAN-1999; 99DE-01000635.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Breitling F, Poustka A, Moldenhauer G;
XX
DR WPI; 2000-499832/45.
XX
DR N-PSDB; AAA71430.
XX
PT Selecting monoclonal antibodies, by expressing them on the surface of
PT hybridomas attached to antibody-binding protein, then reaction with
PT antibody library.
XX
PS Claim 16; Fig 3; 22pp; German.
XX
CC This invention describes a novel method for the selection of monoclonal
CC antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma
CC cells to produce antibody-producing hybridomas such that the antibodies
CC are presented at the surface of the hybridomas by an antibody-binding
CC protein (i); and (ii) binding the antibody to antigens (Ag). The
CC invention also describes antibody-binding proteins (i) that comprise a
CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa
CC chain or a murine MHC (major histocompatibility complex) Class I K(k)
CC transmembrane domain of PDGFR (platelet-derived growth factor receptor)
CC or CD52. The method is used to select Mab with specificity for particular
CC antigens. Mab can be selected without separate culture of hybridomas, and
CC selection can be made against many antigens in a library, optionally on
CC the basis of strength of affinity for a particular antigen. Complex
CC mixtures of hybridomas can be used for selection, reducing the time and
CC cost involved in Mab selection. This sequence represents the bla protein
CC protein contained in the expression vector pSEX15G2 which contains the
CC bla protein, Neo-R and protein G described in the method of the invention
XX
SQ Sequence 286 AA;
Query Match 100.0%; Score 1348; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 2e-132;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 HPEITLVKXKADBDQAGAVGYIELDINGSKILIESRPERPMMSTPYVLGAVLSRID 60
OY |||||||
OY 1 HPEITLVKXKADBDQAGAVGYIELDINGSKILIESRPERPMMSTPYVLGAVLSRID 60
Db 24 HPEITLVKXKADBDQAGAVGYIELDINGSKILIESRPERPMMSTPYVLGAVLSRID 83
OY |||||||
OY 61 AGEOIGRRIRHSQNDLVESPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
Db 84 AGOEOIGRRIRHSQNDLVESPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143
OY |||||||
OY 121 KETLAFIHMGDHVTRLDRWEPELNEAIPNBERDTTTPVAAATTLKLLTGELTLTASRQ 180

Db 144 KETLAFIHMGDHVTRLDRWEPELNEAIPNBERDTTTPVAAATTLKLLTGELTLTASRQ 203
OY |||||||
OY 181 QLIDMMEADKVAGPLLSALPAGMFIADKSGAGERSGIIIALGPDGKPSRIYVITYTG 240
Db 204 QLIDMMEADKVAGPLLSALPAGMFIADKSGAGERSGIIIALGPDGKPSRIYVITYTG 263
OY |||||||
OY 241 SOATMDERNROIAEIGASLICKW 263
Db 264 SOATMDERNROIAEIGASLICKW 286

RESULT 13
AAB10438
ID AAB10438 standard; protein; 286 AA.
XX
AC AAB10438;
XX
DT 01-DEC-2000 (first entry)
XX
DE Expression vector pSEX11L4 bla protein.
XX
KM Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
KM B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.
XX
OS Synthetic.
XX
PD DE1900635-A1.
XX
PD 13-JUL-2000.
XX
PF 11-JAN-1999; 99DE-01000635.
XX
PR 11-JAN-1999; 99DE-01000635.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Breitling F, Poustka A, Moldenhauer G;
XX
DR WPI; 2000-499832/45.
XX
DR N-PSDB; AAA71428.
XX
PT Selecting monoclonal antibodies, by expressing them on the surface of
PT hybridomas attached to antibody-binding protein, then reaction with
PT antibody library.
XX
PS Claim 16; Fig 1; 22pp; German.
XX
CC This invention describes a novel method for the selection of monoclonal
CC antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma
CC cells to produce antibody-producing hybridomas such that the antibodies
CC are presented at the surface of the hybridomas by an antibody-binding
CC protein (i); and (ii) binding the antibody to antigens (Ag). The
CC invention also describes antibody-binding proteins (i) that comprise a
CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa
CC chain or a murine MHC (major histocompatibility complex) Class I K(k)
CC transmembrane domain of PDGFR (platelet-derived growth factor receptor)
CC or CD52. The method is used to select Mab with specificity for particular
CC antigens. Mab can be selected without separate culture of hybridomas, and
CC selection can be made against many antigens in a library, optionally on
CC the basis of strength of affinity for a particular antigen. Complex
CC mixtures of hybridomas can be used for selection, reducing the time and
CC cost involved in Mab selection. This sequence represents the Neo-R
CC protein contained in the expression vector pSEX11L4 which contains the
CC bla protein, Neo-R and protein G described in the method of the invention
XX
SQ Sequence 286 AA;
Query Match 100.0%; Score 1348; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 2e-132;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVAEDQAGARVGYIELDLSNGKILSFREPERPPMSTFKVLLCGAVLSRID 60
 DB 24 HPEITLVKVAEDQAGARVGYIELDLSNGKILSFREPERPPMSTFKVLLCGAVLSRID 83
 QY 61 AGQQLGRRIHYSQNDLVEYSPTVEKHLTDGMTVELCSAAITMSDNTAANLLTTIGSP 120
 DB 84 AGQQLGRRIHYSQNDLVEYSPTVEKHLTDGMTVELCSAAITMSDNTAANLLTTIGSP 143
 QY 121 KELTAFILNMGDHYTRLDRWEPELNEAIPNDERDTMPVAMATTLRKLLTGELTLASRQ 180
 DB 144 KELTAFILNMGDHYTRLDRWEPELNEAIPNDERDTMPVAMATTLRKLLTGELTLASRQ 203
 QY 181 QLIDMEADKVAAGPLLRSGALPAGWFIADKSGAGRSRGITIALGPDGKPSRIVVIYTTG 240
 DB 204 QLIDMEADKVAAGPLLRSGALPAGWFIADKSGAGRSRGITIALGPDGKPSRIVVIYTTG 263
 QY 241 SQATMDERNRQIAEIGASLIRKM 263
 DB 264 SQATMDERNRQIAEIGASLIRKM 286

RESULT 14
 AAB10440
 ID AAB10440 standard; protein; 286 AA.
 AC AAB10440;
 XX 01-DEC-2000 (first entry)
 XX
 DE Expression vector pSEX11G2 bla protein.
 XX
 KM Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
 KM B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.
 XX
 OS Synthetic.
 PN DE1900635-A1.
 PD 13-JUL-2000.
 PF 11-JAN-1999; 99DE-01000635.
 PR 11-JAN-1999; 99DE-01000635.
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 PI Breitling F, Poustka A, Moldenhauer G;
 XX MPI; 2000-499832/45.
 DR N-PSDB; AAA71429.
 PT Selecting monoclonal antibodies, by expressing them on the surface of
 PT hybridomas attached to antibody-binding protein, then reaction with
 PT antibody library.
 XX
 PS Claim 16; Fig 2; 22pp; German.

CC This invention describes a novel method for the selection of monoclonal
 CC antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma
 CC cells to produce antibody-producing hybridomas such that the antibodies
 CC are presented at the surface of the hybridomas by an antibody-binding
 CC protein (I); and (ii) binding the antibody to antigens (Ag). The
 CC invention also describes antibody-binding proteins (I) that comprise a
 CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa
 CC chain or a murine MHC (major histocompatibility complex) Class I k(k)
 CC molecule; an antibody-binding site of proteins A, G, I or Ig, and the
 CC transmembrane domain of PDGFR (platelet-derived growth factor receptor)
 CC or CD52. The method is used to select Mab with specificity for particular
 CC antigens. Mab can be selected without separate culture of hybridomas, and
 CC selection can be made against many antigens in a library, optionally on
 CC the basis of strength of affinity for a particular antigen. Complex
 CC mixtures of hybridomas can be used for selection, reducing the time and
 CC cost involved in Mab selection. This sequence represents the bla protein

CC protein contained in the expression vector pSEX11G2 which contains the
 CC bla protein, Neo-R and protein G described in the method of the invention
 CC
 SQ Sequence 286 AA;
 Query Match 100.0%; Score 1348; DB 3; Length 286;
 Best Local Similarity 100.0%; Pred. No. 2e-132;
 Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVAEDQAGARVGYIELDLSNGKILSFREPERPPMSTFKVLLCGAVLSRID 60
 DB 24 HPEITLVKVAEDQAGARVGYIELDLSNGKILSFREPERPPMSTFKVLLCGAVLSRID 83
 QY 61 AGQQLGRRIHYSQNDLVEYSPTVEKHLTDGMTVELCSAAITMSDNTAANLLTTIGSP 120
 DB 84 AGQQLGRRIHYSQNDLVEYSPTVEKHLTDGMTVELCSAAITMSDNTAANLLTTIGSP 143
 QY 121 KELTAFILNMGDHYTRLDRWEPELNEAIPNDERDTMPVAMATTLRKLLTGELTLASRQ 180
 DB 144 KELTAFILNMGDHYTRLDRWEPELNEAIPNDERDTMPVAMATTLRKLLTGELTLASRQ 203
 QY 181 QLIDMEADKVAAGPLLRSGALPAGWFIADKSGAGRSRGITIALGPDGKPSRIVVIYTTG 240
 DB 204 QLIDMEADKVAAGPLLRSGALPAGWFIADKSGAGRSRGITIALGPDGKPSRIVVIYTTG 263
 QY 241 SQATMDERNRQIAEIGASLIRKM 263
 DB 264 SQATMDERNRQIAEIGASLIRKM 286

RESULT 15
 AAB50898
 ID AAB50898 standard; protein; 286 AA.
 AC AAB50898;
 XX 20-MAR-2001 (first entry)
 XX
 DE Protein encoded by bla resistance marker of integration vector pLO12306.
 XX
 KM bla resistance marker; recombinant host cell; saccharification;
 KM fermentation; polysaccharase; oligosaccharide degradation; celz gene;
 KM glucanase; integration vector; pLO12306.
 XX
 OS Unidentified.
 PN WO200071729-A2.
 PD 30-NOV-2000.
 PF 26-MAY-2000; 2000WO-US014773.
 PR 26-MAY-1999; 99US-0136376P.
 PA (UVFL) UNIV FLORIDA RRS POUND.
 PI Ingram LO, Zhou S;
 XX MPI; 2001-032043/04.
 DR N-PSDB; AAC91455.
 PT Recombinant host cells useful for producing polysaccharase for degrading
 PT polysaccharides, comprises a first heterologous polynucleotide encoding
 PS polysaccharase under control of surrogate promoter.
 XX
 PS Disclosure; Page 82-83; 87pp; English.

CC The present sequence is given in a specification relating to a
 CC recombinant host cell suitable for simultaneous saccharification and
 CC fermentation. The host cell contains at least one heterologous
 CC polynucleotide encoding a polysaccharase under the transcriptional
 CC control of a surrogate promoter capable of increasing expression of the
 CC polysaccharase. The host cell also contains a second heterologous

CC polynucleotide encoding a secretory polypeptide to facilitate the
 CC secretion of the expressed polysaccharase. The recombinant host cell is
 CC useful for producing polysaccharase which is useful for enzymatically
 CC degrading oligosaccharides such as lignocellulose, hemicellulose,
 CC cellulose, pectin or their combinations, and fermenting the product to
 CC ethanol, by simultaneous saccharification and fermentation processes. The
 CC present sequence is encoded by an integration vector which was introduced
 CC into cells to generate recombinant host cells. The vector contains a
 CC surrogate promoter from *Zymomonas mobilis*, the *celZ* gene from *Erwinia*
 CC *chrysanthemi*, resistance markers *bla* and *tet*, and *Klebsiella oxytoca*
 CC target sequence

XX Sequence 286 AA;

Query Match 100.0%; Score 1348; DB 4; Length 286;

Best Local Similarity 100.0%; Pred. No. 2e-132;

Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	HPETLVKVKDAEDQLGARVGYIELDLNSGKILDSFRPRERFPMWSIFKYLICGAVLSRID	60
Db	24	HPETLVKVKDAEDQLGARVGYIELDLNSGKILDSFRPRERFPMWSIFKYLICGAVLSRID	83
Qy	61	AGQEQIGRRIRYSQNDLVEISPTVEKHLTDGWTVAELCSAIIYMSDNTANILITIGSP	120
Db	84	AGQEQIGRRIRYSQNDLVEISPTVEKHLTDGWTVAELCSAIIYMSDNTANILITIGSP	143
Qy	121	KELTAFLHNMGDHYTRLDRMEPELNEALPNDESDITMPVAMATTLRKLTGELLTASRQ	180
Db	144	KELTAFLHNMGDHYTRLDRMEPELNEALPNDESDITMPVAMATTLRKLTGELLTASRQ	203
Qy	181	QLIDWMEADKVAGPLLRGSLPAGWFIADKSGAGERSRGIITIALGPDGKPSRIIVITYTG	240
Db	204	QLIDWMEADKVAGPLLRGSLPAGWFIADKSGAGERSRGIITIALGPDGKPSRIIVITYTG	263
Qy	241	SOATMDERNROIARIASLIRHW	263
Db	264	SOATMDERNROIARIASLIRHW	286

Search completed: June 10, 2005, 10:49:09
 Job time : 103.972 secs

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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:36:31 ; Search time 26.9646 Seconds
(without alignments)
728.091 Million cell updates/sec

Title: US-10-668-778-2

Perfect score: 1348
Sequence: 1 HPEITLVKVDADQUGARVGV.....TMDERNRQIAETGASLIRHW 263

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCITUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1348	100.0	286	1	US-07-721-775A-2	Sequence 2, Appl
2	1348	100.0	286	1	US-08-339-658-2	Sequence 2, Appl
3	1348	100.0	286	3	US-09-263-933-7	Sequence 7, Appl
4	1348	100.0	286	3	US-09-263-933-14	Sequence 14, Appl
5	1348	100.0	286	3	US-09-263-933-21	Sequence 21, Appl
6	1348	100.0	286	3	US-09-025-769B-265	Sequence 265, App
7	1348	100.0	286	3	US-09-025-769B-362	Sequence 362, App
8	1348	100.0	286	4	US-09-919-901-7	Sequence 7, Appl
9	1348	100.0	286	4	US-09-919-901-14	Sequence 14, Appl
10	1348	100.0	286	4	US-09-919-901-21	Sequence 21, Appl
11	1348	100.0	286	4	US-09-490-070A-265	Sequence 265, App
12	1348	100.0	286	4	US-09-490-070A-362	Sequence 362, App
13	1348	100.0	286	4	US-09-490-153-265	Sequence 265, App
14	1348	100.0	286	4	US-09-490-153-362	Sequence 362, App
15	1348	100.0	286	4	US-10-191-966-7	Sequence 7, Appl
16	1348	100.0	286	4	US-10-191-966-14	Sequence 14, Appl
17	1348	100.0	286	4	US-10-191-966-21	Sequence 21, Appl
18	1348	100.0	286	4	US-09-490-324-265	Sequence 265, App
19	1348	100.0	286	4	US-09-490-324-362	Sequence 362, App
20	1348	100.0	286	3	US-09-025-769B-285	Sequence 285, App
21	1348	100.0	286	3	US-09-025-769B-298	Sequence 298, App
22	1348	100.0	286	3	US-09-025-769B-300	Sequence 300, App
23	1348	100.0	286	4	US-09-490-070A-285	Sequence 285, App
24	1348	100.0	286	4	US-09-490-070A-298	Sequence 298, App
25	1348	100.0	286	4	US-09-490-070A-300	Sequence 300, App
26	1348	100.0	286	4	US-09-490-153-285	Sequence 285, App
27	1348	100.0	286	4	US-09-490-153-298	Sequence 298, App

28	1348	100.0	286	4	US-09-490-153-300	Sequence 300, App
29	1348	100.0	286	4	US-09-490-324-285	Sequence 285, App
30	1348	100.0	286	4	US-09-490-324-298	Sequence 298, App
31	1348	100.0	286	4	US-09-490-324-300	Sequence 300, App
32	1348	100.0	286	3	US-09-263-933-2	Sequence 2, Appl
33	1348	100.0	286	3	US-09-263-933-9	Sequence 9, Appl
34	1348	100.0	286	3	US-09-263-933-16	Sequence 16, Appl
35	1348	100.0	286	4	US-09-919-901-2	Sequence 2, Appl
36	1348	100.0	286	4	US-09-919-901-9	Sequence 9, Appl
37	1348	100.0	286	4	US-09-919-901-16	Sequence 16, Appl
38	1348	100.0	286	4	US-10-191-966-2	Sequence 2, Appl
39	1348	100.0	286	4	US-10-191-966-9	Sequence 9, Appl
40	1348	100.0	286	4	US-10-191-966-16	Sequence 16, Appl
41	1347	99.9	286	4	US-09-555-510B-9	Sequence 9, Appl
42	1347	99.9	286	4	US-10-231-013-9	Sequence 9, Appl
43	1347	99.9	1293	4	US-09-170-496D-292	Sequence 292, App
44	1347	99.9	1293	4	US-09-364-425B-57	Sequence 57, Appl
45	1343	99.6	263	1	US-08-407-544-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-07-721-775A-2

Sequence 2, Application US/07721775A

Patent No. 5180666

GENERAL INFORMATION:

APPLICANT: States, J. Christopher

APPLICANT: Hines, Ronald N.

TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING

TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESSES:

ADDRESSES: Relating, Echington, Barnard, Perry & Milton

STREET: P.O. Box 4390

CITY: Troy

STATE: Michigan

COUNTRY: U.S.A.

ZIP: 48099

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07721,775A

FILING DATE: 19910627

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Kohn, Kenneth I.

REGISTRATION NUMBER: 30, 955

REFERENCE/DOCKET NUMBER: P-321WSU

TELECOMMUNICATION INFORMATION:

TELEPHONE: (313) 689-3554

TELEFAX: (313) 689-4071

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 286 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-721-775A-2

Query Match 100.0%, Score 1348, DB 1, Length 286;
Best local Similarity 100.0%, Pred. No. 5.2e-141;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQUGARVGVTELDNGSKILIESRPFPMSTFKVLGAVLSRD 60
DB 24 HPEITLVKVDADQUGARVGVTELDNGSKILIESRPFPMSTFKVLGAVLSRD 83

QY 61 AGOBLGRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGP 120
DB 84 AGOBLGRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGP 143
QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDERDTMPVAMATTLRKLLTGELLTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWEPELNEAIPNDERDTMPVAMATTLRKLLTGELLTLASRQ 203
QY 181 QLIDWMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVITYTG 240
DB 204 QLIDWMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVITYTG 263
QY 241 SOATMDERNROIAETIGASLIRHW 263
DB 264 SOATMDERNROIAETIGASLIRHW 286

RESULT 2

US-08-339-658-2
; Sequence 2, Application US/08339658
; Patent No. 5525482

; GENERAL INFORMATION:
; APPLICANT: States, J. Christopher
; APPLICANT: Hines, Ronald N.
; APPLICANT: No. 5525482ak, Raymond F.
; TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
; TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard, Perry & Milton
; STREET: P. O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: U.S.A.
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339, 658
; FILING DATE: 15-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,295
; FILING DATE: 09-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-321MSU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (313) 689-3554
; TELEFAX: (313) 689-4071
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-339-658-2

Query Match 100.0%; Score 1348; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.2e-141;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELTVKVDADQAGRVGYIELDINSKILSFRRPERPMMSTFKVLLCGAVLSRID 60
DB 24 HPELTVKVDADQAGRVGYIELDINSKILSFRRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGOBLGRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGP 120
DB 84 AGOBLGRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGP 143

QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDERDTMPVAMATTLRKLLTGELLTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWEPELNEAIPNDERDTMPVAMATTLRKLLTGELLTLASRQ 203
QY 181 QLIDWMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVITYTG 240
DB 204 QLIDWMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVITYTG 263
QY 241 SOATMDERNROIAETIGASLIRHW 263
DB 264 SOATMDERNROIAETIGASLIRHW 286

RESULT 3

US-09-263-933-7
; Sequence 7, Application US/09263933
; Patent No. 6280940

; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/263,933
; CURRENT FILING DATE: 1999-03-08
; EARLIER FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; US-09-263-933-7

Query Match 100.0%; Score 1348; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.2e-141;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELTVKVDADQAGRVGYIELDINSKILSFRRPERPMMSTFKVLLCGAVLSRID 60
DB 24 HPELTVKVDADQAGRVGYIELDINSKILSFRRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGOBLGRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGP 120
DB 84 AGOBLGRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGP 143
QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDERDTMPVAMATTLRKLLTGELLTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWEPELNEAIPNDERDTMPVAMATTLRKLLTGELLTLASRQ 203
QY 181 QLIDWMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVITYTG 240
DB 204 QLIDWMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVITYTG 263
QY 241 SOATMDERNROIAETIGASLIRHW 263
DB 264 SOATMDERNROIAETIGASLIRHW 286

RESULT 4
US-09-263-933-14
; Sequence 14, Application US/09263933
; Patent No. 6280940

; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A

;; CURRENT APPLICATION NUMBER: US/09/263,933
;; CURRENT FILING DATE: 1999-03-08
;; EARLIER APPLICATION NUMBER: 09/129,611
;; EARLIER FILING DATE: 1998-08-05
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 14
;; LENGTH: 286
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
US-09-263-933-14

Query Match 100.0%; Score 1348; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.2e-141;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGAVGYIELDLSGKILSFPERPFPMSSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKVDADQAGAVGYIELDLSGKILSFPERPFPMSSTFKVLLCGAVLSRID 83
QY 61 AGQEQIGRIHYSQNDLVEYSPTVEKHLTDGATVRELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQEQIGRIHYSQNDLVEYSPTVEKHLTDGATVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDTTVPVAMATTLRKLLTGELLTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDTTVPVAMATTLRKLLTGELLTLASRQ 203
QY 181 QLIDWMEADKVAGPILRSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 240
DB 204 QLIDWMEADKVAGPILRSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 263
QY 241 SOATMDERNRQIAETGASLIRKM 263
DB 264 SOATMDERNRQIAETGASLIRKM 286

RESULT 5
US-09-263-933-21
;; Sequence 21, Application US/09263933
;; Patent No. 6280940
;; GENERAL INFORMATION:
;; APPLICANT: Potts, Karen E.
;; APPLICANT: Jackson, Roberta L.
;; APPLICANT: Patrick, Amy K.
;; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
;; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
;; FILE REFERENCE: 0125-0005A
;; CURRENT APPLICATION NUMBER: US/09/263,933
;; CURRENT FILING DATE: 1999-03-08
;; EARLIER APPLICATION NUMBER: 09/129,611
;; EARLIER FILING DATE: 1998-08-05
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 21
;; LENGTH: 286
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
US-09-263-933-21

Query Match 100.0%; Score 1348; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.2e-141;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEITLVKVDADQAGAVGYIELDLSGKILSFPERPFPMSSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKVDADQAGAVGYIELDLSGKILSFPERPFPMSSTFKVLLCGAVLSRID 83
QY 61 AGQEQIGRIHYSQNDLVEYSPTVEKHLTDGATVRELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQEQIGRIHYSQNDLVEYSPTVEKHLTDGATVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDTTVPVAMATTLRKLLTGELLTLASRQ 180

DB 144 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDTTVPVAMATTLRKLLTGELLTLASRQ 203
QY 181 QLIDWMEADKVAGPILRSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 240
DB 204 QLIDWMEADKVAGPILRSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 263
QY 241 SOATMDERNRQIAETGASLIRKM 263
DB 264 SOATMDERNRQIAETGASLIRKM 286

RESULT 6
US-09-025-769B-265
;; Sequence 265, Application US/09025769B
;; Patent No. 630064
;; GENERAL INFORMATION:
;; APPLICANT: Knappik, Achim
;; APPLICANT: Pack, Peter
;; APPLICANT: 11ag, Vic
;; APPLICANT: Ge, Liming
;; APPLICANT: Moroney, Simon
;; APPLICANT: Plueckthum, Andreas
;; TITLE OF INVENTION: Protein/(Poly)peptide libraries
;; NUMBER OF SEQUENCES: 373
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;; STREET: 1251 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10021
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/025,769B
;; FILING DATE: 18-FEB-1998
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: EP 95 11 3021.0
;; FILING DATE: 18-AUG-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: James F. Haley, Jr., Esq.
;; REGISTRATION NUMBER: 27,794
;; REFERENCE/DOCKET NUMBER: MORPHO/5
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212)596-9000
;; TELEFAX: (212)596-9090
;; INFORMATION FOR SEQ ID NO: 265:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 286 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-025-769B-265

Query Match 100.0%; Score 1348; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.2e-141;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEITLVKVDADQAGAVGYIELDLSGKILSFPERPFPMSSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKVDADQAGAVGYIELDLSGKILSFPERPFPMSSTFKVLLCGAVLSRID 83
QY 61 AGQEQIGRIHYSQNDLVEYSPTVEKHLTDGATVRELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQEQIGRIHYSQNDLVEYSPTVEKHLTDGATVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDTTVPVAMATTLRKLLTGELLTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDTTVPVAMATTLRKLLTGELLTLASRQ 203

QY 181 OLIDMMEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDKPSRIVIVYTTG 240
DB 204 OLIDMMEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDKPSRIVIVYTTG 263
QY 241 SOATWDERNRQIAETIGASLIRKM 263
DB 264 SOATWDERNRQIAETIGASLIRKM 286

RESULT 7

US-09-025-769B-362
; Sequence 362, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilaq, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 362:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-362

Query Match 100.0%; Score 1348; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.2e-141;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGVGYIELDLSGKILESFRPERPMMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKVKADBDQAGVGYIELDLSGKILESFRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGCP 120
DB 84 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGCP 143
QY 121 KELTAFILNMGDHYTRLDRWEPELNEALPNDERDTMPVAMATTLRKLLTSELTLASRQ 180
DB 144 KELTAFILNMGDHYTRLDRWEPELNEALPNDERDTMPVAMATTLRKLLTSELTLASRQ 203
QY 181 OLIDMMEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDKPSRIVIVYTTG 240

DB 204 OLIDMMEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDKPSRIVIVYTTG 263
QY 241 SOATWDERNRQIAETIGASLIRKM 263
DB 264 SOATWDERNRQIAETIGASLIRKM 286

RESULT 8

US-09-919-901-7
; Sequence 7, Application US/09919901
; Patent No. 6599738
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT FILING DATE: 2001-08-02
; PRIOR FILING DATE: 1999-02-08
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-09-919-901-7

Query Match 100.0%; Score 1348; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.2e-141;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGVGYIELDLSGKILESFRPERPMMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKVKADBDQAGVGYIELDLSGKILESFRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGCP 120
DB 84 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGCP 143
QY 121 KELTAFILNMGDHYTRLDRWEPELNEALPNDERDTMPVAMATTLRKLLTSELTLASRQ 180
DB 144 KELTAFILNMGDHYTRLDRWEPELNEALPNDERDTMPVAMATTLRKLLTSELTLASRQ 203
QY 181 OLIDMMEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDKPSRIVIVYTTG 240
DB 204 OLIDMMEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDKPSRIVIVYTTG 263
QY 241 SOATWDERNRQIAETIGASLIRKM 263
DB 264 SOATWDERNRQIAETIGASLIRKM 286

RESULT 9

US-09-919-901-14
; Sequence 14, Application US/09919901
; Patent No. 6599738
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02

PRIOR APPLICATION NUMBER: 09/263, 933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129, 611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO: 14
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-09-919-901-14

Query Match 100.0%; Score 1348; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.2e-141;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVDADQAGARVGYIELDLSGKILSFPRPERFPMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVDADQAGARVGYIELDLSGKILSFPRPERFPMSTFKVLLCGAVLSRID 83
QY 61 AGQEQGRIRHYSQNDLYEVSPTVEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQEQGRIRHYSQNDLYEVSPTVEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDREPELNEAIPNDERDTTMAPVAMATTIRKLLTGEILTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDREPELNEAIPNDERDTTMAPVAMATTIRKLLTGEILTLASRQ 203
QY 181 QIIDWMEADKVAQPLIRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 240
DB 204 QIIDWMEADKVAQPLIRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 263
QY 241 SQATWDERNRQIAETGASLIKHW 263
DB 264 SQATWDERNRQIAETGASLIKHW 286

RESULT 10
US-09-919-901-21
Sequence 21, Application US/09919901
Patent No. 6599738
GENERAL INFORMATION:
APPLICANT: Potes, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919, 901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263, 933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129, 611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO: 21
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-09-919-901-21

Query Match 100.0%; Score 1348; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.2e-141;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVDADQAGARVGYIELDLSGKILSFPRPERFPMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVDADQAGARVGYIELDLSGKILSFPRPERFPMSTFKVLLCGAVLSRID 83

QY 61 AGQEQGRIRHYSQNDLYEVSPTVEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQEQGRIRHYSQNDLYEVSPTVEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDREPELNEAIPNDERDTTMAPVAMATTIRKLLTGEILTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDREPELNEAIPNDERDTTMAPVAMATTIRKLLTGEILTLASRQ 203
QY 181 QIIDWMEADKVAQPLIRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 240
DB 204 QIIDWMEADKVAQPLIRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 263
QY 241 SQATWDERNRQIAETGASLIKHW 263
DB 264 SQATWDERNRQIAETGASLIKHW 286

RESULT 11
US-09-490-070A-265
Sequence 265, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pach, Peter
Ilaq, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSER: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & Mcauliffe
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490, 070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31, 298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-09-490-070A-265

Query Match 100.0%; Score 1348; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.2e-141;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVDADQAGARVGYIELDLSGKILSFPRPERFPMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVDADQAGARVGYIELDLSGKILSFPRPERFPMSTFKVLLCGAVLSRID 83

QY 61 AGOELGRIRHYSONDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGCP 120
DB 84 AGOELGRIRHYSONDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGCP 143
QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDPTTVPVAMATTLRKLLTGELLTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDPTTVPVAMATTLRKLLTGELLTLASRQ 203
QY 181 OLIMMEADKXAGPLRLRSLPAGWFIADKSGAGRGSGIITAAIGDPGKPSRIVITYTTG 240
DB 204 OLIMMEADKXAGPLRLRSLPAGWFIADKSGAGRGSGIITAAIGDPGKPSRIVITYTTG 263
QY 241 SOATMDERNROIAEIGASLIRKM 263
DB 264 SOATMDERNROIAEIGASLIRKM 286

RESULT 12

US-09-490-070A-362
Sequence 362, Application US/09490070A

Patent No. 6696248

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Pack, Peter

Ilaq, Vic

Ge, Liming

Moreney, Simon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman

White & McLaughlin

STREET: 1666 K Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,070A

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Colin G. Sandercock, Esq.

REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 37629-0005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 912-2000

TELEFAX: (202) 912-2020

INFORMATION FOR SEQ ID NO: 362:

SEQUENCE CHARACTERISTICS:

LENGTH: 286 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 362:

US-09-490-070A-362

Query Match

Best Local Similarity 100.0%; Score 1348; DB 4; Length 286;

Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKXDAEDQAGRVGYTELDLNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60

DB 24 HPEITLVKXDAEDQAGRVGYTELDLNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83

QY 61 AGOELGRIRHYSONDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGCP 120
DB 84 AGOELGRIRHYSONDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGCP 143
QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDPTTVPVAMATTLRKLLTGELLTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDPTTVPVAMATTLRKLLTGELLTLASRQ 203
QY 181 OLIMMEADKXAGPLRLRSLPAGWFIADKSGAGRGSGIITAAIGDPGKPSRIVITYTTG 240
DB 204 OLIMMEADKXAGPLRLRSLPAGWFIADKSGAGRGSGIITAAIGDPGKPSRIVITYTTG 263
QY 241 SOATMDERNROIAEIGASLIRKM 263
DB 264 SOATMDERNROIAEIGASLIRKM 286

RESULT 13

US-09-490-153-265
Sequence 265, Application US/09490153

Patent No. 6706484

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Pack, Peter

Ilaq, Vic

Ge, Liming

Moreney, Simon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,153

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 596-9000

TELEFAX: (212) 596-9090

INFORMATION FOR SEQ ID NO: 265:

SEQUENCE CHARACTERISTICS:

LENGTH: 286 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 265:

US-09-490-153-265

Query Match

Best Local Similarity 100.0%; Score 1348; DB 4; Length 286;

Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKXDAEDQAGRVGYTELDLNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60

DB 24 HPEITLVKXDAEDQAGRVGYTELDLNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83

Db 24 HPE TLVVKVADBDQAGARVGYIELDLSGKILSFRRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGQEBQGRIRIHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGCP 120
Db 84 AGQEBQGRIRIHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGCP 143
QY 121 KELTAFLLNMGDHYTRLDRWPELNEALPNDERDTTVPVAAATTIRKLLTGELTLASRQ 180
Db 144 KELTAFLLNMGDHYTRLDRWPELNEALPNDERDTTVPVAAATTIRKLLTGELTLASRQ 203
QY 181 QLIIDWMEADKVAGPLLRSLPAGWFIADKSGAGERSGIIIALGPDGKPSRIIVITYTG 240
Db 204 QLIIDWMEADKVAGPLLRSLPAGWFIADKSGAGERSGIIIALGPDGKPSRIIVITYTG 263
QY 241 SOATMDERNRQIAETGASLIRKM 263
Db 264 SOATMDERNRQIAETGASLIRKM 286

RESULT 14
US-09-490-153-362

; Sequence 362, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Haag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESS: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 362:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 362:
US-09-490-153-362

Query Match 100.0%; Score 1348; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.2e-141;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPE TLVVKVADBDQAGARVGYIELDLSGKILSFRRPERPMMSTFKVLLCGAVLSRID 60

Db 24 HPE TLVVKVADBDQAGARVGYIELDLSGKILSFRRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGQEBQGRIRIHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGCP 120
Db 84 AGQEBQGRIRIHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGCP 143
QY 121 KELTAFLLNMGDHYTRLDRWPELNEALPNDERDTTVPVAAATTIRKLLTGELTLASRQ 180
Db 144 KELTAFLLNMGDHYTRLDRWPELNEALPNDERDTTVPVAAATTIRKLLTGELTLASRQ 203
QY 181 QLIIDWMEADKVAGPLLRSLPAGWFIADKSGAGERSGIIIALGPDGKPSRIIVITYTG 240
Db 204 QLIIDWMEADKVAGPLLRSLPAGWFIADKSGAGERSGIIIALGPDGKPSRIIVITYTG 263
QY 241 SOATMDERNRQIAETGASLIRKM 263
Db 264 SOATMDERNRQIAETGASLIRKM 286

RESULT 15

US-10-191-966-7
; Sequence 7, Application US/10191966
; Patent No. 6790612
; GENERAL INFORMATION:
; APPLICANT: Potes, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-7

Query Match 100.0%; Score 1348; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.2e-141;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPE TLVVKVADBDQAGARVGYIELDLSGKILSFRRPERPMMSTFKVLLCGAVLSRID 60
Db 24 HPE TLVVKVADBDQAGARVGYIELDLSGKILSFRRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGQEBQGRIRIHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGCP 120
Db 84 AGQEBQGRIRIHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGCP 143
QY 121 KELTAFLLNMGDHYTRLDRWPELNEALPNDERDTTVPVAAATTIRKLLTGELTLASRQ 180
Db 144 KELTAFLLNMGDHYTRLDRWPELNEALPNDERDTTVPVAAATTIRKLLTGELTLASRQ 203
QY 181 QLIIDWMEADKVAGPLLRSLPAGWFIADKSGAGERSGIIIALGPDGKPSRIIVITYTG 240
Db 204 QLIIDWMEADKVAGPLLRSLPAGWFIADKSGAGERSGIIIALGPDGKPSRIIVITYTG 263
QY 241 SOATMDERNRQIAETGASLIRKM 263
Db 264 SOATMDERNRQIAETGASLIRKM 286

Search completed: June 10, 2005, 11:01:13

Fri Jun 10 14:22:56 2005

us-10-668-778-2.rat

Page 8

Job time : 27.9646 secs

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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:36:31 ; Search time 15.2765 Seconds

(without alignments)
728.091 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_149

Perfect score: 770
Sequence: 1 HPELVKVKADBDQAGARVG.....MGDHYTRDRKPELNEAIP 149

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 7464964 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents AA:*

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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
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5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	770	100.0	286	1	US-07-721-775A-2
2	770	100.0	286	1	US-08-339-658-2
3	770	100.0	286	3	US-09-263-933-7
4	770	100.0	286	3	US-09-263-933-14
5	770	100.0	286	3	US-09-263-933-21
6	770	100.0	286	3	US-09-025-769B-265
7	770	100.0	286	3	US-09-025-769B-362
8	770	100.0	286	4	US-09-919-901-7
9	770	100.0	286	4	US-09-919-901-14
10	770	100.0	286	4	US-09-919-901-21
11	770	100.0	286	4	US-09-490-070A-265
12	770	100.0	286	4	US-09-490-070A-362
13	770	100.0	286	4	US-09-490-153-265
14	770	100.0	286	4	US-09-490-153-362
15	770	100.0	286	4	US-10-191-966-7
16	770	100.0	286	4	US-10-191-966-14
17	770	100.0	286	4	US-10-191-966-21
18	770	100.0	286	4	US-09-490-324-265
19	770	100.0	286	4	US-09-490-324-362
20	770	100.0	286	4	US-09-025-769B-285
21	770	100.0	286	4	US-09-025-769B-298
22	770	100.0	286	4	US-09-025-769B-300
23	770	100.0	286	4	US-09-490-070A-285
24	770	100.0	286	4	US-09-490-070A-298
25	770	100.0	286	4	US-09-490-070A-300
26	770	100.0	286	4	US-09-490-153-285
27	770	100.0	286	4	US-09-490-153-298

28	770	100.0	299	4	US-09-490-153-300	Sequence 300, App
29	770	100.0	299	4	US-09-490-324-285	Sequence 285, App
30	770	100.0	299	4	US-09-490-324-298	Sequence 298, App
31	770	100.0	299	4	US-09-490-324-300	Sequence 300, App
32	770	100.0	2307	3	US-09-263-933-2	Sequence 2, Appl1
33	770	100.0	2307	3	US-09-263-933-9	Sequence 9, Appl1
34	770	100.0	2307	3	US-09-263-933-16	Sequence 16, Appl1
35	770	100.0	2307	4	US-09-919-901-2	Sequence 2, Appl1
36	770	100.0	2307	4	US-09-919-901-9	Sequence 9, Appl1
37	770	100.0	2307	4	US-09-919-901-16	Sequence 16, Appl1
38	770	100.0	2307	4	US-10-191-966-2	Sequence 2, Appl1
39	770	100.0	2307	4	US-10-191-966-9	Sequence 9, Appl1
40	770	100.0	2307	4	US-10-191-966-16	Sequence 16, Appl1
41	769	99.9	263	1	US-08-407-544-2	Sequence 2, Appl1
42	769	99.9	265	2	US-08-719-697-2	Sequence 2, Appl1
43	769	99.9	265	3	US-08-727-616A-2	Sequence 2, Appl1
44	769	99.9	265	4	US-09-481-756-2	Sequence 2, Appl1
45	769	99.9	286	2	US-08-719-697-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-07-721-775A-2
; Sequence 2, Application US/07721775A
; Patent No. 5180666
; GENERAL INFORMATION:
; APPLICANT: States, J. Christopher
; APPLICANT: Hines, Ronald N.
; APPLICANT: No. 5180666ak, Raymond F.
; TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
; TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Relating, Ethington, Barnard, Perry & Milton
; STREET: P. O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: U.S.A.
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07721,775A
; FILING DATE: 19910627
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-321WSU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (313) 689-3554
; TELEFAX: (313) 689-4071
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-721-775A-2

Query Match 100.0%; Score 770; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.98-84;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADBDQAGARVGIIEDLNSGKILSFRRPRPPMSTFVLLCGAVLSRID 60
DB 24 HPELVKVKADBDQAGARVGIIEDLNSGKILSFRRPRPPMSTFVLLCGAVLSRID 83

Qy 61 AGOBOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120
Db 84 AGOBOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 143
Qy 121 KETLAFHNMGDHVTRLDRMEPELNEAIP 149
Db 144 KETLAFHNMGDHVTRLDRMEPELNEAIP 172

RESULT 2

US-08-339-658-2
Sequence 2, Application US/08339658
Patent No. 5525482
GENERAL INFORMATION:
APPLICANT: States, J. Christopher
APPLICANT: Hines, Ronald N.
APPLICANT: No. 5525482ak, Raymond F.
TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
NUMBER OF SEQUENCES: 2
MUTAGENICITY OF A CHEMICAL
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reising, Ethington, Barnard, Perry & Milton
STREET: P.O. Box 4390
CITY: Troy
STATE: Michigan
COUNTRY: U.S.A.
ZIP: 48099
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,658
FILING DATE: 15-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,295
FILING DATE: 09-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: P-321WSU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 689-3554
TELEFAX: (313) 689-4071
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-339-658-2

Query Match 100.0%; Score 770; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.9e-84;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPEPLVVKVKAEDQLGARVGYIELDLSNGKILSFREPERPPMSTFKVLLCGAVLSRID 60
Db 24 HPEPLVVKVKAEDQLGARVGYIELDLSNGKILSFREPERPPMSTFKVLLCGAVLSRID 83
Qy 61 AGOBOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120
Db 84 AGOBOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 143
Qy 121 KETLAFHNMGDHVTRLDRMEPELNEAIP 149
Db 144 KETLAFHNMGDHVTRLDRMEPELNEAIP 172

RESULT 3
US-09-263-933-7

Sequence 7, Application US/09263933
Patent No. 6280940
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
NUMBER OF SEQUENCES: 2
MUTAGENICITY OF A CHEMICAL
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reising, Ethington, Barnard, Perry & Milton
STREET: P.O. Box 4390
CITY: Troy
STATE: Michigan
COUNTRY: U.S.A.
ZIP: 48099
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,933
FILING DATE: 1998-08-05
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,295
FILING DATE: 09-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: P-321WSU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 689-3554
TELEFAX: (313) 689-4071
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-263-933-7

Query Match 100.0%; Score 770; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.9e-84;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPEPLVVKVKAEDQLGARVGYIELDLSNGKILSFREPERPPMSTFKVLLCGAVLSRID 60
Db 24 HPEPLVVKVKAEDQLGARVGYIELDLSNGKILSFREPERPPMSTFKVLLCGAVLSRID 83
Qy 61 AGOBOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120
Db 84 AGOBOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 143
Qy 121 KETLAFHNMGDHVTRLDRMEPELNEAIP 149
Db 144 KETLAFHNMGDHVTRLDRMEPELNEAIP 172

RESULT 4

US-09-263-933-14
Sequence 14, Application US/09263933
Patent No. 6280940
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
NUMBER OF SEQUENCES: 2
MUTAGENICITY OF A CHEMICAL
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reising, Ethington, Barnard, Perry & Milton
STREET: P.O. Box 4390
CITY: Troy
STATE: Michigan
COUNTRY: U.S.A.
ZIP: 48099
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,933
FILING DATE: 1998-08-05
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,295
FILING DATE: 09-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: P-321WSU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 689-3554
TELEFAX: (313) 689-4071
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-263-933-14

Query Match 100.0%; Score 770; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.9e-84;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPEPLVVKVKAEDQLGARVGYIELDLSNGKILSFREPERPPMSTFKVLLCGAVLSRID 60
Db 24 HPEPLVVKVKAEDQLGARVGYIELDLSNGKILSFREPERPPMSTFKVLLCGAVLSRID 83
Qy 61 AGOBOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120
Db 84 AGOBOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 143

Qy 121 KETLAFHNMGDHVTRLDRWEPLEALP 149
Db 144 KETLAFHNMGDHVTRLDRWEPLEALP 172

RESULT 5
US-09-263-933-21
Sequence 21, Application US/09263933
Patent No. 6280940
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
US-09-263-933-21

Query Match 100.0%; Score 770; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.9e-84;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPELTIVVKQAEQDQGVGVGIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 60
Db 24 HPELTIVVKQAEQDQGVGVGIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 83

Qy 61 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAIIITMSDNTAANLLTTIGCP 120
Db 84 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAIIITMSDNTAANLLTTIGCP 143

Qy 121 KETLAFHNMGDHVTRLDRWEPLEALP 149
Db 144 KETLAFHNMGDHVTRLDRWEPLEALP 172

RESULT 6
US-09-025-769B-265
Sequence 265, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998

PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-265

Query Match 100.0%; Score 770; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.9e-84;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPELTIVVKQAEQDQGVGVGIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 60
Db 24 HPELTIVVKQAEQDQGVGVGIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 83

Qy 61 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAIIITMSDNTAANLLTTIGCP 120
Db 84 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAIIITMSDNTAANLLTTIGCP 143

Qy 121 KETLAFHNMGDHVTRLDRWEPLEALP 149
Db 144 KETLAFHNMGDHVTRLDRWEPLEALP 172

RESULT 7
US-09-025-769B-362
Sequence 362, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090

;; INFORMATION FOR SEQ ID NO: 362;
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 286 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-025-769B-362

Query Match 100.0%; Score 770; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.9e-84;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVVYKDAEDQLGARVGYIELDLSNGKILSFREPERPPMMSTFKVLLCGAVLSRID 60
DB 24 HPELVVYKDAEDQLGARVGYIELDLSNGKILSFREPERPPMMSTFKVLLCGAVLSRID 83
QY 61 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGGP 120
DB 84 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGGP 143
QY 121 KELTSFLHNMGDHVTRLDRWEPELNEAIP 149
DB 144 KELTSFLHNMGDHVTRLDRWEPELNEAIP 172

RESULT 8
US-09-919-901-7

;; Sequence 7, Application US/09919901
;; Patent No. 6599738
;; GENERAL INFORMATION:
;; APPLICANT: Jackson, Robert A.
;; APPLICANT: Potts, Karen E.
;; APPLICANT: Patrick, Amy K.
;; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
;; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
;; FILE REFERENCE: 0125-0005A
;; CURRENT APPLICATION NUMBER: US/09/919,901
;; PRIOR FILING DATE: 2001-08-02
;; PRIOR APPLICATION NUMBER: 09/263,933
;; PRIOR FILING DATE: 1999-02-08
;; PRIOR APPLICATION NUMBER: 09/129,611
;; PRIOR FILING DATE: 1998-08-05
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 7
;; LENGTH: 286
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: :
US-09-919-901-7

Query Match 100.0%; Score 770; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.9e-84;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVVYKDAEDQLGARVGYIELDLSNGKILSFREPERPPMMSTFKVLLCGAVLSRID 60
DB 24 HPELVVYKDAEDQLGARVGYIELDLSNGKILSFREPERPPMMSTFKVLLCGAVLSRID 83
QY 61 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGGP 120
DB 84 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGGP 143
QY 121 KELTSFLHNMGDHVTRLDRWEPELNEAIP 149
DB 144 KELTSFLHNMGDHVTRLDRWEPELNEAIP 172

RESULT 9
US-09-919-901-14
;; Sequence 14, Application US/09919901
;; Patent No. 6599738

;; GENERAL INFORMATION:
;; APPLICANT: Potts, Karen E.
;; APPLICANT: Jackson, Robert A.
;; APPLICANT: Patrick, Amy K.
;; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
;; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
;; FILE REFERENCE: 0125-0005A
;; CURRENT APPLICATION NUMBER: US/09/919,901
;; PRIOR FILING DATE: 2001-08-02
;; PRIOR APPLICATION NUMBER: 09/263,933
;; PRIOR FILING DATE: 1999-02-08
;; PRIOR APPLICATION NUMBER: 09/129,611
;; PRIOR FILING DATE: 1998-08-05
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 14
;; LENGTH: 286
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: :
US-09-919-901-14

Query Match 100.0%; Score 770; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.9e-84;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVVYKDAEDQLGARVGYIELDLSNGKILSFREPERPPMMSTFKVLLCGAVLSRID 60
DB 24 HPELVVYKDAEDQLGARVGYIELDLSNGKILSFREPERPPMMSTFKVLLCGAVLSRID 83
QY 61 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGGP 120
DB 84 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGGP 143
QY 121 KELTSFLHNMGDHVTRLDRWEPELNEAIP 149
DB 144 KELTSFLHNMGDHVTRLDRWEPELNEAIP 172

RESULT 10
US-09-919-901-21

;; Sequence 21, Application US/09919901
;; Patent No. 6599738
;; GENERAL INFORMATION:
;; APPLICANT: Potts, Karen E.
;; APPLICANT: Jackson, Robert A.
;; APPLICANT: Patrick, Amy K.
;; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
;; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
;; FILE REFERENCE: 0125-0005A
;; CURRENT APPLICATION NUMBER: US/09/919,901
;; PRIOR FILING DATE: 2001-08-02
;; PRIOR APPLICATION NUMBER: 09/263,933
;; PRIOR FILING DATE: 1999-02-08
;; PRIOR APPLICATION NUMBER: 09/129,611
;; PRIOR FILING DATE: 1998-08-05
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 21
;; LENGTH: 286
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: :
US-09-919-901-21

Query Match 100.0%; Score 770; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.9e-84;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVVYKDAEDQLGARVGYIELDLSNGKILSFREPERPPMMSTFKVLLCGAVLSRID 60
DB 24 HPELVVYKDAEDQLGARVGYIELDLSNGKILSFREPERPPMMSTFKVLLCGAVLSRID 83
QY 61 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGGP 120
DB 84 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGGP 143
QY 121 KELTSFLHNMGDHVTRLDRWEPELNEAIP 149
DB 144 KELTSFLHNMGDHVTRLDRWEPELNEAIP 172

Db 24 HPEITLVKVDADDOUGARVGIETLDLNSGKILSFPRPERFPMWSTFKVLLCGAVLSRID 83
 QY 61 AGQEQIGRRIRIHSQNDLVEYSPYTEKHLTDGNTVRELCSAATMWDNTAANLLTTIGSP 120
 Db 84 AGQEQIGRRIRIHSQNDLVEYSPYTEKHLTDGNTVRELCSAATMWDNTAANLLTTIGSP 143
 QY 121 KELTSFLLNMGDHVTRLDRWEPELNEAIP 149
 Db 144 KELTSFLLNMGDHVTRLDRWEPELNEAIP 172

RESULT 11

US-09-490-070A-265
 ; Sequence 265, Application US/09490070A
 ; Patent No. 6696248
 ; GENERAL INFORMATION:
 ; APPLICANT: Knappik, Achim
 ; Pack, Peter
 ; Ilag, Vic
 ; Ge, Liming
 ; Moroney, Simon
 ; Plueckthun, Andreas
 ; TITLE OF INVENTION: Protein/(Poly)peptide libraries
 ; NUMBER OF SEQUENCES: 373
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: Colin G. Sandercock, Esq. c/o Heller Ehrman
 ; White & McAuliffe
 ; STREET: 1666 K Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20006
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/490,070A
 ; FILING DATE: 24-Jan-2000
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 95 11 3021.0
 ; FILING DATE: 18-AUG-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Colin G. Sandercock, Esq.
 ; REGISTRATION NUMBER: 31,298
 ; REFERENCE/DOCKET NUMBER: 37629-0005
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 912-2000
 ; TELEFAX: (202) 912-2020
 ; INFORMATION FOR SEQ ID NO: 265:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 286 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 265:
 ; US-09-490-070A-265

Query Match 100.0%; Score 770; DB 4; Length 286;
 Best Local Similarity 100.0%; Pred. No. 2.9e-84;
 Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADDOUGARVGIETLDLNSGKILSFPRPERFPMWSTFKVLLCGAVLSRID 60
 Db 24 HPEITLVKVDADDOUGARVGIETLDLNSGKILSFPRPERFPMWSTFKVLLCGAVLSRID 83
 QY 61 AGQEQIGRRIRIHSQNDLVEYSPYTEKHLTDGNTVRELCSAATMWDNTAANLLTTIGSP 120
 Db 84 AGQEQIGRRIRIHSQNDLVEYSPYTEKHLTDGNTVRELCSAATMWDNTAANLLTTIGSP 143
 QY 121 KELTSFLLNMGDHVTRLDRWEPELNEAIP 149
 Db 144 KELTSFLLNMGDHVTRLDRWEPELNEAIP 172

Db 144 KELTSFLLNMGDHVTRLDRWEPELNEAIP 172

RESULT 12

US-09-490-070A-362
 ; Sequence 362, Application US/09490070A
 ; Patent No. 6696248
 ; GENERAL INFORMATION:
 ; APPLICANT: Knappik, Achim
 ; Pack, Peter
 ; Ilag, Vic
 ; Ge, Liming
 ; Moroney, Simon
 ; Plueckthun, Andreas
 ; TITLE OF INVENTION: Protein/(Poly)peptide libraries
 ; NUMBER OF SEQUENCES: 373
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: Colin G. Sandercock, Esq. c/o Heller Ehrman
 ; White & McAuliffe
 ; STREET: 1666 K Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20006
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/490,070A
 ; FILING DATE: 24-Jan-2000
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 95 11 3021.0
 ; FILING DATE: 18-AUG-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Colin G. Sandercock, Esq.
 ; REGISTRATION NUMBER: 31,298
 ; REFERENCE/DOCKET NUMBER: 37629-0005
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 912-2000
 ; TELEFAX: (202) 912-2020
 ; INFORMATION FOR SEQ ID NO: 362:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 286 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 362:
 ; US-09-490-070A-362

Query Match 100.0%; Score 770; DB 4; Length 286;
 Best Local Similarity 100.0%; Pred. No. 2.9e-84;
 Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADDOUGARVGIETLDLNSGKILSFPRPERFPMWSTFKVLLCGAVLSRID 60
 Db 24 HPEITLVKVDADDOUGARVGIETLDLNSGKILSFPRPERFPMWSTFKVLLCGAVLSRID 83
 QY 61 AGQEQIGRRIRIHSQNDLVEYSPYTEKHLTDGNTVRELCSAATMWDNTAANLLTTIGSP 120
 Db 84 AGQEQIGRRIRIHSQNDLVEYSPYTEKHLTDGNTVRELCSAATMWDNTAANLLTTIGSP 143
 QY 121 KELTSFLLNMGDHVTRLDRWEPELNEAIP 149
 Db 144 KELTSFLLNMGDHVTRLDRWEPELNEAIP 172

RESULT 13

US-09-490-153-265
 ; Sequence 265, Application US/09490153
 ; Patent No. 6706484
 ; GENERAL INFORMATION:

APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESS: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 265;
US-09-490-153-265
Query Match 100.0%; Score 770; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.9e-84;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEVLVKKDAEDQIGARVGYIEIDLNSGKILSFRRPFRPPMSTFVLLCGAVLSRID 60
DB 24 HPEVLVKKDAEDQIGARVGYIEIDLNSGKILSFRRPFRPPMSTFVLLCGAVLSRID 83
QY 61 AGGQGLGRRIHSQNDLVEYSPTVEKHLTDGMYRELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGGQGLGRRIHSQNDLVEYSPTVEKHLTDGMYRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KETLAFILNMGDHYTRLDRMEPELNEAIP 149
DB 144 KETLAFILNMGDHYTRLDRMEPELNEAIP 172

RESULT 14
US-09-490-153-362
Sequence 362, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESS: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 362;
US-09-490-153-362
Query Match 100.0%; Score 770; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.9e-84;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEVLVKKDAEDQIGARVGYIEIDLNSGKILSFRRPFRPPMSTFVLLCGAVLSRID 60
DB 24 HPEVLVKKDAEDQIGARVGYIEIDLNSGKILSFRRPFRPPMSTFVLLCGAVLSRID 83
QY 61 AGGQGLGRRIHSQNDLVEYSPTVEKHLTDGMYRELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGGQGLGRRIHSQNDLVEYSPTVEKHLTDGMYRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KETLAFILNMGDHYTRLDRMEPELNEAIP 149
DB 144 KETLAFILNMGDHYTRLDRMEPELNEAIP 172

RESULT 15
US-10-191-966-7
Sequence 7, Application US/10191966
Patent No. 6790612
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
PRIOR FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 7
 LENGTH: 286
 TYPE: prt
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: :
 US-10-191-966-7

Query Match 100.0%; Score 770; DB 4; Length 286;
 Best Local Similarity 100.0%; Pred. No. 2.9e-84;
 Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	HPETLVKVDADPDQGARVGYIELDLSGKILESFRPERPMMSTFEKYLGGAVLSRID	60
Db	24	HPETLVKVDADPDQGARVGYIELDLSGKILESFRPERPMMSTFEKYLGGAVLSRID	83
Qy	61	AGQEQLGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTANILLTTIGSP	120
Db	84	AGQEQLGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTANILLTTIGSP	143
Qy	121	KELTAFLNMGDPVTRLDRMEPELNEAIP	149
Db	144	KELTAFLNMGDPVTRLDRMEPELNEAIP	172

Search completed: June 10, 2005, 11:01:14
 Job time : 15.2765 secs

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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:36:31 ; Search time 23.3762 Seconds
(without alignments)
728.091 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_228

Perfect score: 1170
Sequence: 1 HPEITLVKVDADQAGRVG.....KSGAGERSRGIIALGPDG 228

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1170	100.0	286	1	US-08-339-658-2
3	1170	100.0	286	3	US-09-263-933-7
4	1170	100.0	286	3	US-09-263-933-14
5	1170	100.0	286	3	US-09-263-933-21
6	1170	100.0	286	3	US-09-025-769B-265
7	1170	100.0	286	3	US-09-025-769B-362
8	1170	100.0	286	4	US-09-919-901-7
9	1170	100.0	286	4	US-09-919-901-14
10	1170	100.0	286	4	US-09-919-901-21
11	1170	100.0	286	4	US-09-490-070A-265
12	1170	100.0	286	4	US-09-490-070A-362
13	1170	100.0	286	4	US-09-490-153-265
14	1170	100.0	286	4	US-09-490-153-362
15	1170	100.0	286	4	US-10-191-966-7
16	1170	100.0	286	4	US-10-191-966-14
17	1170	100.0	286	4	US-10-191-966-21
18	1170	100.0	286	4	US-09-490-324-265
19	1170	100.0	286	4	US-09-490-324-362
20	1170	100.0	286	3	US-09-025-769B-285
21	1170	100.0	286	3	US-09-025-769B-298
22	1170	100.0	286	3	US-09-025-769B-300
23	1170	100.0	286	4	US-09-490-070A-285
24	1170	100.0	286	4	US-09-490-070A-298
25	1170	100.0	286	4	US-09-490-070A-300
26	1170	100.0	286	4	US-09-490-153-285
27	1170	100.0	286	4	US-09-490-153-298

28	1170	100.0	299	4	US-09-490-153-300	Sequence 300, App
29	1170	100.0	299	4	US-09-490-324-285	Sequence 285, App
30	1170	100.0	299	4	US-09-490-324-298	Sequence 298, App
31	1170	100.0	299	4	US-09-490-324-300	Sequence 300, App
32	1170	100.0	299	3	US-09-263-933-2	Sequence 2, Appl
33	1170	100.0	299	3	US-09-263-933-9	Sequence 9, Appl
34	1170	100.0	299	3	US-09-263-933-16	Sequence 16, Appl
35	1170	100.0	299	3	US-09-263-933-21	Sequence 21, Appl
36	1170	100.0	299	4	US-09-919-901-16	Sequence 16, Appl
37	1170	100.0	299	4	US-09-919-901-21	Sequence 21, Appl
38	1170	100.0	299	4	US-10-191-966-2	Sequence 2, Appl
39	1170	100.0	299	4	US-10-191-966-9	Sequence 9, Appl
40	1170	100.0	299	4	US-10-191-966-16	Sequence 16, Appl
41	1169	99.9	286	4	US-09-555-510B-9	Sequence 9, Appl
42	1169	99.9	286	4	US-10-231-013-9	Sequence 9, Appl
43	1169	99.9	1293	4	US-09-170-496D-292	Sequence 292, App
44	1169	99.9	1293	4	US-09-364-425B-57	Sequence 57, Appl
45	1165	99.6	263	1	US-08-407-544-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-07-721-775A-2
Sequence 2, Application US/07721775A
Patent No. 5180666
GENERAL INFORMATION:
APPLICANT: States, J. Christopher
APPLICANT: Hines, Ronald N.
APPLICANT: No. 5180666ak, Raymond F.
TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSES: Relating, Echington, Barnard, Perry & Milton
STREET: P. O. Box 4390
CITY: Troy
STATE: Michigan
COUNTRY: U.S.A.
ZIP: 48099
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07721,775A
FILING DATE: 19910627
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: P-321WSU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 689-3554
TELEFAX: (313) 689-4071
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-721-775A-2

Query Match 100.0%; Score 1170; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 6.7e-122;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGRVGTYELDINSKTLIESFRPEERPPMSTFYVLGAVLSRID 60
DB 24 HPEITLVKVDADQAGRVGTYELDINSKTLIESFRPEERPPMSTFYVLGAVLSRID 83

QY 61 AGGOLGRIHYSQNDLVEYSPVTEKHLTDGTVRELCSAITSNDNTAANLLTTTIGP 120
DB 84 AGGOLGRIHYSQNDLVEYSPVTEKHLTDGTVRELCSAITSNDNTAANLLTTTIGP 143
QY 121 KETLAFILNMGDHVTRLDRMBEPELNEALPNDERDTTVPVAAATTLRKLLTGBLLTLASRQ 180
DB 144 KETLAFILNMGDHVTRLDRMBEPELNEALPNDERDTTVPVAAATTLRKLLTGBLLTLASRQ 203
QY 181 QLIDMMEADKVAGPLRLSALPAGWFIADKSGAGERSGRTIAALGPDG 228
DB 204 QLIDMMEADKVAGPLRLSALPAGWFIADKSGAGERSGRTIAALGPDG 251

RESULT 2

US-08-339-658-2
; Sequence 2, Application US/08339658
; Patent No. 5525482
; GENERAL INFORMATION:
; APPLICANT: States, J. Christopher
; APPLICANT: Hines, Ronald N.
; APPLICANT: No. 5525482ak, Raymond P.
; TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
; TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: Reising, Ethington, Barnard, Perry & Milton
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: U.S.A.
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,658
; FILING DATE: 15-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,295
; FILING DATE: 09-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-321WSU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (313) 689-3554
; TELEFAX: (313) 689-4071
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-339-658-2

Query Match 100.0%; Score 1170; DB 1: Length 286;
Best Local Similarity 100.0%; Pred. No. 6.7e-122;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVAEDQAGARVGYIEIDLNSGKILSFRRPERPPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKVAEDQAGARVGYIEIDLNSGKILSFRRPERPPMSTFVLLCGAVLSRID 83
QY 61 AGGOLGRIHYSQNDLVEYSPVTEKHLTDGTVRELCSAITSNDNTAANLLTTTIGP 120
DB 84 AGGOLGRIHYSQNDLVEYSPVTEKHLTDGTVRELCSAITSNDNTAANLLTTTIGP 143
QY 121 KETLAFILNMGDHVTRLDRMBEPELNEALPNDERDTTVPVAAATTLRKLLTGBLLTLASRQ 180
DB 144 KETLAFILNMGDHVTRLDRMBEPELNEALPNDERDTTVPVAAATTLRKLLTGBLLTLASRQ 203

QY 181 QLIDMMEADKVAGPLRLSALPAGWFIADKSGAGERSGRTIAALGPDG 228
DB 204 QLIDMMEADKVAGPLRLSALPAGWFIADKSGAGERSGRTIAALGPDG 251

RESULT 3

US-09-263-933-7
; Sequence 7, Application US/09263933
; Patent No. 6280940
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/263,933
; EARLIER FILING DATE: 1999-03-08
; EARLIER APPLICATION NUMBER: 09/129,611
; EARLIER FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 7
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; US-09-263-933-7

Query Match 100.0%; Score 1170; DB 3: Length 286;
Best Local Similarity 100.0%; Pred. No. 6.7e-122;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVAEDQAGARVGYIEIDLNSGKILSFRRPERPPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKVAEDQAGARVGYIEIDLNSGKILSFRRPERPPMSTFVLLCGAVLSRID 83
QY 61 AGGOLGRIHYSQNDLVEYSPVTEKHLTDGTVRELCSAITSNDNTAANLLTTTIGP 120
DB 84 AGGOLGRIHYSQNDLVEYSPVTEKHLTDGTVRELCSAITSNDNTAANLLTTTIGP 143
QY 121 KETLAFILNMGDHVTRLDRMBEPELNEALPNDERDTTVPVAAATTLRKLLTGBLLTLASRQ 180
DB 144 KETLAFILNMGDHVTRLDRMBEPELNEALPNDERDTTVPVAAATTLRKLLTGBLLTLASRQ 203
QY 181 QLIDMMEADKVAGPLRLSALPAGWFIADKSGAGERSGRTIAALGPDG 228
DB 204 QLIDMMEADKVAGPLRLSALPAGWFIADKSGAGERSGRTIAALGPDG 251

RESULT 4

US-09-263-933-14
; Sequence 14, Application US/09263933
; Patent No. 6280940
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/263,933
; EARLIER FILING DATE: 1999-03-08
; EARLIER APPLICATION NUMBER: 09/129,611
; EARLIER FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 14
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; US-09-263-933-14

Query Match 100.0%; Score 1170; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 6.7e-122;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVDADQAGVGYELDINSKILSFRRPFRPMSTFKVLCGAVLSRID 60
DB HPELVKVDADQAGVGYELDINSKILSFRRPFRPMSTFKVLCGAVLSRID 83
QY 61 AGQEQGRIRIHVSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
DB AGQEQGRIRIHVSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFINMGDHTRLDRWPELNEAIPNDRDRTMPVAMATTIRKLLTGELLTLASRQ 180
DB KELTAFINMGDHTRLDRWPELNEAIPNDRDRTMPVAMATTIRKLLTGELLTLASRQ 203
QY 191 QUIDMEADKVAQPLLRSLPAGWFIADKSGAGSGRSIIAALGPDG 228
DB 204 QUIDMEADKVAQPLLRSLPAGWFIADKSGAGSGRSIIAALGPDG 251

RESULT 5

US-09-263-933-21
Sequence 21, Application US/09263933
Patent No. 6280940

GENERAL INFORMATION:
APPLICANT: Potte, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
EARLIER FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
US-09-263-933-21

Query Match 100.0%; Score 1170; DB 3; Length 286;

Best Local Similarity 100.0%; Pred. No. 6.7e-122;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVDADQAGVGYELDINSKILSFRRPFRPMSTFKVLCGAVLSRID 60
DB HPELVKVDADQAGVGYELDINSKILSFRRPFRPMSTFKVLCGAVLSRID 83
QY 61 AGQEQGRIRIHVSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
DB AGQEQGRIRIHVSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFINMGDHTRLDRWPELNEAIPNDRDRTMPVAMATTIRKLLTGELLTLASRQ 180
DB KELTAFINMGDHTRLDRWPELNEAIPNDRDRTMPVAMATTIRKLLTGELLTLASRQ 203
QY 181 QUIDMEADKVAQPLLRSLPAGWFIADKSGAGSGRSIIAALGPDG 228
DB 204 QUIDMEADKVAQPLLRSLPAGWFIADKSGAGSGRSIIAALGPDG 251

RESULT 6

US-09-025-769B-265
Sequence 265, Application US/09025769B
Patent No. 6300064

GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic

APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5

TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 265:

SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-265

Query Match 100.0%; Score 1170; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 6.7e-122;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVDADQAGVGYELDINSKILSFRRPFRPMSTFKVLCGAVLSRID 60
DB HPELVKVDADQAGVGYELDINSKILSFRRPFRPMSTFKVLCGAVLSRID 83
QY 61 AGQEQGRIRIHVSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
DB AGQEQGRIRIHVSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFINMGDHTRLDRWPELNEAIPNDRDRTMPVAMATTIRKLLTGELLTLASRQ 180
DB KELTAFINMGDHTRLDRWPELNEAIPNDRDRTMPVAMATTIRKLLTGELLTLASRQ 203
QY 181 QUIDMEADKVAQPLLRSLPAGWFIADKSGAGSGRSIIAALGPDG 228
DB 204 QUIDMEADKVAQPLLRSLPAGWFIADKSGAGSGRSIIAALGPDG 251

RESULT 7

US-09-025-769B-362
Sequence 362, Application US/09025769B
Patent No. 6300064

GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 362:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-362

Query Match 100.0%; Score 1170; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 6,7e-122;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADQDQAGVGYIEIDLSNGKILSFRRPFRPPMSTFVLLCGAVLSRID 60
DB HPEITLVKVKADQDQAGVGYIEIDLSNGKILSFRRPFRPPMSTFVLLCGAVLSRID 83
QY 61 AGGOLGRRIHYSONDLVEYSPVTEKHLTDGMYRELCSAIIYMSDNTAAILLTTIGCP 120
DB AGGOLGRRIHYSONDLVEYSPVTEKHLTDGMYRELCSAIIYMSDNTAAILLTTIGCP 143
QY 121 KETLAFHNMGDHYTRLDRWPEPEINEAIPNDRDITMVPVAAATTLRKLLTGELLTLASRQ 180
DB KETLAFHNMGDHYTRLDRWPEPEINEAIPNDRDITMVPVAAATTLRKLLTGELLTLASRQ 203
QY 181 QLIWMKADKVAAGPLRSALPAGWFIADKSGAGRGSRGIIAALGPDG 228
DB QLIWMKADKVAAGPLRSALPAGWFIADKSGAGRGSRGIIAALGPDG 251

RESULT 8
US-09-919-901-7
Sequence 7, Application US/09919901
Patent No. 6599738
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7

LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-09-919-901-7

Query Match 100.0%; Score 1170; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 6,7e-122;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADQDQAGVGYIEIDLSNGKILSFRRPFRPPMSTFVLLCGAVLSRID 60
DB HPEITLVKVKADQDQAGVGYIEIDLSNGKILSFRRPFRPPMSTFVLLCGAVLSRID 83
QY 61 AGGOLGRRIHYSONDLVEYSPVTEKHLTDGMYRELCSAIIYMSDNTAAILLTTIGCP 120
DB AGGOLGRRIHYSONDLVEYSPVTEKHLTDGMYRELCSAIIYMSDNTAAILLTTIGCP 143
QY 121 KETLAFHNMGDHYTRLDRWPEPEINEAIPNDRDITMVPVAAATTLRKLLTGELLTLASRQ 180
DB KETLAFHNMGDHYTRLDRWPEPEINEAIPNDRDITMVPVAAATTLRKLLTGELLTLASRQ 203
QY 181 QLIWMKADKVAAGPLRSALPAGWFIADKSGAGRGSRGIIAALGPDG 228
DB QLIWMKADKVAAGPLRSALPAGWFIADKSGAGRGSRGIIAALGPDG 251

RESULT 9
US-09-919-901-14
Sequence 14, Application US/09919901
Patent No. 6599738
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-09-919-901-14

Query Match 100.0%; Score 1170; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 6,7e-122;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADQDQAGVGYIEIDLSNGKILSFRRPFRPPMSTFVLLCGAVLSRID 60
DB HPEITLVKVKADQDQAGVGYIEIDLSNGKILSFRRPFRPPMSTFVLLCGAVLSRID 83
QY 61 AGGOLGRRIHYSONDLVEYSPVTEKHLTDGMYRELCSAIIYMSDNTAAILLTTIGCP 120
DB AGGOLGRRIHYSONDLVEYSPVTEKHLTDGMYRELCSAIIYMSDNTAAILLTTIGCP 143
QY 121 KETLAFHNMGDHYTRLDRWPEPEINEAIPNDRDITMVPVAAATTLRKLLTGELLTLASRQ 180
DB KETLAFHNMGDHYTRLDRWPEPEINEAIPNDRDITMVPVAAATTLRKLLTGELLTLASRQ 203
QY 181 QLIWMKADKVAAGPLRSALPAGWFIADKSGAGRGSRGIIAALGPDG 228
DB QLIWMKADKVAAGPLRSALPAGWFIADKSGAGRGSRGIIAALGPDG 251

Db 204 QUIDMEADKVAGPILRSALPAGWFIADKSGAGERSGIIAALGPDG 251

RESULT 10
US-09-919-901-21
Sequence 21, Application US/09919901
Patent No. 6599738
GENERAL INFORMATION:
APPLICANT: Potte, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 21
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION:
US-09-919-901-21

Query Match 100.0%; Score 1170; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 6.7e-122;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPELVKVKADBDQAGRVGYIELDLSGKILIESFRPERPFPMSTFKVLLCGAVLSRID 60
Db 24 HPELVKVKADBDQAGRVGYIELDLSGKILIESFRPERPFPMSTFKVLLCGAVLSRID 83

Qy 61 AGQELGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGSP 120
Db 84 AGQELGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGSP 143

Qy 121 KELTFALNMGDHYRLDRWPELNEALPNDERDTTMAPVAMATTIRKLLTGELTLASRQ 180
Db 144 KELTFALNMGDHYRLDRWPELNEALPNDERDTTMAPVAMATTIRKLLTGELTLASRQ 203

Qy 181 QUIDMEADKVAGPILRSALPAGWFIADKSGAGERSGIIAALGPDG 228
Db 204 QUIDMEADKVAGPILRSALPAGWFIADKSGAGERSGIIAALGPDG 251

RESULT 11
US-09-490-070A-265
Sequence 265, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McLaughlin
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-09-490-070A-265

Query Match 100.0%; Score 1170; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 6.7e-122;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPELVKVKADBDQAGRVGYIELDLSGKILIESFRPERPFPMSTFKVLLCGAVLSRID 60
Db 24 HPELVKVKADBDQAGRVGYIELDLSGKILIESFRPERPFPMSTFKVLLCGAVLSRID 83

Qy 61 AGQELGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGSP 120
Db 84 AGQELGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGSP 143

Qy 121 KELTFALNMGDHYRLDRWPELNEALPNDERDTTMAPVAMATTIRKLLTGELTLASRQ 180
Db 144 KELTFALNMGDHYRLDRWPELNEALPNDERDTTMAPVAMATTIRKLLTGELTLASRQ 203

Qy 181 QUIDMEADKVAGPILRSALPAGWFIADKSGAGERSGIIAALGPDG 228
Db 204 QUIDMEADKVAGPILRSALPAGWFIADKSGAGERSGIIAALGPDG 251

RESULT 12
US-09-490-070A-362
Sequence 362, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McLaughlin
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 362:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 362:
US-09-490-070A-362

Query Match 100.0%; Score 1170; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 6,7e-122;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 24 HPEITLVKKAEDQAGRVGYIELDLSNGKILLESFRPEPRPMMSTFVLLCGAVLSRID 83
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DB 84 AGQOLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAAILLTITGCP 143
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QY 181 QLIIMWEADKVAAGPLRSALPAGWFIADKSGAGRGSRGIIAALGPDG 228
DB 204 QLIIMWEADKVAAGPLRSALPAGWFIADKSGAGRGSRGIIAALGPDG 251

RESULT 13
US-09-490-153-265
Sequence 265, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-09-490-153-265

Query Match 100.0%; Score 1170; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 6,7e-122;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14
US-09-490-153-362
Sequence 362, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 362:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
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TOPOLOGY: linear
MOLECULE TYPE: protein
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US-09-490-153-362

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RESULT 15

US-10-191-966-7
Sequence 7, Application US/10191966
Patent No. 6790612
GENERAL INFORMATION:
APPLICANT: Poter, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-10-191-966-7

Query Match 100.0%; Score 1170; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 6.7e-122;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 QLIDMWEADKVAAGPILRSALPAGWFIADKSGAGERGSRGIIAALGPDG 228
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2005, 10:40:16 ; Search time 76.3841 Seconds
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Title: US-10-668-778-2_COPY_1_228

Perfect score: 1170
Sequence: 1 HPEITLVKVKDAEDQLGARVG.....KSGAGERSGRLIALLGPDG 228

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Total number of hits satisfying chosen parameters: 1710399

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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2	1170	100.0	286 10 US-09-919-901-7	Sequence 7, Appl1
3	1170	100.0	286 10 US-09-919-901-14	Sequence 14, Appl1
4	1170	100.0	286 10 US-09-919-901-21	Sequence 21, Appl1
5	1170	100.0	286 11 US-09-837-306-354	Sequence 354, App
6	1170	100.0	286 14 US-10-191-966-7	Sequence 7, Appl1
7	1170	100.0	286 14 US-10-191-966-14	Sequence 14, Appl1
8	1170	100.0	286 14 US-10-191-966-21	Sequence 21, Appl1
9	1170	100.0	286 15 US-10-045-674-523	Sequence 523, App
10	1170	100.0	286 16 US-10-416-708A-73	Sequence 73, Appl1
11	1170	100.0	2307 10 US-09-919-901-2	Sequence 2, Appl1

12	1170	100.0	2307 10 US-09-919-901-9	Sequence 9, Appl1
13	1170	100.0	2307 10 US-09-919-901-16	Sequence 16, Appl1
14	1170	100.0	2307 14 US-10-191-966-2	Sequence 2, Appl1
15	1170	100.0	2307 14 US-10-191-966-9	Sequence 9, Appl1
16	1170	100.0	2307 14 US-10-191-966-16	Sequence 16, Appl1
17	1169	99.9	286 14 US-10-231-013-9	Sequence 9, Appl1
18	1169	99.9	286 14 US-10-842-534-9	Sequence 9, Appl1
19	1169	99.9	1293 14 US-10-251-385-192	Sequence 232, App
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21	1165	99.6	265 9 US-09-772-114-6	Sequence 6, Appl1
22	1165	99.6	265 14 US-10-280-482-2	Sequence 2, Appl1
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25	1165	99.6	286 14 US-10-016-668-5	Sequence 5, Appl1
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27	1165	99.6	286 17 US-10-656-029-4	Sequence 4, Appl1
28	1165	99.6	286 17 US-10-877-952-26	Sequence 26, Appl1
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30	1162	99.3	264 17 US-10-877-952-18	Sequence 18, Appl1
31	1162	99.3	362 15 US-10-469-199-2	Sequence 2, Appl1
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35	1158	99.0	265 16 US-10-622-088-114	Sequence 114, App
36	1158	99.0	265 17 US-10-656-029-6	Sequence 6, Appl1
37	1157	98.9	265 17 US-10-877-952-154	Sequence 154, App
38	1157	98.9	264 9 US-09-772-114-9	Sequence 9, Appl1
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43	1142	97.6	498 15 US-10-491-653-146	Sequence 146, App
44	1121	95.8	284 15 US-10-052-188-2	Sequence 2, Appl1
45	470.5	40.2	288 14 US-10-016-668-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-10-668-778-2
Sequence 2, Application US/10668778
Publication No. US2004003817A1
GENERAL INFORMATION:
APPLICANT: Ballint, Robert F.
APPLICANT: Her, Deng-Hong
APPLICANT: Kalobilos, Inc.
TITLE OF INVENTION: Interaction-Activated Proteins
FILE REFERENCE: 021167-000700US
CURRENT APPLICATION NUMBER: US/10/668, 778
CURRENT FILING DATE: 2003-09-22
PRIOR APPLICATION NUMBER: US/09/526, 106
PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: US 60/124,339
PRIOR FILING DATE: 1999-03-15
PRIOR APPLICATION NUMBER: US 60/135,926
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 60/175,968
PRIOR FILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 263
TYPE: PRT
ORGANISM: Escherichia coli
FEATURE:
OTHER INFORMATION: TEM-1 beta-lactamase
US-10-668-778-2

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Best Local Similarity 100.0%; Pred. No. 8.1e-113;
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RESULT 2
US-09-919-901-7
; Sequence 7, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-09-919-901-7

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Best Local Similarity 100.0%; Pred. No. 9.2e-113;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 24 HPEITLVKVKADBDLGARVGYIEIDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 83
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Db 144 KELTAFILNMGDHVTRLDRWPEPELNEAIPNDERDTPVMAATTLRKLLTGELLTLASRQ 203
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Db 204 QIIMWEADKVAAGPLRSALPAGWFIADKSGAGERSGIIAALGPDG 251

RESULT 3
US-09-919-901-14
; Sequence 14, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.

; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
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; OTHER INFORMATION: :
US-09-919-901-14

- Query Match 100.0%; Score 1170; DB 10; Length 286;
Best Local Similarity 100.0%; Pred. No. 9.2e-113;
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RESULT 4
US-09-919-901-21
; Sequence 21, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
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; PRIOR FILING DATE: 1998-08-05
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; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: :
US-09-919-901-21

- Query Match 100.0%; Score 1170; DB 10; Length 286;
Best Local Similarity 100.0%; Pred. No. 9.2e-113;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 61 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATWSDNTAANLLTTIGSP 120
Db 84 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATWSDNTAANLLTTIGSP 143
Qy 121 KELTAFILNMGDHYTRLDRMEPELNEAIPNDRDRTTMVAAATTIRKLLTGSELLTLASRQ 180
Db 144 KELTAFILNMGDHYTRLDRMEPELNEAIPNDRDRTTMVAAATTIRKLLTGSELLTLASRQ 203
Qy 181 QLIDMEADKVAAGPLIRLSALPAGWFIADKSGAGERSGIIAALGPDG 228
Db 204 QLIDMEADKVAAGPLIRLSALPAGWFIADKSGAGERSGIIAALGPDG 251
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```
RESULT 5
US-09-837-306-354
; Sequence 354, Application US/09837306
; Publication No. US20040029113A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, ROBERT C.
; APPLICANT: COHEN, EDWARD H.
; APPLICANT: NASTRI, HORACIO G.
; APPLICANT: ROOKEY, KRISTIN L.
; APPLICANT: HOET, RENE
; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC
; TITLE OF INVENTION: PACKAGES THAT COLLECTIVELY DISPLAY THE MEMBERS OF A
; TITLE OF INVENTION: DIVERSE FAMILY OF PEPTIDES, POLYPEPTIDES OR PROTEINS
; FILE REFERENCE: DYAK/002
; CURRENT APPLICATION NUMBER: US/09/837,306
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/1198,069
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 354
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: pCESS5
US-09-837-306-354
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Query Match 100.0%; Score 1170; DB 11; Length 286;
Best Local Similarity 100.0%; Pred. No. 9.2e-113;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPEITLVKVDADQAGARVGYIELDLSNGKILSFRRPERPMMSTFKVLLCGAVLSRID 60
Db 24 HPEITLVKVDADQAGARVGYIELDLSNGKILSFRRPERPMMSTFKVLLCGAVLSRID 83
Qy 61 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATWSDNTAANLLTTIGSP 120
Db 84 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATWSDNTAANLLTTIGSP 143
Qy 121 KELTAFILNMGDHYTRLDRMEPELNEAIPNDRDRTTMVAAATTIRKLLTGSELLTLASRQ 180
Db 144 KELTAFILNMGDHYTRLDRMEPELNEAIPNDRDRTTMVAAATTIRKLLTGSELLTLASRQ 203
Qy 181 QLIDMEADKVAAGPLIRLSALPAGWFIADKSGAGERSGIIAALGPDG 228
Db 204 QLIDMEADKVAAGPLIRLSALPAGWFIADKSGAGERSGIIAALGPDG 251
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```
RESULT 6
US-10-191-966-7
; Sequence 7, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potes, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
```

```
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-10-191-966-7
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Query Match 100.0%; Score 1170; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 9.2e-113;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPEITLVKVDADQAGARVGYIELDLSNGKILSFRRPERPMMSTFKVLLCGAVLSRID 60
Db 24 HPEITLVKVDADQAGARVGYIELDLSNGKILSFRRPERPMMSTFKVLLCGAVLSRID 83
Qy 61 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATWSDNTAANLLTTIGSP 120
Db 84 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATWSDNTAANLLTTIGSP 143
Qy 121 KELTAFILNMGDHYTRLDRMEPELNEAIPNDRDRTTMVAAATTIRKLLTGSELLTLASRQ 180
Db 144 KELTAFILNMGDHYTRLDRMEPELNEAIPNDRDRTTMVAAATTIRKLLTGSELLTLASRQ 203
Qy 181 QLIDMEADKVAAGPLIRLSALPAGWFIADKSGAGERSGIIAALGPDG 228
Db 204 QLIDMEADKVAAGPLIRLSALPAGWFIADKSGAGERSGIIAALGPDG 251
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```
RESULT 7
US-10-191-966-14
; Sequence 14, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potes, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-10-191-966-14
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Query Match 100.0%; Score 1170; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 9.2e-113;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPEITLVKVDADQAGARVGYIELDLSNGKILSFRRPERPMMSTFKVLLCGAVLSRID 60
Db 24 HPEITLVKVDADQAGARVGYIELDLSNGKILSFRRPERPMMSTFKVLLCGAVLSRID 83
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QY 61 AGGOLGRRIHYSONDIVEYSPVTEKHLTDGTVRELCSAAITMSDNTAANLLTTIGP 120
 DB 84 AGGOLGRRIHYSONDIVEYSPVTEKHLTDGTVRELCSAAITMSDNTAANLLTTIGP 143
 QY 121 KETLAFLLNMGDHTRLDREPELNEALPNDERDTTVPVMAATTLRKLLTGBLLTLASRQ 180
 DB 144 KETLAFLLNMGDHTRLDREPELNEALPNDERDTTVPVMAATTLRKLLTGBLLTLASRQ 203
 QY 181 QLIIMMEADKVAAGPLRLSALPAGWFIADKSGAGERGSGIITIALGPDG 228
 DB 204 QLIIMMEADKVAAGPLRLSALPAGWFIADKSGAGERGSGIITIALGPDG 251

RESULT 8

US-10-191-966-21
 ; Sequence 21, Application US/10191966
 ; Publication No. US20030175692A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Potts, Karen E.
 ; APPLICANT: Jackson, Roberta L.
 ; APPLICANT: Patick, Amy K.
 ; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
 ; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
 ; FILE REFERENCE: 0125-0005A
 ; CURRENT APPLICATION NUMBER: US/10/191,966
 ; PRIOR FILING DATE: 2002-07-10
 ; PRIOR APPLICATION NUMBER: US/09/263,933
 ; PRIOR FILING DATE: 1999-03-08
 ; PRIOR APPLICATION NUMBER: 09/129,611
 ; PRIOR FILING DATE: 1998-08-05
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 21
 ; LENGTH: 286
 ; TYPE: PRP
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: :
 US-10-191-966-21

Query Match 100.0%; Score 1170; DB 14; Length 286;
 Best Local Similarity 100.0%; Pred. No. 9.2e-113;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVAEDDQAGRVGTELDLNSGKILSFREPERPMMSTFKVLICGAVLSRID 60
 DB 24 HPEITLVKVAEDDQAGRVGTELDLNSGKILSFREPERPMMSTFKVLICGAVLSRID 83
 QY 61 AGGOLGRRIHYSONDIVEYSPVTEKHLTDGTVRELCSAAITMSDNTAANLLTTIGP 120
 DB 84 AGGOLGRRIHYSONDIVEYSPVTEKHLTDGTVRELCSAAITMSDNTAANLLTTIGP 143
 QY 121 KETLAFLLNMGDHTRLDREPELNEALPNDERDTTVPVMAATTLRKLLTGBLLTLASRQ 180
 DB 144 KETLAFLLNMGDHTRLDREPELNEALPNDERDTTVPVMAATTLRKLLTGBLLTLASRQ 203
 QY 181 QLIIMMEADKVAAGPLRLSALPAGWFIADKSGAGERGSGIITIALGPDG 228
 DB 204 QLIIMMEADKVAAGPLRLSALPAGWFIADKSGAGERGSGIITIALGPDG 251

RESULT 9

US-10-045-674-523
 ; Sequence 523, Application US/10045674
 ; Publication No. US2003023233A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LADNER, ROBERT C.
 ; APPLICANT: COHEN, EDWARD H.
 ; APPLICANT: NASTRI, HORACIO G.
 ; APPLICANT: ROOKEY, KRISTIN L.
 ; APPLICANT: HOET, RENE
 ; APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.

; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
 ; TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
 ; TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
 ; TITLE OF INVENTION: LIBRARIES
 ; FILE REFERENCE: DVA/002 CIP2
 ; CURRENT APPLICATION NUMBER: US/10/045,674
 ; CURRENT FILING DATE: 2001-10-25
 ; PRIOR APPLICATION NUMBER: 60/198,069
 ; PRIOR FILING DATE: 2000-04-17
 ; PRIOR APPLICATION NUMBER: 09/837,306
 ; PRIOR FILING DATE: 2001-04-17
 ; NUMBER OF SEQ ID NOS: 635
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 523
 ; LENGTH: 286
 ; TYPE: PRP
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Vector pCESS
 ; OTHER INFORMATION: protein sequence
 US-10-045-674-523

Query Match 100.0%; Score 1170; DB 15; Length 286;
 Best Local Similarity 100.0%; Pred. No. 9.2e-113;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVAEDDQAGRVGTELDLNSGKILSFREPERPMMSTFKVLICGAVLSRID 60
 DB 24 HPEITLVKVAEDDQAGRVGTELDLNSGKILSFREPERPMMSTFKVLICGAVLSRID 83
 QY 61 AGGOLGRRIHYSONDIVEYSPVTEKHLTDGTVRELCSAAITMSDNTAANLLTTIGP 120
 DB 84 AGGOLGRRIHYSONDIVEYSPVTEKHLTDGTVRELCSAAITMSDNTAANLLTTIGP 143
 QY 121 KETLAFLLNMGDHTRLDREPELNEALPNDERDTTVPVMAATTLRKLLTGBLLTLASRQ 180
 DB 144 KETLAFLLNMGDHTRLDREPELNEALPNDERDTTVPVMAATTLRKLLTGBLLTLASRQ 203
 QY 181 QLIIMMEADKVAAGPLRLSALPAGWFIADKSGAGERGSGIITIALGPDG 228
 DB 204 QLIIMMEADKVAAGPLRLSALPAGWFIADKSGAGERGSGIITIALGPDG 251

RESULT 10

US-10-416-708A-73
 ; Sequence 73, Application US/10416708A
 ; Publication No. US20040161753A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wise, John G.
 ; APPLICANT: Fromknecht, Katja
 ; TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING
 ; TITLE OF INVENTION: SPECIFICITIES
 ; FILE REFERENCE: 37779-0004
 ; CURRENT APPLICATION NUMBER: US/10/416,708A
 ; CURRENT FILING DATE: 2004-01-28
 ; NUMBER OF SEQ ID NOS: 89
 ; SOFTWARE: Patent In version 3.2
 ; SEQ ID NO 73
 ; LENGTH: 286
 ; TYPE: PRP
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic Construct
 US-10-416-708A-73

Query Match 100.0%; Score 1170; DB 16; Length 286;
 Best Local Similarity 100.0%; Pred. No. 9.2e-113;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVAEDDQAGRVGTELDLNSGKILSFREPERPMMSTFKVLICGAVLSRID 60
 DB 24 HPEITLVKVAEDDQAGRVGTELDLNSGKILSFREPERPMMSTFKVLICGAVLSRID 83

Qy 61 AGOEOLGRIRIHSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGCP 120
Db 84 AGOEOLGRIRIHSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGCP 143
Qy 121 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDITMPVAMATTIRKLLTGELTLTASRQ 180
Db 144 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDITMPVAMATTIRKLLTGELTLTASRQ 203
Qy 181 OLIDMEADKVAAGPLRSALPAGWFIADKSGGERSGIIAALGPDG 228
Db 204 OLIDMEADKVAAGPLRSALPAGWFIADKSGGERSGIIAALGPDG 251

RESULT 11

US-09-919-901-2
; Sequence 2, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-09-919-901-2

Query Match 100.0%; Score 1170; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 1.7e-111;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HPEITLVKVKDAEDQAGAVGYIELDLSNGKILSRPERPFPMSFTFVLLCGAVLSRID 60
Db 2045 HPEITLVKVKDAEDQAGAVGYIELDLSNGKILSRPERPFPMSFTFVLLCGAVLSRID 2104
Qy 61 AGOEOLGRIRIHSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGCP 120
Db 2105 AGOEOLGRIRIHSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGCP 2164
Qy 121 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDITMPVAMATTIRKLLTGELTLTASRQ 180
Db 2165 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDITMPVAMATTIRKLLTGELTLTASRQ 2224
Qy 181 OLIDMEADKVAAGPLRSALPAGWFIADKSGGERSGIIAALGPDG 228
Db 2225 OLIDMEADKVAAGPLRSALPAGWFIADKSGGERSGIIAALGPDG 2272

RESULT 12

US-09-919-901-9
; Sequence 9, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901

; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-09-919-901-9

Query Match 100.0%; Score 1170; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 1.7e-111;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HPEITLVKVKDAEDQAGAVGYIELDLSNGKILSRPERPFPMSFTFVLLCGAVLSRID 60
Db 2045 HPEITLVKVKDAEDQAGAVGYIELDLSNGKILSRPERPFPMSFTFVLLCGAVLSRID 2104
Qy 61 AGOEOLGRIRIHSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGCP 120
Db 2105 AGOEOLGRIRIHSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGCP 2164
Qy 121 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDITMPVAMATTIRKLLTGELTLTASRQ 180
Db 2165 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDITMPVAMATTIRKLLTGELTLTASRQ 2224
Qy 181 OLIDMEADKVAAGPLRSALPAGWFIADKSGGERSGIIAALGPDG 228
Db 2225 OLIDMEADKVAAGPLRSALPAGWFIADKSGGERSGIIAALGPDG 2272

RESULT 13

US-09-919-901-16
; Sequence 16, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-09-919-901-16

Query Match 100.0%; Score 1170; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 1.7e-111;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HPEITLVKVKDAEDQAGAVGYIELDLSNGKILSRPERPFPMSFTFVLLCGAVLSRID 60
Db 2045 HPEITLVKVKDAEDQAGAVGYIELDLSNGKILSRPERPFPMSFTFVLLCGAVLSRID 2104
Qy 61 AGOEOLGRIRIHSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGCP 120

Db 2105 AGOQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGCP 2164
QY 121 KETAFALHNMGDHVTRLDRWPEPELNEAIPNDERDTMPVAMATTLRKLLTGELLTLASRQ 180
Db 2165 KETAFALHNMGDHVTRLDRWPEPELNEAIPNDERDTMPVAMATTLRKLLTGELLTLASRQ 2224
QY 181 QLIDMMEADKVAGPLRLSALPAGWFIADKSGAGERSGRTIITGALGPDG 228
Db 2225 QLIDMMEADKVAGPLRLSALPAGWFIADKSGAGERSGRTIITGALGPDG 2272

RESULT 14
US-10-191-966-2
Sequence 2, Application US/10191966
Publication No. US20030175692A1
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 2307
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-10-191-966-2

Query Match 100.0%; Score 1170; DB 14; Length 2307;
Best Local Similarity 100.0%; Pred. No. 1,7e-111;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKDAEDQIGARVGYIEIDLNSGKILSFREPERPPMSTFVLLCGAVLSRID 60
Db 2045 HPEITLVKVKDAEDQIGARVGYIEIDLNSGKILSFREPERPPMSTFVLLCGAVLSRID 2104
QY 61 AGOQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGCP 120
Db 2105 AGOQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGCP 2164
QY 121 KETAFALHNMGDHVTRLDRWPEPELNEAIPNDERDTMPVAMATTLRKLLTGELLTLASRQ 180
Db 2165 KETAFALHNMGDHVTRLDRWPEPELNEAIPNDERDTMPVAMATTLRKLLTGELLTLASRQ 2224
QY 181 QLIDMMEADKVAGPLRLSALPAGWFIADKSGAGERSGRTIITGALGPDG 228
Db 2225 QLIDMMEADKVAGPLRLSALPAGWFIADKSGAGERSGRTIITGALGPDG 2272

RESULT 15
US-10-191-966-9
Sequence 9, Application US/10191966
Publication No. US20030175692A1
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933

; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-9

Query Match 100.0%; Score 1170; DB 14; Length 2307;
Best Local Similarity 100.0%; Pred. No. 1,7e-111;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKDAEDQIGARVGYIEIDLNSGKILSFREPERPPMSTFVLLCGAVLSRID 60
Db 2045 HPEITLVKVKDAEDQIGARVGYIEIDLNSGKILSFREPERPPMSTFVLLCGAVLSRID 2104
QY 61 AGOQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGCP 120
Db 2105 AGOQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGCP 2164
QY 121 KETAFALHNMGDHVTRLDRWPEPELNEAIPNDERDTMPVAMATTLRKLLTGELLTLASRQ 180
Db 2165 KETAFALHNMGDHVTRLDRWPEPELNEAIPNDERDTMPVAMATTLRKLLTGELLTLASRQ 2224
QY 181 QLIDMMEADKVAGPLRLSALPAGWFIADKSGAGERSGRTIITGALGPDG 228
Db 2225 QLIDMMEADKVAGPLRLSALPAGWFIADKSGAGERSGRTIITGALGPDG 2272

Search completed: June 10, 2005, 11:09:07
Job time : 77.3841 secs

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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:23:36 ; Search time 63.6534 Seconds

(without alignments)
1528.512 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_190

Perfect score: 975
Sequence: 1 HPELVKVKYKADBDQAGARVG.....GELITLASRQQLIDMWEADK 190

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	975	100.0	229	2	06WVY5 Klebsiella
2	975	100.0	232	2	06WVY4 Hafnia alve
3	975	100.0	241	2	06WVY8 Klebsiella
4	975	100.0	242	2	06WVY3 Escherichia
5	975	100.0	285	2	06KB67 hordeum vul
6	975	100.0	286	2	038058 bacterioph
7	975	100.0	286	2	000626 staphylococ
8	975	100.0	286	2	079CL6 methylobact
9	975	100.0	286	2	079DR3 Escherichia
10	970	99.5	225	2	038212 bacterioph
11	970	99.5	232	2	06PRU7 Escherichia
12	970	99.5	255	2	084H50 Escherichia
13	970	99.5	261	2	084H49 Escherichia
14	970	99.5	264	2	06FRU6 acinetobact
15	970	99.5	281	2	06QIV0 Escherichia
16	970	99.5	282	2	06QIV1 Escherichia
17	970	99.5	286	1	BLAT_ECOLI
18	970	99.5	286	1	BLAT_SALTI
19	970	99.5	286	2	053043 Klebsiella
20	970	99.5	286	2	08KSD3 Klebsiella
21	970	99.5	286	2	08VFA3 Klebsiella
22	970	99.5	286	2	08VFA3 Klebsiella
23	970	99.5	286	2	093A77 Escherichia
24	970	99.5	286	2	093A77 Escherichia
25	970	99.5	286	2	093A77 Escherichia
26	970	99.5	286	2	06A253 Klebsiella
27	970	99.5	286	2	06LBN9 pseudomonas
28	970	99.5	286	2	06LBN9 pseudomonas
29	970	99.5	286	2	06LBN9 pseudomonas
30	970	99.5	286	2	06LBN9 pseudomonas
31	970	99.5	286	2	06WJ74 Escherichia

32	970	99.5	286	2	06WJ11 enterobacte
33	970	99.5	286	2	06WJ11 enterobacte
34	970	99.5	286	2	06WJ11 enterobacte
35	970	99.5	286	2	07B3X5 citrobacter
36	970	99.5	286	2	07B899 Klebsiella
37	970	99.5	286	2	07B899 Klebsiella
38	970	99.5	286	2	07B899 Klebsiella
39	970	99.5	286	2	07B899 Klebsiella
40	970	99.5	286	2	07DHD3 Klebsiella
41	970	99.5	286	2	0844X1 Klebsiella
42	970	99.5	286	2	0844X1 Klebsiella
43	970	99.5	286	2	09EYX1 Escherichia
44	970	99.5	286	2	09EYX1 Escherichia
45	970	99.5	286	2	09EYX1 Escherichia

ALIGNMENTS

RESULT 1									
ID	06WVY5	PRELIMINARY;	PRT;	229	AA.				
AC	06WVY5;								
DT	05-JUL-2004 (TREMBLrel. 27, Created)								
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)								
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)								
DE	Beta-lactamase (Fragment).								
GN	Name=Blactem;								
OS	Klebsiella oxytoca.								
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;								
OC	Enterobacteriaceae; Klebsiella.								
OX	NCBI_TaxID=571;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=Misc126;								
RA	Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;								
RL	Submitted (Apr-2004) to the EMBL/Genbank/DBJ databases.								
DR	EMBL; AY265885; AAP3843.1; -								
DR	HSP; P00807; IKGE.								
DR	InterPro; IPR000871; Beta_lactamase_A.								
DR	PRINTS; PR00118; BLACTAMASEA.								
DR	PROSITE; PS00146; BETA_LACTAMASE_A; 1.								
FT	NON_TER 1 1								
FT	NON_TER 229 229								
SQ	SEQUENCE 229 AA; 25067 MW; C85582C2617F4467 CRC64;								
Query Match 100.0%; Score 975; DB 2; Length 229;									
Best Local Similarity 100.0%; Pred. No. 2.5e-74;									
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	HPELVKVKYKADBDQAGARVGITELDINSKLTIESFRPERPPMSTFKVLUCGAVLSRID	60						
DB	2	HPELVKVKYKADBDQAGARVGITELDINSKLTIESFRPERPPMSTFKVLUCGAVLSRID	61						
QY	61	AGQELGRIRHSQNDLVESPVTEKHLTDGATVRELCSAITSNDTAAANLLTTIGCP	120						
DB	62	AGQELGRIRHSQNDLVESPVTEKHLTDGATVRELCSAITSNDTAAANLLTTIGCP	121						
QY	121	KELTAFILNMGDHYRLDRWPELNEALPNDERDTTMEVAAATTKLITGELLTASRQ	180						
DB	122	KELTAFILNMGDHYRLDRWPELNEALPNDERDTTMEVAAATTKLITGELLTASRQ	181						
QY	181	QILIDMWEADK 190							
DB	182	QILIDMWEADK 191							
RESULT 2									
ID	06WVY4	PRELIMINARY;	PRT;	232	AA.				
AC	06WVY4;								
DT	05-JUL-2004 (TREMBLrel. 27, Created)								
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)								

DT 05-JUL-2004 (TREMBLrel. 27, last annotation update)
 DE Beta-lactamase (Fragment).
 GN Name=blatEM;
 OS Hafnia alvei.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Hafnia.
 OX NCBI_TaxID=569;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MISC198;
 RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
 RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY265886; AAP3844.1; -.
 DR HSSP; P00807; 1KGE.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 FT NON_TER 1
 FT 232
 SQ SEQUENCE 232 AA; 25380 MW; 3D5DFD85582C261 CRC64;

Query Match 100.0%; Score 975; DB 2; Length 232;
 Best Local Similarity 100.0%; Pred. No. 2.5e-74;
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADBDQAGAVGYIELDINSKILSFRRPFRPMMSTFVLLCGAVLSRID 60
 DB 2 HPELVKVKADBDQAGAVGYIELDINSKILSFRRPFRPMMSTFVLLCGAVLSRID 61
 QY 61 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120
 DB 62 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 121
 QY 121 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDTTTPVAAATTLRKLLTGBLLTLASRQ 180
 DB 122 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDTTTPVAAATTLRKLLTGBLLTLASRQ 181
 QY 181 QLIIDMMEADK 190
 DB 182 QLIIDMMEADK 191

RESULT 3

Q6MWY8 PRELIMINARY; PRT; 241 AA.
 AC Q6MWY8;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, last annotation update)
 DE Beta-lactamase (Fragment).
 GN Name=blatEM;
 OS Klebsiella pneumoniae.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Klebsiella.
 OX NCBI_TaxID=573;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MISC112;
 RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
 RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY265882; AAP3840.1; -.
 DR HSSP; P00807; 1KGE.
 DR InterPro; IPR00146; Beta_lactamase.
 DR pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 FT NON_TER 1
 FT 241
 SQ SEQUENCE 241 AA; 26407 MW; 38DF2AFDF0C5807D CRC64;

Query Match 100.0%; Score 975; DB 2; Length 241;
 Best Local Similarity 100.0%; Pred. No. 2.6e-74;

Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADBDQAGAVGYIELDINSKILSFRRPFRPMMSTFVLLCGAVLSRID 60
 DB 7 HPELVKVKADBDQAGAVGYIELDINSKILSFRRPFRPMMSTFVLLCGAVLSRID 66
 QY 61 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120
 DB 67 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 126
 QY 121 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDTTTPVAAATTLRKLLTGBLLTLASRQ 180
 DB 127 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDTTTPVAAATTLRKLLTGBLLTLASRQ 186
 QY 181 QLIIDMMEADK 190
 DB 187 QLIIDMMEADK 196

RESULT 4

Q6MWY3 PRELIMINARY; PRT; 242 AA.
 AC Q6MWY3;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, last annotation update)
 DE Beta-lactamase (Fragment).
 GN Name=blatEM;
 OS Escherichia coli.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TA005;
 RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
 RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY265887; AAP3845.1; -.
 DR HSSP; P00807; 1KGE.
 DR InterPro; IPR00146; Beta_lactamase.
 DR pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 FT NON_TER 1
 FT 242
 SQ SEQUENCE 242 AA; 26554 MW; 38C3DFA8A5A3807D CRC64;

Query Match 100.0%; Score 975; DB 2; Length 242;
 Best Local Similarity 100.0%; Pred. No. 2.6e-74;
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADBDQAGAVGYIELDINSKILSFRRPFRPMMSTFVLLCGAVLSRID 60
 DB 8 HPELVKVKADBDQAGAVGYIELDINSKILSFRRPFRPMMSTFVLLCGAVLSRID 67
 QY 61 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120
 DB 68 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 127
 QY 121 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDTTTPVAAATTLRKLLTGBLLTLASRQ 180
 DB 128 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDTTTPVAAATTLRKLLTGBLLTLASRQ 187
 QY 181 QLIIDMMEADK 190
 DB 188 QLIIDMMEADK 197

RESULT 5

Q6KB67 PRELIMINARY; PRT; 285 AA.
 AC Q6KB67;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, last annotation update)
 DE Beta-lactamase (Fragment).
 GN Name=blatEM;
 OS Escherichia coli.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TA005;
 RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
 RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY265887; AAP3845.1; -.
 DR HSSP; P00807; 1KGE.
 DR InterPro; IPR00146; Beta_lactamase.
 DR pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 FT NON_TER 1
 FT 285
 SQ SEQUENCE 285 AA; 30800 MW; 38C3DFA8A5A3807D CRC64;

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DR 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DB 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DS Hypothetical protein (Fragment).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
OC NCBI_TaxId=4513;
OX [1]
RN SEQUENCE FROM N.A.
RP TISSUE=First leaf;
RA Jansen C., Korell M., Bekey C., Biedenkopf D., Kogel K.H.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ717739; CAG30723.1; -.
DR HSSP: P00807; 1A0.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR000871; Beta_lactamase_A.
DR Pfam: PF00144; Beta_lactamase; 1.
DR PRINTS: PR00118; BLACTAMASE.
DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
KW Hypothetical protein.
FT NON_TER 285
SQ SEQUENCE 285 AA; 31371 MW; A2P22753375FA930 CRC64;

Query Match 100.0%; Score 975; DB 2; Length 285;
Best Local Similarity 100.0%; Pred. No. 3.2e-74;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGYIELDLSGKILSFSPRPERPFPMSTFKVLLCGAVLSRID 60
DB HPEITLVKVDADQAGARVGYIELDLSGKILSFSPRPERPFPMSTFKVLLCGAVLSRID 83
QY 61 AGQEQIGRRIRHSQNDLVEYSPTVEKHLTDGNTVELCSAATMSDNTAANLLTTIGSP 120
DB AGQEQIGRRIRHSQNDLVEYSPTVEKHLTDGNTVELCSAATMSDNTAANLLTTIGSP 143
QY 84 AGQEQIGRRIRHSQNDLVEYSPTVEKHLTDGNTVELCSAATMSDNTAANLLTTIGSP 143
DB 84 KETLAFILNMGDHVRRLDRWPELNEAIPNDRDITMPVAMATTIRKLLTGLLTLASRQ 180
QY 121 KETLAFILNMGDHVRRLDRWPELNEAIPNDRDITMPVAMATTIRKLLTGLLTLASRQ 180
DB 144 KETLAFILNMGDHVRRLDRWPELNEAIPNDRDITMPVAMATTIRKLLTGLLTLASRQ 203
QY 181 QLIDWMEADK 190
DB 204 QLIDWMEADK 213

RESULT 6
Q38058 PRELIMINARY; PRT; 286 AA.
ID Q38058
AC Q38058;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Beta lactamase.
GN Name=bla;
OS Bacteriophage phi-X174.
OC Viruses; ssDNA viruses; Microviridae; Microvirinae.
OC NCBI_TaxId=10847;
OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=95172401; PubMed=7867948; DOI=10.1016/0378-1119(94)00839-K;
RA Henrich B., Schmidberger B.;
RL "A variant of phiX174 gene B-based positive selection vectors with
RT enhanced lytic potential.";
RL Gene 154:51-54(1995).
RL EMBL: Z35638; CAA84692.1; -.
DR PIR: S47061; S47061.
DR HSSP: Q9R435; 1HTZ.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR000871; Beta_lactamase_A.
DR Pfam: PF00144; Beta_lactamase; 1.
DR PRINTS: PR00118; BLACTAMASE.
DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.

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SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;

Query Match 100.0%; Score 975; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.2e-74;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGYIELDLSGKILSFSPRPERPFPMSTFKVLLCGAVLSRID 60
DB HPEITLVKVDADQAGARVGYIELDLSGKILSFSPRPERPFPMSTFKVLLCGAVLSRID 83
QY 24 HPEITLVKVDADQAGARVGYIELDLSGKILSFSPRPERPFPMSTFKVLLCGAVLSRID 83
DB 24 HPEITLVKVDADQAGARVGYIELDLSGKILSFSPRPERPFPMSTFKVLLCGAVLSRID 83
QY 61 AGQEQIGRRIRHSQNDLVEYSPTVEKHLTDGNTVELCSAATMSDNTAANLLTTIGSP 120
DB AGQEQIGRRIRHSQNDLVEYSPTVEKHLTDGNTVELCSAATMSDNTAANLLTTIGSP 143
QY 84 AGQEQIGRRIRHSQNDLVEYSPTVEKHLTDGNTVELCSAATMSDNTAANLLTTIGSP 143
DB 84 KETLAFILNMGDHVRRLDRWPELNEAIPNDRDITMPVAMATTIRKLLTGLLTLASRQ 180
QY 121 KETLAFILNMGDHVRRLDRWPELNEAIPNDRDITMPVAMATTIRKLLTGLLTLASRQ 180
DB 144 KETLAFILNMGDHVRRLDRWPELNEAIPNDRDITMPVAMATTIRKLLTGLLTLASRQ 203
QY 181 QLIDWMEADK 190
DB 204 QLIDWMEADK 213

RESULT 7
Q00626 PRELIMINARY; PRT; 286 AA.
ID Q00626
AC Q00626; O08022; O08102; O09393; O09396; O09397; O09398; O09399;
AC O09400; O09401; O09402; O09403; O09404; O09405; O09406; O09407;
AC O09408; O09481; O09482; O09483; O09490; Q57339;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Beta-lactamase.
OS Staphylococcus aureus.
OC Plasmid J3356/POX7/3, and Plasmid J3356/POX7/1.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC PLASMID=J3356/POX7/3, and J3356/POX7/1;
RA MEDLINE=9642275; PubMed=8825372; DOI=10.1006/plas.1995.0005;
RA Needham C., Noble W.C., Dyke K.G.;
RT "The staphylococcal insertion sequence IS257 is active.";
RL Plasmid 34:198-205(1995).
DR EMBL: U36912; AAB39957.1; -.
DR EMBL: U36911; AAB39956.1; -.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR000871; Beta_lactamase_A.
DR Pfam: PF00144; Beta_lactamase; 1.
DR PRINTS: PR00118; BLACTAMASE.
DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
KW Plasmid.
SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;

Query Match 100.0%; Score 975; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.2e-74;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGYIELDLSGKILSFSPRPERPFPMSTFKVLLCGAVLSRID 60
DB HPEITLVKVDADQAGARVGYIELDLSGKILSFSPRPERPFPMSTFKVLLCGAVLSRID 83
QY 24 HPEITLVKVDADQAGARVGYIELDLSGKILSFSPRPERPFPMSTFKVLLCGAVLSRID 83
DB 24 HPEITLVKVDADQAGARVGYIELDLSGKILSFSPRPERPFPMSTFKVLLCGAVLSRID 83
QY 61 AGQEQIGRRIRHSQNDLVEYSPTVEKHLTDGNTVELCSAATMSDNTAANLLTTIGSP 120
DB AGQEQIGRRIRHSQNDLVEYSPTVEKHLTDGNTVELCSAATMSDNTAANLLTTIGSP 143
QY 84 AGQEQIGRRIRHSQNDLVEYSPTVEKHLTDGNTVELCSAATMSDNTAANLLTTIGSP 143
DB 84 KETLAFILNMGDHVRRLDRWPELNEAIPNDRDITMPVAMATTIRKLLTGLLTLASRQ 180
QY 121 KETLAFILNMGDHVRRLDRWPELNEAIPNDRDITMPVAMATTIRKLLTGLLTLASRQ 180
DB 144 KETLAFILNMGDHVRRLDRWPELNEAIPNDRDITMPVAMATTIRKLLTGLLTLASRQ 203
QY 181 QLIDWMEADK 190
DB 204 QLIDWMEADK 213

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OS Bacteriophage f1.
OC Viruses; ssDNA viruses; Inoviridae; Inovirus.
OX NCBI_TaxID=10863;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86278026; PubMed=3525535;
RA Topal M.D., Radie J.S., Conrad M.;
RT "O-6-methylguanine mutation and repair is nonuniform: Selection for
  DNA motif interactive with O-6-methylguanine.";
RL J. Biol. Chem. 261:9879-9885(1986).
DR EMBL; M14017; AAA32208.1; -.
DR HSSP; Q9R435; 1HTZ.
DR InterPro; IPR001466; Beta_lactamase.
DR Pfam; PF00144; Beta_lactamase_A.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER
SQ SEQUENCE 225 AA; 25022 MW; 009BF841D618BA09 CRC64;

Query Match 99.5%; Score 970; DB 2; Length 225;
Best Local Similarity 98.9%; Pred. No. 6,4e-74;
Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HPEITVKKVADBDQAGRVGYIELDLSGKILSFPRPERFPMSTFKYLLCGAVLSRID 60
DB 24 HPEITVKKVADBDQAGRVGYIELDLSGKILSFPRPERFPMSTFKYLLCGAVLSRID 83
OY 61 AGQBLGRRIRHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANILLTTIGSP 120
DB 84 AGQBLGRRIRHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANILLTTIGSP 143
OY 121 KELITAFLNMGDGHVRLDRWPELNEAIPNDRDITMPAAMATTIRKLLTGELTLASRQ 180
DB 144 KELITAFLNMGDGHVRLDRWPELNEAIPNDRDITMPAAMATTIRKLLTGELTLASRQ 203
OY 181 OLIDWMEADK 190
DB 204 OLIDWMEADK 213

RESULT 11
O6PRU7 PRELIMINARY; PRT; 232 AA.
AC O6PRU7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Inhibitor-resistant TEM beta-lactamase (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RA Ghandili S., Hosseini-Mazini S.M.;
RL Submitted (Mar-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY583761; AAS86427.1; -.
DR HSSP; P00807; 1ALQ.
DR InterPro; IPR001466; Beta_lactamase.
DR Pfam; PF00144; Beta_lactamase_A.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER
SQ SEQUENCE 232 AA; 25558 MW; 5791CD285BE70EB0 CRC64;

Query Match 99.5%; Score 970; DB 2; Length 232;
Best Local Similarity 98.9%; Pred. No. 6,6e-74;
Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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OY 1 HPEITVKKVADBDQAGRVGYIELDLSGKILSFPRPERFPMSTFKYLLCGAVLSRID 60
DB 15 HPEITVKKVADBDQAGRVGYIELDLSGKILSFPRPERFPMSTFKYLLCGAVLSRID 74
OY 61 AGQBLGRRIRHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANILLTTIGSP 120
DB 75 AGQBLGRRIRHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANILLTTIGSP 134
OY 121 KELITAFLNMGDGHVRLDRWPELNEAIPNDRDITMPAAMATTIRKLLTGELTLASRQ 180
DB 135 KELITAFLNMGDGHVRLDRWPELNEAIPNDRDITMPAAMATTIRKLLTGELTLASRQ 194
OY 181 OLIDWMEADK 190
DB 195 OLIDWMEADK 204

RESULT 12
O84H50 PRELIMINARY; PRT; 255 AA.
AC O84H50;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE TEM-117 beta-lactamase (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RA Box A.T.A., Pauw A., Laverstein-vanhal M.A.;
RL Submitted (Jul-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; A1130282; AAN05026.1; -.
DR HSSP; Q9R435; 1HTZ.
DR InterPro; IPR001466; Beta_lactamase.
DR Pfam; PF00144; Beta_lactamase_A.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER
SQ SEQUENCE 255 AA; 27906 MW; DCBB28B65978C3A6 CRC64;

Query Match 99.5%; Score 970; DB 2; Length 255;
Best Local Similarity 98.9%; Pred. No. 7,4e-74;
Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HPEITVKKVADBDQAGRVGYIELDLSGKILSFPRPERFPMSTFKYLLCGAVLSRID 60
DB 12 HPEITVKKVADBDQAGRVGYIELDLSGKILSFPRPERFPMSTFKYLLCGAVLSRID 71
OY 61 AGQBLGRRIRHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANILLTTIGSP 120
DB 72 AGQBLGRRIRHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANILLTTIGSP 131
OY 121 KELITAFLNMGDGHVRLDRWPELNEAIPNDRDITMPAAMATTIRKLLTGELTLASRQ 180
DB 132 KELITAFLNMGDGHVRLDRWPELNEAIPNDRDITMPAAMATTIRKLLTGELTLASRQ 191
OY 181 OLIDWMEADK 190
DB 192 OLIDWMEADK 201

RESULT 13
O84H49 PRELIMINARY; PRT; 261 AA.
AC O84H49;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE TEM-110 beta-lactamase (Fragment).
```

OS Klebsiella oxytoca.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=571;
RN [1]
RP SEQUENCE FROM N.A.
RA Box A.T.A., Pauw A., Leverstein-vanhal M.A., Verhoef J., Fluit A.C.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY130283; AAN05027.1; -.
DR HSSP; Q9R435; IHTZ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON TER 1
FT NON TER 261
SQ SEQUENCE 261 AA; 28738 MW; 4F748F773A08CB8 CRC64;

Query Match 99.5%; Score 970; DB 2; Length 261;
Best Local Similarity 98.9%; Pred. No. 7.7e-74;
Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGARVGYIELDLSGKILIESFRPERPMMSTPFVLLCGAVLSRID 60
DB 12 HPEITLVKVKADBDQAGARVGYIELDLSGKILIESFRPERPMMSTPFVLLCGAVLSRID 71
QY 61 AGQOLGRIRIHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANILLTTIGSP 120
DB 72 AGQOLGRIRIHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANILLTTIGSP 131
QY 121 KETLAFILNMGDHYTRLDWRPELNEAIPNDRDITPMVAATTLRKLLTGELLTLASRQ 180
DB 132 KETLAFILNMGDHYTRLDWRPELNEAIPNDRDITPMVAATTLRKLLTGELLTLASRQ 191
QY 181 QLIDWMEADK 190
DB 192 QLIDWMEADK 201

RESULT 14

ID Q6PRU6 PRELIMINARY; PRT; 264 AA.
AC Q6PRU6;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE TEM beta-lactamase (Fragment).
OS Acinetobacter sp. U11.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=269266;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=U11;
RA Ghandili S., Hosseini-Maziani S.M.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY583762; AAS86428.1; -.
DR HSSP; P00807; IALQ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON TER 1
FT NON TER 264
SQ SEQUENCE 264 AA; 28986 MW; A4F071CF7489352C CRC64;

Query Match 99.5%; Score 970; DB 2; Length 264;
Best Local Similarity 98.9%; Pred. No. 7.8e-74;
Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGARVGYIELDLSGKILIESFRPERPMMSTPFVLLCGAVLSRID 60

DB 12 HPEITLVKVKADBDQAGARVGYIELDLSGKILIESFRPERPMMSTPFVLLCGAVLSRID 71
QY 61 AGQOLGRIRIHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANILLTTIGSP 120
DB 72 AGQOLGRIRIHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANILLTTIGSP 131
QY 121 KETLAFILNMGDHYTRLDWRPELNEAIPNDRDITPMVAATTLRKLLTGELLTLASRQ 180
DB 132 KETLAFILNMGDHYTRLDWRPELNEAIPNDRDITPMVAATTLRKLLTGELLTLASRQ 191
QY 181 QLIDWMEADK 190
DB 192 QLIDWMEADK 201

RESULT 15

ID Q6QIV0 PRELIMINARY; PRT; 281 AA.
AC Q6QIV0;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE TEM-1 beta-lactamase (Fragment).
GN Name=BlatEM-1;
OS Serratia marcescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ES-42, ES-46, ES-71, and ES-11;
RA Yatsuyama J., Saito S., Harata S., Suzuki N., Amano K.-I.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY538700; AAS46846.1; -.
DR EMBL; AY538701; AAS46847.1; -.
DR EMBL; AY538702; AAS46848.1; -.
DR EMBL; AY538698; AAS46844.1; -.
DR HSSP; P00807; IALQ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON TER 281
FT NON TER 281
SQ SEQUENCE 281 AA; 30837 MW; C6934B9C696057BF CRC64;

Query Match 99.5%; Score 970; DB 2; Length 281;
Best Local Similarity 98.9%; Pred. No. 8.4e-74;
Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGARVGYIELDLSGKILIESFRPERPMMSTPFVLLCGAVLSRID 60
DB 24 HPEITLVKVKADBDQAGARVGYIELDLSGKILIESFRPERPMMSTPFVLLCGAVLSRID 83
QY 61 AGQOLGRIRIHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANILLTTIGSP 120
DB 84 AGQOLGRIRIHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANILLTTIGSP 143
QY 121 KETLAFILNMGDHYTRLDWRPELNEAIPNDRDITPMVAATTLRKLLTGELLTLASRQ 180
DB 144 KETLAFILNMGDHYTRLDWRPELNEAIPNDRDITPMVAATTLRKLLTGELLTLASRQ 203
QY 181 QLIDWMEADK 190
DB 204 QLIDWMEADK 213

Search completed: June 10, 2005, 10:57:02
Job time : 63.6534 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:22:36 ; Search time 66.6888 Seconds
(without alignments)
997.510 Million cell updates/sec

Title: US-10-6668-778-2_COPY_1_172

```

      FELICL SCORE: 885
Sequence: 1 HPETLVKVKDAEDQLGARV.....RDTTMVAMATTIRKLTLGE 172

```

Scoring table: BLOSUM62

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing:	Minimum Match	0%
	Maximum Match	100%

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	885	100.0	263	4	AAE05544	Aae05544 E. coli m
2	885	100.0	263	4	AAB36692	Aab36692 Escherichia
3	885	100.0	263	8	ADJ67709	Adj67709 Escherichia
4	885	100.0	264	2	AAW16634	Aaw16634 Beta-lactam
5	885	100.0	264	2	AAW18680	Aaw18680 Intracellular
6	885	100.0	286	2	AAR31575	Aar31575 Ampicillin
7	885	100.0	286	2	AAAR37619	Aar37619 Secretory
8	885	100.0	286	2	AAAR6423	Aar6423 Cytochrom
9	885	100.0	286	2	AAW16635	Aaw16635 Beta-lactam
10	885	100.0	286	2	AAW18679	Aaw18679 Secretory
11	885	100.0	286	2	AAAY08529	Aay08529 Vector pA
12	885	100.0	286	3	AAAB10442	Aab10442 Expressid
13	885	100.0	286	3	AAAB10438	Aab10438 Expressid
14	885	100.0	286	3	AAAB10440	Aab10440 Expressid
15	885	100.0	286	4	AAAB50898	Aab50898 Protein e
16	885	100.0	286	4	AAAB31173	Aab31173 Amino acid
17	885	100.0	286	5	AAU75551	Aau75551 celJ inte
18	885	100.0	286	6	ABP55474	Abp55474 Vector pC
19	885	100.0	286	6	ABR43622	Ab43622 Cloning v
20	885	100.0	286	8	ADRW70422	Adr70422 Vector pA
21	885	100.0	286	8	ADRW70410	Adr70410 Vector pA
22	885	100.0	286	8	ADRW70404	Adr70404 Vector pA
23	885	100.0	286	8	ADRW70416	Adr70416 Vector pA
24	885	100.0	286	8	ADRW70428	Adr70428 Vector pA
25	885	100.0	290	4	AAU23219	Aau23219 Novel hum

45	880	99.4	265	2	AAH48613
44	880	99.4	265	2	AAH08232
43	880	99.4	265	2	AAH08233
42	884	99.9	1967	6	ABH82793
41	884	99.9	1253	7	ADH14284
40	884	99.9	1253	7	ADG22811
39	884	99.9	872	7	ADK65686
38	884	99.9	286	2	AAH06551
37	885	100.0	2761	2	ADH11249
36	885	100.0	2307	3	AAH70066
35	885	100.0	2307	3	AAH70065
34	885	100.0	2307	3	AAH70064
33	885	100.0	2377	2	AAH52701
32	885	100.0	1088	5	ADH46109
31	885	100.0	1031	5	ADH46109
30	885	100.0	585	6	ADA67747
29	885	100.0	408	6	ABH55981
28	885	100.0	327	2	AAH18681
27	885	100.0	327	2	AAH16636
26	885	100.0	290	4	AAH84362
25	885	100.0	290	4	AAH84362
24	885	100.0	290	4	AAH84362
23	885	100.0	290	4	AAH84362
22	885	100.0	290	4	AAH84362
21	885	100.0	290	4	AAH84362
20	885	100.0	290	4	AAH84362
19	885	100.0	290	4	AAH84362
18	885	100.0	290	4	AAH84362
17	885	100.0	290	4	AAH84362
16	885	100.0	290	4	AAH84362
15	885	100.0	290	4	AAH84362
14	885	100.0	290	4	AAH84362
13	885	100.0	290	4	AAH84362
12	885	100.0	290	4	AAH84362
11	885	100.0	290	4	AAH84362
10	885	100.0	290	4	AAH84362
9	885	100.0	290	4	AAH84362
8	885	100.0	290	4	AAH84362
7	885	100.0	290	4	AAH84362
6	885	100.0	290	4	AAH84362
5	885	100.0	290	4	AAH84362
4	885	100.0	290	4	AAH84362
3	885	100.0	290	4	AAH84362
2	885	100.0	290	4	AAH84362
1	885	100.0	290	4	AAH84362

ALIGNMENTS

RESULT	1
AAE05544	
ID	AAE05544 standard; protein; 263 AA.
AC	
XX	AAE05544;
DT	24-SEP-2001 (first entry)
XX	
DE	E. coli mature TEM-1 beta-lactamase.
KM	Interaction-dependent enzyme association; IDEA system; biosensor;
KW	circularly permuted interaction-activated protein; marker protein;
KM	type A beta-lactamase; TEM-1 beta-lactamase; protein-protein interaction.
XX	therapeutic; drug screening; thioredoxin; ampicillin resistance.
OS	Escherichia coli.
XX	
Key	Location/Qualifiers
FH	Cleavage-site
FT	/note= "Break-point between alpha and omega fragments"
PT	27..28
PT	36..40
Region	/note= "inter-sub-domain loop"
FT	39..39
FT	/note= "Break-point between alpha and omega fragments"
FT	45
Active-site	74..75
Cleavage-site	/note= "Break-point between alpha and omega fragments"
FT	149..150
FT	/note= "Break-point between alpha and omega fragments"
FT	172..173
Cleavage-site	/note= "Break-point between alpha and omega fragments"
FT	189..204
Region	/note= "inter-sub-domain loop"
FT	190..191
Cleavage-site	/note= "Break-point between alpha and omega fragments"
FT	202..203
Cleavage-site	/note= "Break-point between alpha and omega fragments"
FT	228..229
Cleavage-site	/note= "Break-point between alpha and omega fragments"
PT	
PN	WO200151629-A2.
XX	
PD	19-JUL-2001.
XX	
Pf	16-JAN-2001, 2001MO-US001651.
XX	
DR	13-JAN-2000, 2000US-0175968P.
PR	15-MAR-2000, 2000US-00526106.

ID ADJ67709 standard; protein; 263 AA.
 XX ADJ67709;
 XX 20-MAY-2004 (first entry)
 XX Escherichia coli TEM-1 beta-lactamase.
 DE
 XX
 KM fragment complementation system; marker protein;
 KM multiple genetic element incorporation; antibiotic resistance;
 KM beta-lactam derivative activation; anti-tumour compound;
 KM functional reassembly; protein-protein interaction; proteome interaction;
 KM immunoglobulin variable region; immune cell protein; CD40;
 KM phosphorylation-regulated cell signal transducer; TEM-1 beta-lactamase;
 KM enzyme.
 XX Escherichia coli.
 OS
 XX
 PN US2004038317-A1.
 XX
 PD 26-FEB-2004.
 XX
 PF 22-SEP-2003; 2003US-00668778.
 XX
 PR 15-MAR-1999; 99US-0124339P.
 XX
 PR 25-MAY-1999; 99US-0135826P.
 PR 13-JAN-2000; 2000US-0175868P.
 PR 15-MAR-2000; 2000US-00526106.
 XX
 PA (KALO-) KALOBIO5 INC.
 XX
 PI Balint RF, Her J;
 XX
 DR WPI; 2004-203222/19.
 DR N-PSDB; ADJ67708.
 XX
 PT Fragment complementation system for detecting immunoglobulin epitope, has
 PT first oligopeptide containing N-terminal fragment with C-terminal break-
 PT point, second oligopeptide containing C-terminal fragment with N-terminal
 PT break-point.
 XX
 PS Disclosure; SEQ ID NO 2; 47pp; English.
 XX
 XX The invention describes a fragment complementation system (I) comprising
 CC a first oligopeptide having an N-terminal fragment with a C-terminal
 CC break-point, and a second oligopeptide having a C-terminal fragment with
 CC a N-terminal break-point, where the N-terminal fragment and the C-
 CC terminal fragment each are derived from a marker protein and reassemble
 CC to form a functionally reconstituted marker protein. (I) is useful for
 CC selecting simultaneous incorporation of multiple genetic elements into a
 CC host cell, and activating a beta-lactam derivative of an anti-tumour
 CC compound in a host. The method described is useful for identifying a
 CC second oligopeptide to which a first oligopeptide binds, involving co-
 CC expressing the first and second oligopeptides. Binding of the first
 CC oligopeptide to the second oligopeptide results in the functional
 CC reassembly of the marker protein. The method is also useful for
 CC monitoring the occurrence of protein-protein interactions in a sample;
 CC identifying oligopeptide interactions between two different proteomes;
 CC and identifying epitopes that bind to an immunoglobulin variable region.
 CC (I) or an expression cassette (II), encoding a selectable N or C-terminal
 CC peptide, is useful for identifying interactions between an extra cellular
 CC domain of a transmembrane protein and a polypeptide, where the
 CC transmembrane protein is an immune cell protein, preferably CD40. (I) or
 CC (II) is useful for high-throughput identification of compound that
 CC inhibit phosphorylation-regulated cell signal transducers. (I)
 CC efficiently detects multiple interaction between extracellular and
 CC intracellular protein with high throughput format. This is the amino acid
 CC sequence of antibiotic resistance enzyme TEM-1 beta-lactamase that can be
 CC used as a selectable gene in the fragment complementation system of the
 CC invention.
 CC
 CC Sequence 263 AA;
 XX
 XX

Query Match 100.0%; Score 885; DB 8; Length 263;
 Best Local Similarity 100.0%; Pred. No. 5.2e-90;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 HPETLVKVDADPDQARVGYIELDLSGKILESFRPERFPMSTFKYLICGAVLSRID 60
 DB 1 HPETLVKVDADPDQARVGYIELDLSGKILESFRPERFPMSTFKYLICGAVLSRID 60
 OY 61 AGQEQIGRRIRHVSQNDLVESPYTEKHLTDGKTTRELCSAAITMSDNTAANLLTTIGCP 120
 DB 61 AGQEQIGRRIRHVSQNDLVESPYTEKHLTDGKTTRELCSAAITMSDNTAANLLTTIGCP 120
 OY 121 KELLTAFLHMGSHVTRLDKRWPELINAIFPNDERDTPVYMAATTLLKLTGE 172
 DB 121 KELLTAFLHMGSHVTRLDKRWPELINAIFPNDERDTPVYMAATTLLKLTGE 172
 RESULT 4
 ID AAM16634
 XX AAM16634 standard; protein; 264 AA.
 AC AAM16634;
 XX
 DT 09-AUG-1997 (first entry)
 XX
 DE Beta-lactamase (including signal peptide).
 XX
 KM Gene directed enzyme prodng therapy; GDEPT;
 KM virus directed enzyme prodng therapy; VDEPT; beta-lactamase; cancer;
 KM HIV; inflammation.
 XX
 OS Escherichia coli.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..23
 FT /label= Sig_peptide
 XX
 PN MO9719180-A2.
 XX
 PD 29-MAY-1997.
 XX
 PF 19-NOV-1996; 96WO-GB002845.
 XX
 PR 20-NOV-1995; 95GB-00023703.
 XX
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Dev I, Moore JT, Ohmstede C;
 XX
 DR WPI; 1997-298117/27.
 DR N-PSDB; AAT66736.
 XX
 PT Molecular chimera for gene or virus directed enzyme prodng therapy -
 PT useful for treatment of cancer, viral infection or inflammation.
 XX
 PS Example; Page 28; 38pp; English.
 XX
 XX Escherichia coli beta-lactamase (AAM16634), including the signal peptide,
 CC is the expression product of a molecular chimera, designated pCMV-BL
 CC (AAT66737), in which the beta-lactamase gene is under control of the CMV
 CC intermediate/early promoter. Vectors consisting of a transcriptional
 CC regulatory DNA sequence linked to a beta-lactamase gene can be used for
 CC enzyme prodng therapy. Expression of the beta-lactamase in a targeted
 CC cell allows conversion of a prodng into an agent toxic to the cell for
 CC treatment of cancer, viral (e.g. HIV) infection or inflammation.
 CC Secretion of the enzyme has the advantage of increasing neighbouring cell
 CC kill
 XX
 XX Sequence 264 AA;
 XX
 XX Query Match 100.0%; Score 885; DB 2; Length 264;
 XX Best Local Similarity 100.0%; Pred. No. 5.2e-90;
 XX Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 HPELVKVKADBDQAGARVGYIELDLSNGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
DB      2 HPELVKVKADBDQAGARVGYIELDLSNGKILSFRRPFRPMMSTFKVLLCGAVLSRID 61
QY      61 AGOBLGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGGP 120
DB      62 AGOBLGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGGP 121
QY      121 KELTAFLEHMGDHTRLDRWEPELNEAIPNDRDRTTVPVAAATTIRKLLTGE 172
DB      122 KELTAFLEHMGDHTRLDRWEPELNEAIPNDRDRTTVPVAAATTIRKLLTGE 173

RESULT 5
AAM18680
ID      AAM18680 standard; protein; 264 AA.
XX      AC
XX      AAM18680;
XX      DT
XX      13-AUG-1997 (first entry)
XX      DE
XX      Intracellularly-expressed beta-lactamase.
XX      KW
XX      Producing therapy; gene directed enzyme producing therapy; GDBPT;
XX      virus directed enzyme producing therapy; VDEPT; lung cancer;
XX      beta-lactamase; PCMV-delBL.
XX      OS
XX      Escherichia coli.
XX      PN
XX      WO9719183-A2.
XX      PD
XX      29-MAY-1997.
XX      PF
XX      19-NOV-1996; 96WO-GB002846.
XX      PR
XX      20-NOV-1995; 95GB-00023703.
XX      PA
XX      (GLAXO) GLAXO GROUP LTD.
XX      PI
XX      Dev I, Moore JT, Sethna PB;
XX      WPI; 1997-298118/27.
XX      DR
XX      N-PSDB; AAT70311.
XX      PT
XX      DNA construct for gene-directed enzyme producing therapy of lung cancer -
XX      comprises lung- or neuroendocrine-specific promoter controlling
XX      expression of producing-converting enzyme.
XX      PS
XX      Example 811; Page 32-34; 53pp; English.
XX      CC
XX      The intracellular form (AAM18680) of TEM beta-lactamase is expressed by
XX      PCMV-delBL (AAT70311) in which a PCR-amplified beta-lactamase coding
XX      sequence, minus the signal sequence, is placed under control of the
XX      immediate/early promoter of cytomegalovirus. Intracellular beta-
XX      lactamase constructs, placed under control of promoter/enhancer elements
XX      of lung-associated protein or neuroendocrine marker protein genes, can be
XX      used in novel chimaeric molecules for use in producing therapy of lung
XX      cancer.
XX      SQ
XX      Sequence 264 AA;

Query Match      100.0%; Score 885; DB 2; Length 264;
Best Local Similarity 100.0%; Pred. No. 5.2e-90;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      121 KELTAFLEHMGDHTRLDRWEPELNEAIPNDRDRTTVPVAAATTIRKLLTGE 172
DB      122 KELTAFLEHMGDHTRLDRWEPELNEAIPNDRDRTTVPVAAATTIRKLLTGE 173

RESULT 6
AAR31575
ID      AAR31575 standard; protein; 286 AA.
XX      AC
XX      AAR31575;
XX      DT
XX      10-MAR-2003 (revised)
XX      04-JUN-1993 (first entry)
XX      DE
XX      Ampicillin resistance protein.
XX      KW
XX      CYP1A1; PRNH127; PRNH155; xeroderma pigmentosum group A; XPA;
XX      xenobiotics; circular; chimeric cytochrome P450IA1.
XX      OS
XX      Homo sapiens.
XX      PN
XX      US5180666-A.
XX      PD
XX      19-JAN-1993.
XX      PF
XX      27-JUN-1991; 91US-00721775.
XX      PR
XX      27-JUN-1991; 91US-00721775.
XX      PA
XX      (UYMA-) UNIV WAYNE STATE.
XX      PI
XX      States JC, Hines RN, Novak RF;
XX      WPI; 1993-052845/06.
XX      DR
XX      N-PSDB; AAQ36498.
XX      PT
XX      In vitro method for testing mutagenicity of a chemical - by metabolising
XX      chemical cell line consisting of transformed fibroblasts having
XX      detectable cytochrome P450 mixed function oxidase activity and detecting
XX      gene damage.
XX      PS
XX      Disclosure; Col 21-24; 24pp; English.
XX      CC
XX      The expression constructs PRNH127 and PRNH155 contain identical sequences
XX      but were constructed using different strategies (see AAQ36498). The
XX      constructs comprise exons 2-7 of human CYP1A1 gene under the control of
XX      the inducible mouse metallothionein (MMT-1) promoter. The constructs also
XX      contain an open reading frame in the opposite orientation to the
XX      cytochrome P450 exons. This ORF encodes ampicillin resistance. The
XX      constructs are suitable for transformation of human fibroblasts derived
XX      from the xeroderma pigmentosum group A. Cultures of the transformed
XX      fibroblasts can be used to test substances for mutagenicity. The presence
XX      of the inducible cytochrome P450 gene allows metabolism of the substance
XX      to mutagenic metabolites. (Updated on 10-MAR-2003 to add missing OS
XX      field.)
XX      SQ
XX      Sequence 286 AA;

Query Match      100.0%; Score 885; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.8e-90;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Db 144 KELTAFILNMGDHVTRLDRWBEPELNEAIPNDRDRTTTPVAAATTIRKLLTGE 195

RESULT 7

AAR97619
ID AAR97619 standard; protein; 286 AA.

AC AAR97619;

XX 20-AUG-1996 (first entry)

XX Secretory beta-lactamase.

XX Gene therapy; gene directed enzyme prodnug therapy; GDEPT;

XX virus directed enzyme prodnug therapy; VDBPT; prodnug activation;

XX cytotoxic; cycostatic; cancer; tumour; retrovirus; vector;

XX beta-lactamase; cephalosporin.

XX Synthetic.

XX WO9616179-A1.

XX 30-MAY-1996.

XX 20-NOV-1995; 95WO-GB002716.

XX 18-NOV-1994; 94GB-00023367.

XX (WELL) WELLCOME FOUND LTD.

XX Dev IK, Moore JT, Ohmsted C;

XX WPI; 1996-268615/27.

XX N-PSDB; AAT29220.

XX Molecular chimaera for use in enzyme gene therapy - is activated in a

XX target cell to express a secretable enzyme which cleaves a prodnug

XX outside the cell into a cytotoxic or cycostatic agent.

XX Example 3; Page 57-58; 73pp; English.

XX A secretory beta-lactamase (AAR97619) is expressed from DNA construct

XX PCMV-BL (AAT29220), in which the beta-lactamase coding sequence is under

XX the control of the intermediate/early cytomagalovirus promoter. Beta-

XX lactamase delivery to mammalian cells confers sensitivity to

XX cephalosporin prodnugs. Liposomal DNA/5-fluorouracil prodnug combinations

XX resulted in 8.c. tumour regression in mice bearing A549 tumours. Survival

XX of mice bearing human large cell lung H460 intrathoracic (i.t.) tumours

XX was increased upon i.t. injection of the secretory beta-lactamase DNA

XX construct

XX Sequence 286 AA;

XX Query Match 100.0%; Score 885; DB 2; Length 286;

XX Best Local Similarity 100.0%; Pred. No. 5.8e-90;

XX Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Db 1 HPEITLVKVKADBDQAGARVGYIELDLSGKILIESFRPERFPFMSTFKYLICGAVLSRID 60

XX 24 HPEITLVKVKADBDQAGARVGYIELDLSGKILIESFRPERFPFMSTFKYLICGAVLSRID 83

XX 61 AGQEBOLGRIRIHVSQNDLVEYSPVTEKHLTDGWTVELCSAATWSDNTAAANLLTTIGGP 120

XX 84 AGQEBOLGRIRIHVSQNDLVEYSPVTEKHLTDGWTVELCSAATWSDNTAAANLLTTIGGP 143

XX 121 KELTAFILNMGDHVTRLDRWBEPELNEAIPNDRDRTTTPVAAATTIRKLLTGE 172

XX 144 KELTAFILNMGDHVTRLDRWBEPELNEAIPNDRDRTTTPVAAATTIRKLLTGE 195

XX AAR96423;

XX 25-MAR-2003 (revised)

XX 25-NOV-1996 (first entry)

XX Cytochrome P450 (CYP1A1 construct).

XX cytochrome; P450; metallothionein; mouse; human; cytotoxicity; assay;

XX metabolism.

XX Homo sapiens.

XX US5525482-A.

XX 11-JUN-1996.

XX 15-NOV-1994; 94US-00339658.

XX 27-JUN-1991; 91US-00721775.

XX 09-DEC-1992; 92US-00980295.

XX (UYMA-) UNITV WAYNE STATE.

XX Hines RN, Novak RF, States JC;

XX WPI; 1996-2686397/29.

XX N-PSDB; AAT30354.

XX Testing chemicals for cytotoxicity to human by detecting gene damage -

XX using recombinant fibroblasts transformed with cytochrome P450 gene under

XX control of inducible promoter.

XX Disclosure; Col 17-24; 26pp; English.

XX The present sequence is encoded by a chimeric mouse metallothionein-

XX cytochrome P450IAl (CYP1A1) expression construct. Two clones, PRNH127 and

XX PRNH15, were isolated by different methods and which both had the same

XX sequence. The CYP1A1 construct is used in assays to test for cytotoxicity

XX of humans to a chemical. The method comprises exposing human fibroblast

XX cells normally not including any cytochrome P450 activity to potentially

XX toxic chemicals. The cells having been transformed to express cytochrome

XX P450, under the control of a controllable promoter through the CYP1A1

XX gene, upon exposure to the chemical in vitro. The chemical is metabolised

XX intracellularly into a cytochrome metabolite by oxidation within the

XX fibroblasts through the intracellular cytochrome P450 mixed function

XX oxidase enzymes expressed by the cells. Gene damage in the test cells is

XX detected as an indication of cytotoxicity of the chemical. (Updated on 25

XX -MAR-2003 to correct PF field.)

XX Sequence 286 AA;

XX Query Match 100.0%; Score 885; DB 2; Length 286;

XX Best Local Similarity 100.0%; Pred. No. 5.8e-90;

XX Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Db 1 HPEITLVKVKADBDQAGARVGYIELDLSGKILIESFRPERFPFMSTFKYLICGAVLSRID 60

XX 24 HPEITLVKVKADBDQAGARVGYIELDLSGKILIESFRPERFPFMSTFKYLICGAVLSRID 83

XX 61 AGQEBOLGRIRIHVSQNDLVEYSPVTEKHLTDGWTVELCSAATWSDNTAAANLLTTIGGP 120

XX 84 AGQEBOLGRIRIHVSQNDLVEYSPVTEKHLTDGWTVELCSAATWSDNTAAANLLTTIGGP 143

XX 121 KELTAFILNMGDHVTRLDRWBEPELNEAIPNDRDRTTTPVAAATTIRKLLTGE 172

XX 144 KELTAFILNMGDHVTRLDRWBEPELNEAIPNDRDRTTTPVAAATTIRKLLTGE 195

RESULT 9

AAW16635
ID AAW16635 standard; protein; 286 AA.

XX AAW16635;

XX 25-MAR-2003 (revised)

XX 25-NOV-1996 (first entry)

XX Cytochrome P450 (CYP1A1 construct).

XX cytochrome; P450; metallothionein; mouse; human; cytotoxicity; assay;

XX metabolism.

XX Homo sapiens.

XX US5525482-A.

XX 11-JUN-1996.

XX 15-NOV-1994; 94US-00339658.

XX 27-JUN-1991; 91US-00721775.

XX 09-DEC-1992; 92US-00980295.

XX (UYMA-) UNITV WAYNE STATE.

XX Hines RN, Novak RF, States JC;

XX WPI; 1996-2686397/29.

XX N-PSDB; AAT30354.

XX Testing chemicals for cytotoxicity to human by detecting gene damage -

XX using recombinant fibroblasts transformed with cytochrome P450 gene under

XX control of inducible promoter.

XX Disclosure; Col 17-24; 26pp; English.

XX The present sequence is encoded by a chimeric mouse metallothionein-

XX cytochrome P450IAl (CYP1A1) expression construct. Two clones, PRNH127 and

XX PRNH15, were isolated by different methods and which both had the same

XX sequence. The CYP1A1 construct is used in assays to test for cytotoxicity

XX of humans to a chemical. The method comprises exposing human fibroblast

XX cells normally not including any cytochrome P450 activity to potentially

XX toxic chemicals. The cells having been transformed to express cytochrome

XX P450, under the control of a controllable promoter through the CYP1A1

XX gene, upon exposure to the chemical in vitro. The chemical is metabolised

XX intracellularly into a cytochrome metabolite by oxidation within the

XX fibroblasts through the intracellular cytochrome P450 mixed function

XX oxidase enzymes expressed by the cells. Gene damage in the test cells is

XX detected as an indication of cytotoxicity of the chemical. (Updated on 25

XX -MAR-2003 to correct PF field.)

XX Sequence 286 AA;

XX Query Match 100.0%; Score 885; DB 2; Length 286;

XX Best Local Similarity 100.0%; Pred. No. 5.8e-90;

XX Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Db 1 HPEITLVKVKADBDQAGARVGYIELDLSGKILIESFRPERFPFMSTFKYLICGAVLSRID 60

XX 24 HPEITLVKVKADBDQAGARVGYIELDLSGKILIESFRPERFPFMSTFKYLICGAVLSRID 83

XX 61 AGQEBOLGRIRIHVSQNDLVEYSPVTEKHLTDGWTVELCSAATWSDNTAAANLLTTIGGP 120

XX 84 AGQEBOLGRIRIHVSQNDLVEYSPVTEKHLTDGWTVELCSAATWSDNTAAANLLTTIGGP 143

XX 121 KELTAFILNMGDHVTRLDRWBEPELNEAIPNDRDRTTTPVAAATTIRKLLTGE 172

XX 144 KELTAFILNMGDHVTRLDRWBEPELNEAIPNDRDRTTTPVAAATTIRKLLTGE 195

AC AAW16635;
 XX
 DT 09-AUG-1997 (first entry)
 XX
 DE Beta-lactamase (no signal peptide).
 XX
 KW Gene directed enzyme prodnrg therapy; GDEPT;
 KW virus directed enzyme prodnrg therapy; VDEPT; beta-lactamase; cancer;
 KW HIV; inflammation.
 XX
 OS Escherichia coli.
 XX
 PN WO9719180-A2.
 XX
 PD 29-MAY-1997.
 XX
 PF 19-NOV-1996; 96WO-GB002845.
 XX
 PR 20-NOV-1995; 95GB-00023703.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Dev I, Moore JT, Ohmstede C;
 XX
 DR WPI; 1997-298117/27.
 DR N-PSDB; AAT66737.
 XX
 PT Molecular chimera for gene or virus directed enzyme prodnrg therapy -
 PT useful for treatment of cancer, viral infection or inflammation.
 XX
 PS Example; Page 26; 38pp; English.
 XX
 CC Escherichia coli beta-lactamase (AAW16635), lacking the signal peptide,
 CC is the expression product of a molecular chimera, designated PCMV-delBL
 CC (AAT66738), in which the beta-lactamase gene is under control of the CMV
 CC intermediate/early promoter. Vectors consisting of a transcriptional
 CC regulatory DNA sequence linked to a beta-lactamase gene can be used for
 CC enzyme prodnrg therapy. Intracellular expression of the beta-lactamase in
 CC a targeted cell allows conversion of a prodnrg into an agent toxic to
 CC the cell for treatment of cancer, viral (e.g. HIV) infection or
 CC inflammation
 CC
 XX
 CC Sequence 286 AA;
 CC SQ
 Query Match 100.0%; Score 885; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 5.8e-90;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HPEITLVKKVKAEDDQAGARVGYIEIDLNSGKILSFRRPFRPMMSTFVLLCGAVLSRID 60
 DB 24 HPEITLVKKVKAEDDQAGARVGYIEIDLNSGKILSFRRPFRPMMSTFVLLCGAVLSRID 83
 QY 61 AGGQQLGRRIRHSQNDLVEYSPVTEKHLTDGMTVRELCSAAITWSDNTAANLLTTTGGP 120
 DB 84 AGGQQLGRRIRHSQNDLVEYSPVTEKHLTDGMTVRELCSAAITWSDNTAANLLTTTGGP 143
 QY 121 KETLAFILNMGDHVTRLDRWPEPELNEALPNDERDITMVAATTLRKLLTGE 172
 DB 144 KETLAFILNMGDHVTRLDRWPEPELNEALPNDERDITMVAATTLRKLLTGE 195

KW beta-lactamase; PCMV-BL.
 XX
 OS Escherichia coli.
 XX
 PN Key location/Qualifiers
 FT Peptide 1..23
 FT /label= Sig_peptide
 FT Protein 24..286
 FT /label= Mat_protein
 XX
 PN WO9719183-A2.
 XX
 PD 29-MAY-1997.
 XX
 PF 19-NOV-1996; 96WO-GB002846.
 XX
 PR 20-NOV-1995; 95GB-00023703.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Dev I, Moore JT, Sethna PB;
 XX
 DR WPI; 1997-298118/27.
 DR N-PSDB; AAT70309.
 XX
 PT DNA construct for gene-directed enzyme prodnrg therapy of lung cancer -
 PT comprises lung- or neuroendocrine-specific promoter controlling
 PT expression of prodnrg-converting enzyme.
 XX
 PS Example 81; Page 26-27; 53pp; English.
 XX
 CC The secreted form (AAW18679) of TEM beta-lactamase is expressed by PCMV-
 CC BL (AAT70309) in which a PCR-amplified beta-lactamase coding sequence is
 CC placed under control of the intermediate/early promoter of
 CC cytomegalovirus. Secretory beta-lactamase constructs, placed under
 CC control of promoter/enhancer elements of lung- associated protein or
 CC neuroendocrine marker protein genes, can be used in novel chimeric
 CC molecules for use in prodnrg therapy of lung cancer
 CC
 XX
 CC Sequence 286 AA;
 CC SQ
 Query Match 100.0%; Score 885; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 5.8e-90;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HPEITLVKKVKAEDDQAGARVGYIEIDLNSGKILSFRRPFRPMMSTFVLLCGAVLSRID 60
 DB 24 HPEITLVKKVKAEDDQAGARVGYIEIDLNSGKILSFRRPFRPMMSTFVLLCGAVLSRID 83
 QY 61 AGGQQLGRRIRHSQNDLVEYSPVTEKHLTDGMTVRELCSAAITWSDNTAANLLTTTGGP 120
 DB 84 AGGQQLGRRIRHSQNDLVEYSPVTEKHLTDGMTVRELCSAAITWSDNTAANLLTTTGGP 143
 QY 121 KETLAFILNMGDHVTRLDRWPEPELNEALPNDERDITMVAATTLRKLLTGE 172
 DB 144 KETLAFILNMGDHVTRLDRWPEPELNEALPNDERDITMVAATTLRKLLTGE 195

RESULT 11
 ID AAY08529
 AC AAY08529;
 XX
 DT 03-AUG-1999 (first entry)
 XX
 DE Vector pASK75 beta-la protein.
 XX
 KW Firefly; luciferase; tetracycline; transcriptional control; TetR; TetA;
 KW tetracycline repressor; tetracycline promoter; luminescence; luxCDABE;
 KW insect; Tn10; medicine; dosage; cheese production; antibiotic; foodstuff;
 KW allergy.
 XX

OS Synthetic.
XX
XX MO9925866-A1.
XX
XX 27-MAY-1999.
XX
XX 11-NOV-1998; 98MO-FI000873.
XX
XX 14-NOV-1997; 97FI-00004235.
XX
XX (KORP/) KORBELA M.
XX (KARP/) KARP M.
XX (KURI/) KURITU J.
XX
XX Korpela M, Karp M, Kuritu J;
XX
XX WPI; 1999-338015/28.
XX N-PSDB; AAV72418.
XX
XX Assaying for tetracycline using recombinant prokaryotic cells.
XX
XX Disclosure; Page 47-48; 67pp; English.
XX
XX This invention describes a novel tetracycline assay that uses recombinant
CC prokaryotic cells comprising a luciferase gene under the transcriptional
CC control of a tetracycline repressor and tetracycline promoter and
CC involves the detection of luminescence emitted from the cells. The assay
CC can be used to distinguish tetracycline from other microbial agents. The
CC invention also describes a novel plasmid comprising either the luxDABE
CC genes, a tetracycline repressor (Tetr) and a tetracycline promoter (Tetr)
CC from Thio, or the insect luciferase gene, a tetracycline repressor (Tetr)
CC and a tetracycline promoter (Tetr) from Thio. The tetracycline assay
CC method can be used for the determination of tetracycline in a sample,
CC e.g. to study the dosage and penetration of the medicine. The method can
CC also be used to test cheese production, as cheese making bacteria are not
CC able to work in the presence of tetracycline. The method can also be used
CC to determine the presence or concentration of antibiotics in foodstuffs,
CC e.g. for allergic people. The present assay method does not rely on the
CC growth of microbes as do conventional tests, and so is much more rapid.
CC The present assay is also more sensitive, as even a small amount of
CC luminescence can be detected
XX
XX Sequence 286 AA;
SQ
Query Match 100.0%; Score 885; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.8e-90;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEITVKKDADDOUGARVGYIELDLSNGKILSFRRPFRPMSFPVYLGGAVLSRID 60
DB 24 HPEITVKKDADDOUGARVGYIELDLSNGKILSFRRPFRPMSFPVYLGGAVLSRID 83
QY 61 AGOELGRIRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGOELGRIRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTSFLLNMGDHTRLDRWEPBELNEAIPNDRDRTTVPVAAATTIRKLLTGE 172
DB 144 KELTSFLLNMGDHTRLDRWEPBELNEAIPNDRDRTTVPVAAATTIRKLLTGE 195
RESULT 12
AAB10442
ID AAB10442 standard; protein; 286 AA.
XX
XX AAB10442;
XX
XX 01-DEC-2000 (first entry)
XX
XX Expression vector pSEX15G2 bla protein.
XX
XX Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
KW B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.

XX
XX OS Synthetic.
XX
XX DE19900635-A1.
XX
XX 13-JUL-2000.
XX
XX 11-JAN-1999; 99DE-01000635.
XX
XX 11-JAN-1999; 99DE-01000635.
XX
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
XX Bretling F, Poustka A, Moldenhauer G;
XX
XX WPI; 2000-499632/45.
XX N-PSDB; AAA71430.
XX
XX Selecting monoclonal antibodies, by expressing them on the surface of
PT hybridomas attached to antibody-binding protein, then reaction with
PT antibody library.
XX
XX Claim 16; Fig 3; 22pp; German.
XX
XX This invention describes a novel method for the selection of monoclonal
CC antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma
CC cells to produce antibody-producing hybridomas such that the antibodies
CC are presented at the surface of the hybridomas by an antibody-binding
CC protein (i); and (ii) binding the antibody to antigens (Ag). The
CC invention also describes antibody-binding proteins (i) that comprise a
CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa
CC chain or a murine MHC (major histocompatibility complex) Class I K(K)
CC molecule; an antibody-binding site of proteins A, G, I or Ig; and the
CC transmembrane domain of PDGFR (platelet-derived growth factor receptor)
CC or CD52. The method is used to select Mab with specificity for particular
CC antigens. Mab can be selected without separate culture of hybridomas, and
CC selection can be made against many antigens in a library, optionally on
CC the basis of strength of affinity for a particular antigen. Complex
CC mixtures of hybridomas can be used for selection, reducing the time and
CC cost involved in Mab selection. This sequence represents the bla protein
CC protein contained in the expression vector pSEX15G2 which contains the
CC bla protein, Neo-R and protein G described in the method of the invention
XX
XX Sequence 286 AA;
SQ
Query Match 100.0%; Score 885; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.8e-90;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEITVKKDADDOUGARVGYIELDLSNGKILSFRRPFRPMSFPVYLGGAVLSRID 60
DB 24 HPEITVKKDADDOUGARVGYIELDLSNGKILSFRRPFRPMSFPVYLGGAVLSRID 83
QY 61 AGOELGRIRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGOELGRIRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTSFLLNMGDHTRLDRWEPBELNEAIPNDRDRTTVPVAAATTIRKLLTGE 172
DB 144 KELTSFLLNMGDHTRLDRWEPBELNEAIPNDRDRTTVPVAAATTIRKLLTGE 195
RESULT 13
AAB10438
ID AAB10438 standard; protein; 286 AA.
XX
XX AAB10438;
XX
XX 01-DEC-2000 (first entry)
XX
XX Expression vector pSEX11L4 bla protein.
XX
XX Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
KW

XX bla resistance marker; recombinant host cell; saccharification;
KM fermentation; polysaccharase; oligosaccharide degradation; celz gene;
KM glucanase; Integration vector; pUD12306.
XX
OS unidentified.
XX
PN WO200071729-A2.
XX
PD 30-NOV-2000.
XX
PF 26-MAY-2000; 2000WO-US014773.
XX
PR 26-MAY-1999; 99US-0136376P.
XX (UYFL) UNIV FLORIDA RES FOUND.
XX
PI Ingram LO, Zhou S;
XX
XX
DR WPI: 2001-032043/04.
DR N-PADB; AAC91455.
XX
PT Recombinant host cells useful for producing polysaccharase for degrading
PT oligosaccharides, comprises a first heterologous polynucleotide encoding
PT polysaccharase under control of surrogate promoter.
XX
XX
PS Disclosure; Page 82-83; 87pp; English.
XX
XX The present sequence is given in a specification relating to a
CC recombinant host cell suitable for simultaneous saccharification and
CC fermentation. The host cell contains at least one heterologous
CC polynucleotide encoding a polysaccharase under the transcriptional
CC control of a surrogate promoter capable of increasing expression of the
CC polysaccharase. The host cell also contains a second heterologous
CC polynucleotide encoding a secretory polypeptide to facilitate the
CC secretion of the expressed polysaccharase. The recombinant host cell is
CC useful for producing polysaccharase which is useful for enzymatically
CC degrading oligosaccharides such as lignocellulose, hemicellulose,
CC cellulose, pectin or their combinations, and fermenting the product to
CC ethanol, by simultaneous saccharification and fermentation processes. The
CC present sequence is encoded by an integration vector which was introduced
CC into cells to generate recombinant host cells. The vector contains a
CC surrogate promoter from *Zymomonas mobilis*, the celz gene from *Erwinia*
CC chrysanthemi, resistance markers bla and tet, and *Klebsiella oxytoca*
CC target sequence
XX
SQ Sequence 286 AA;
XX
XX
Query Match 100.0%; Score 885; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.8e-90;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 HPEITLVKVAEDQIGARVGYIELDLSGKILBSFRPEPRPMMSTFKVLLCGAVLSRID 60
24 HPEITLVKVAEDQIGARVGYIELDLSGKILBSFRPEPRPMMSTFKVLLCGAVLSRID 83
QY 61 AGQEQLGRRIRYSQNDLVESYPTVKHITDGMTVRELCSAATMSDNTAAILLTTIGSP 120
DB 84 AGQEQLGRRIRYSQNDLVESYPTVKHITDGMTVRELCSAATMSDNTAAILLTTIGSP 143
QY 121 KETAFAPLHNMGDHVTRLDRWEPELNEAIPNDRDPTMPVAAATTLRKLLTGE 172
DB 144 KETAFAPLHNMGDHVTRLDRWEPELNEAIPNDRDPTMPVAAATTLRKLLTGE 195

Search completed: June 10, 2005, 10:49:12
Job time : 67.6888 secs

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```
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Hafnia.
OX NCBI_TaxID=569;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MISC198;
RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
RL Submitted (APR-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY265886; AAP93844.1; -
DR HSP; P00807; IKGE.
DR InterPro; IPR000871; Beta_lactamase_A.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1 1
FT NON_TER 232 232
SQ SEQUENCE 232 AA; 25380 MW; 3D5DFD85582C261 CRC64;

Query Match 100.0%; Score 770; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 1,7e-62;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVVKQKAEDELGARGVGTIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
D 2 HPELVVKQKAEDELGARGVGTIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 61
QY 61 AGOQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAALTMSDNTAANLLTTTGGP 120
D 62 AGOQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAALTMSDNTAANLLTTTGGP 121
QY 121 KETLAFHNMGDHVTRLDRWPELNEAIP 149
D 122 KETLAFHNMGDHVTRLDRWPELNEAIP 150

RESULT 3
Q6MWY8 PRELIMINARY; PRT; 241 AA.
AC Q6MWY8;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Beta-lactamase (Fragment).
GN Name=blatEM;
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MISC112;
RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
RL Submitted (APR-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY265882; AAP93840.1; -
DR HSP; P00807; IKGE.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1 1
FT NON_TER 241 241
SQ SEQUENCE 241 AA; 26407 MW; 38DF2AFDF0C5807D CRC64;

Query Match 100.0%; Score 770; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.8e-62;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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D 67 AGOQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAALTMSDNTAANLLTTTGGP 126
QY 121 KETLAFHNMGDHVTRLDRWPELNEAIP 149
D 127 KETLAFHNMGDHVTRLDRWPELNEAIP 155

RESULT 4
Q6MWY3 PRELIMINARY; PRT; 242 AA.
AC Q6MWY3;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Beta-lactamase (Fragment).
GN Name=blatEM;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=7A005;
RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
RL Submitted (APR-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY265887; AAP93845.1; -
DR HSP; P00807; IKGE.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1 1
FT NON_TER 242 242
SQ SEQUENCE 242 AA; 26554 MW; 38C3DPA8A5A3807D CRC64;

Query Match 100.0%; Score 770; DB 2; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.8e-62;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVVKQKAEDELGARGVGTIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
D 8 HPELVVKQKAEDELGARGVGTIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 67
QY 61 AGOQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAALTMSDNTAANLLTTTGGP 120
D 68 AGOQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAALTMSDNTAANLLTTTGGP 127
QY 121 KETLAFHNMGDHVTRLDRWPELNEAIP 149
D 128 KETLAFHNMGDHVTRLDRWPELNEAIP 156

RESULT 5
Q6KB67 PRELIMINARY; PRT; 285 AA.
AC Q6KB67;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
DE Hordeum vulgare (Barley).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticaceae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=first leaf;
RA Jansen C., Korell M., Bockey C., Biedenkopf D., Kogel K.H.;
RL Submitted (MAY-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ717739; CAG30723.1; -
DR HSP; P00807; IALQ.
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DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR000871; Beta_lactamase_A.
DR Pfam: PF00144; Beta_lactamase_1.
DR PRINTS: PR00118; BLACTAMASEA.
DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
DR Hypothetical protein.
FT NON TER 285
SEQUENCE 285 AA; 31371 MW; A2P22753375FA930 CRC64;

Query Match 100.0%; Score 770; DB 2; Length 285;
Best Local Similarity 100.0%; Pred. No. 2.2e-62;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKQADQEDQARVGYIELDLSGKILSFPRPERPMMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKQADQEDQARVGYIELDLSGKILSFPRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGOQOLGRRIHYSONDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTTIGP 120
DB 84 AGOQOLGRRIHYSONDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTTIGP 143
QY 121 KETLAFILNMGDHVTRLDRMEPELNEAIP 149
DB 144 KETLAFILNMGDHVTRLDRMEPELNEAIP 172

RESULT 6

QJ38058 PRELIMINARY; PRT; 286 AA.
AC Q38058;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Beta_lactamase.
OS Bacteriophage phi-X174.
OC Viruses; ssDNA viruses; Microviridae; Microvirus.
OX NCBI_TaxID=10847;

RN [1]
RP SEQUENCE FROM N. A.
RA MEDLINE=95172401; PubMed=7867948; DOI=10.1016/0378-1119(94)00839-K;
RX Henrich B., Schmidberger B.;
RT "A variant of phiX174 gene B-based positive selection vectors with
enhanced lytic potential.";
RL Gene 154:51-54(1995).
DR EMBL; Z35638; CAA84692.1; -.
DR PIR; S47061; S47061.
DR HSSP; Q9R435; 1HTZ.
DR InterPro: IPR000871; Beta_lactamase.
DR Pfam; PR00144; Beta_lactamase_1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;

Query Match 100.0%; Score 770; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.2e-62;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKQADQEDQARVGYIELDLSGKILSFPRPERPMMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKQADQEDQARVGYIELDLSGKILSFPRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGOQOLGRRIHYSONDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTTIGP 120
DB 84 AGOQOLGRRIHYSONDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTTIGP 143
QY 121 KETLAFILNMGDHVTRLDRMEPELNEAIP 149
DB 144 KETLAFILNMGDHVTRLDRMEPELNEAIP 172

RESULT 7

Q00626 PRELIMINARY; PRT; 286 AA.
ID Q00626
AC Q00626; 008022; 008102; 009393; 009396; 009397; 009398; 009399;
AC 009400; 009401; 009402; 009403; 009404; 009405; 009406; 009407;
AC 009408; 009481; 009482; 009483; 009490; 057333;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 01, Last annotation update)
DE Beta_lactamase.
OS Staphylococcus aureus.
OC Plasmid J3356/POX7/3, and Plasmid J3356/POX7/1.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N. A.
RC PLASMID=J3356/POX7/3, and J3356/POX7/1;
RX MEDLINE=96422755; PubMed=8825372; DOI=10.1006/plae.1995.0005;
RA Needham C., Noble W.C., Dyke K.G.;
RT "The staphylococcal insertion sequence IS257 is active.";
RL Plasmid 34:198-205(1995).
DR EMBL; U36912; AAB39957.1; -.
DR EMBL; U36911; AAB39956.1; -.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase_1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
DR Plasmid.
KM Plasmid.
SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;

Query Match 100.0%; Score 770; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.2e-62;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKQADQEDQARVGYIELDLSGKILSFPRPERPMMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKQADQEDQARVGYIELDLSGKILSFPRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGOQOLGRRIHYSONDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTTIGP 120
DB 84 AGOQOLGRRIHYSONDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTTIGP 143
QY 121 KETLAFILNMGDHVTRLDRMEPELNEAIP 149
DB 144 KETLAFILNMGDHVTRLDRMEPELNEAIP 172

RESULT 8

Q79CL6 PRELIMINARY; PRT; 286 AA.
ID Q79CL6
AC Q79CL6;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Beta_lactamase.
GN Name-bla;
OS Methylobacillus flagellatum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Methylobacterales;
OC Bacteria; Proteobacteria; Methylobacterales.
OX NCBI_TaxID=405;
RN [1]

RP SEQUENCE FROM N. A.
RX MEDLINE=97074643; PubMed=8917070; DOI=10.1016/0378-1119(96)00114-X;
RA Serebrijski I.G., Vasein V.M., Teygankov Y.D.;
RT "Two new members of the BioB superfamily: cloning, sequencing and
expression of bioB genes of Methylobacillus flagellatum and
Corynebacterium glutamicum.";
RL Gene 175:15-22(1996).
RN [2]
RP SEQUENCE FROM N. A.
RA Serebrijski I., Vasein V., Teygankov Y.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U31280; AAC44581.1; -.

DR HSSP; P00807; 1ALQ.
DR InterPro; IPR001466; Beta_lactamase_A.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;
Query Match 100.0%; Score 770; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.2e-62;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEVLVVKQAEADQAGRVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 60
DB 24 HPEVLVVKQAEADQAGRVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 83
QY 61 AGGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTTGGP 120
DB 84 AGGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTTGGP 143
QY 121 KETLAFLLHMGDHYTRLDRWEPELNEAIP 149
DB 144 KETLAFLLHMGDHYTRLDRWEPELNEAIP 172
RESULT 9
ID Q79DR3 PRELIMINARY; PRT; 286 AA.
AC Q79DR3;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Mutant extended-spectrum beta-lactamase precursor (EC 3.5.2.6).
GN Name:bla; Synonyms=blatEM-116;
OS Escherichia coli.
OC Plasmid pBP4, and plasmid pCAPS.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K-12;
RA Maneewannakul K., Maneewannakul S., Ippen-Ihler K.;
RL Submitted (AUG-1991) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12; PLASMID=pBP4;
RA Rondot S., Anthony K., Dubel S., Ida N., Beyreuther K., Frost L.,
RA Little M., Breitling F.;
RL Submitted (APR-1997) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC PLASMID=pCAPS;
RA MEDLINE=96189310; PubMed=9514792; DOI=10.1006/abio.1997.2558;
RA Schlepper D., Von Wilcken-Bergmann B., Schmidt M., Sobek H.,
RA Mueller-Hill B.;
RT "A positive selection vector for cloning of long polymerase chain
RT reaction fragments based on a lethal mutant of the cfp gene
RT Escherichia coli.";
RL Anal. Biochem. 257:203-209(1998).
RN [4]
RP SEQUENCE FROM N.A.
RX PubMed=1524306;
RA Jeong S.H., Bae I.K., Lee J.H., Sohn S.G., Kang G.H., Jeon G.J.,
RA Kim Y.H., Jeong B.C., Lee S.H.;
RT "Molecular Characterization of Extended-Spectrum Beta-Lactamase
RT Produced by Clinical Isolates of Klebsiella pneumoniae and Escherichia
RT coli from a Korean Nationwide Survey.";
RL J. Clin. Microbiol. 42:2902-2906(2004).
DR EMBL; M74750; AAA24057.1; -;
DR EMBL; Y12694; CAA73226.1; -;
DR EMBL; AJ001614; CAA04868.1; -;
DR EMBL; AY425988; AAQ95605.1; -;

DR HSSP; P00807; 1ALQ.
DR GO; GO:0008800; F:beta-lactamase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR001466; Beta_lactamase_A.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW Hydrolyase; Plasmid; Signal.
FT SIGNAL 1 23 Potential.
SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;
Query Match 100.0%; Score 770; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.2e-62;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEVLVVKQAEADQAGRVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 60
DB 24 HPEVLVVKQAEADQAGRVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 83
QY 61 AGGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTTGGP 120
DB 84 AGGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTTGGP 143
QY 121 KETLAFLLHMGDHYTRLDRWEPELNEAIP 149
DB 144 KETLAFLLHMGDHYTRLDRWEPELNEAIP 172

RESULT 10
ID Q38212 PRELIMINARY; PRT; 225 AA.
AC Q38212;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Bacteriophage phi-R208 amplicillinase gene mutation. (fragment).
OS Bacteriophage phi.
OC Viruses; ssDNA viruses; Inoviridae; Inovirus.
OX NCBI_TaxID=10863;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=86278026; PubMed=3525535;
RA Topal M.D., Badie J.S., Conrad M.;
RT "O-6-methylguanine mutation and repair is nonuniform. Selection for
RT DNA most interactive with O-6-methylguanine.";
RL J. Biol. Chem. 261:9879-9885(1986).
DR EMBL; M14017; AAA32208.1; -;
DR HSSP; Q9R435; HTZ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1 1
SQ SEQUENCE 225 AA; 25022 MW; 009BF841D618BA09 CRC64;
Query Match 99.9%; Score 769; DB 2; Length 225;
Best Local Similarity 99.3%; Pred. No. 2.1e-62;
Matches 148; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEVLVVKQAEADQAGRVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 60
DB 24 HPEVLVVKQAEADQAGRVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 83
QY 61 AGGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTTGGP 120
DB 84 AGGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTTGGP 143
QY 121 KETLAFLLHMGDHYTRLDRWEPELNEAIP 149
DB 144 KETLAFLLHMGDHYTRLDRWEPELNEAIP 172


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RESULT 11
Q6PRU7 PRELIMINARY; PRT; 232 AA.
ID Q6PRU7
AC Q6PRU7
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Inhibitor-resistant TEM beta-lactamase (Fragment).
OS Escherichia coli.
OC Bacteriophage; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OC NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=U33;
RA Ghadiali S., Hosseini-Mazinan S.M.;
RL Submitted (MAR-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY583761; AAS86427.1; -.
DR HSSP; P00807; IALO.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1
FT NON_TER 232
SQ SEQUENCE 232 AA; 25558 MW; 5791CD285EE70B80 CRC64;

Query Match 99.9%; Score 769; DB 2; Length 232;
Best Local Similarity 99.3%; Pred. No. 2,1e-62;
Matches 148; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVAEDQAGAVGYIEIDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
DB 15 HPEITLVKVAEDQAGAVGYIEIDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 74
QY 61 AGOGLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120
DB 75 AGOGLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 134
QY 121 KETLAFILNMGDHVTIRLDREWEPELNEAIP 149
DB 135 KETLAFILNMGDHVTIRLDREWEPELNEAIP 163

RESULT 12
Q84H50 PRELIMINARY; PRT; 255 AA.
ID Q84H50
AC Q84H50
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE TEM-117 beta-lactamase (Fragment).
OS Escherichia coli.
OC Bacteriophage; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OC NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC Box A.T.A., Pauw A., Leverstein-vanhal M.A.;
RL Submitted (JUL-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY130282; AAN05026.1; -.
DR HSSP; Q9R435; IHTZ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1
FT NON_TER 255
SQ SEQUENCE 255 AA; 27906 MW; DCBB28B65978C3A6 CRC64;
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Query Match 99.9%; Score 769; DB 2; Length 255;
Best Local Similarity 99.3%; Pred. No. 2,4e-62;
Matches 148; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVAEDQAGAVGYIEIDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
DB 12 HPEITLVKVAEDQAGAVGYIEIDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 71
QY 61 AGOGLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120
DB 72 AGOGLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 131
QY 121 KETLAFILNMGDHVTIRLDREWEPELNEAIP 149
DB 132 KETLAFILNMGDHVTIRLDREWEPELNEAIP 160

RESULT 13
Q84H49 PRELIMINARY; PRT; 261 AA.
ID Q84H49
AC Q84H49
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE TEM-110 beta-lactamase (Fragment).
OS Klebsiella oxytoca.
OC Bacteriophage; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OC NCBI_TaxID=571;
RN [1]
RP SEQUENCE FROM N.A.
RC Box A.T.A., Pauw A., Leverstein-vanhal M.A., Verhoeve J., Fluit A.C.;
RL Submitted (JUL-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY130283; AAN05027.1; -.
DR HSSP; Q9R435; IHTZ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1
FT NON_TER 261
SQ SEQUENCE 261 AA; 28738 MW; 4F748F773A08CB8 CRC64;

Query Match 99.9%; Score 769; DB 2; Length 261;
Best Local Similarity 99.3%; Pred. No. 2,5e-62;
Matches 148; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVAEDQAGAVGYIEIDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
DB 12 HPEITLVKVAEDQAGAVGYIEIDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 71
QY 61 AGOGLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120
DB 72 AGOGLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 131
QY 121 KETLAFILNMGDHVTIRLDREWEPELNEAIP 149
DB 132 KETLAFILNMGDHVTIRLDREWEPELNEAIP 160

RESULT 14
Q6PRU6 PRELIMINARY; PRT; 264 AA.
ID Q6PRU6
AC Q6PRU6
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE TEM beta-lactamase (Fragment).
OS Acinetobacter sp. U11.
OC Bacteriophage; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OC NCBI_TaxID=269266;
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RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=U1;
RA      Ghandli S., Hoseeini-Mazinaní S.M.;
RL      Submitted (MAR-2004) to the EMBL/Genbank/DBJ databases.
DR      EMBL; AY563762; AAC86428.1; -.
DR      HSSP; P00807; IALO.
DR      InterPro; IPR001466; Beta_lactamase.
DR      InterPro; IPR000871; Beta_lactamase_A.
DR      Pfam; PF00144; Beta_lactamase_1.
DR      PRINTS; PR00118; BLACTAMASEA.
DR      PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT      NON_TER      1      1
FT      NON_TER      264      264
SQ      SEQUENCE      264 AA; 28986 MW; AAF071C67489352C CRC64;

```

Query Match	99.9%;	Score 769;	DB 2;	Length 264;
Best Local Similarity	99.3%;	Pred. No. 2.5e-62;		
Matches 148; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 1 HPELVKVDABDOLGARVGIETDLNSGKILIESRPEREFPMMSTFKVLLCGAVLSRD 60
Db 12 HPELVKVDABDOLGARVGIETDLNSGKILIESRPEREFPMMSTFKVLLCGAVLSRD 71

Qy	61	AGGEGQLGRRIHYSNDLVESSPVEKEHLTDGMTRELCSAITSNDNTANLLLTIGCP	120
Db	72	AGGEGQLGRRIHYSNDLVESSPVEKEHLTDGMTRELCSAITSNDNTANLLLTIGCP	131

Oy	121	KELTAF LHM GDH VTR LD RWE PEI NEA IP	149
Db	132	KELTAF LHM GDH VTR LD RWE PEI NEA IP	160

RESULT 15

ID	Q6Q1V0	PRELIMINARY;	PRT;	281 AA.
AC	Q6Q1V0			
DT	05-JUL-2004 (TREMBlrel. 27, Created)			
DT	05-JUL-2004 (TREMBlrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBlrel. 27, Last annotation update)			
DE	TEM-1 beta-lactamase (Fragment).			
GN	Name=blatEM-1;			
OS	Serratia marcescens.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Serratia.			
OX	NCBI_TaxId=615;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=ES-42, ES-46, ES-71, and ES-11;			
RA	Yasuyanaei J., Salto S., Harata S., Suzuki N., Amano K.-I.;			
RL	Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AY538700; AAS46846.1; -			
DR	EMBL; AY538701; AAS46847.1; -			
DR	EMBL; AY538702; AAS46848.1; -			
DR	EMBL; AY538698; AAS46844.1; -			
DR	HSSP; P00807; IALO.			
DR	InterPro; IPR001466; Beta_lactamase.			
DR	InterPro; IPR000671; Beta_lactamase_A.			
DR	Pfam; PF00144; Beta_lactamase_1.			
DR	PRINTS; PRO0118; BLACTAMASEA.			
DR	PROSITE; PS00146; BETA_LACTAMASE_A; 1.			
FT	NON_TER	281	281	
Q0	SEQUENCE	281 AA;	30837 MW;	C8934B9C696057BF CRC64;

Query Match	99.9%	Score 769;	DB 2;	Length 281;
Best Local Similarity	99.3%	Pred. No. 2.7e-62;		
Matches 148; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 HPEPLVKKVDAEDDGLGARVGIETDILNSGKILBESRPEREPPMNSTFKVLLCGAVLSRID 60
24 HPEPLVKKVDAEDDGLGARVGIETDILNSGKILBESRPEREPPMNSTFKVLLCGAVLSRID 83

61 AGQEQGRRIHYSÖNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120

Db 84 AGGEQIGRIHNSQNDLVREYSPVTEKHLTDGHTRELCSAIITMSDNTAAILLITIGP 143

Qy 121 KETLAFLANNGDVTRLDREPELNEAIP 149

Db 144 KETLAFLANNGDVTRLDREPELNEAIP 172

Search completed: June 10, 2005, 10:57:01
Job time : 50.9177 secs

Fri Jun 10 14:22:58 2005

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:35:06 ; Search time 10.8657 seconds
(without alignments)
1319.408 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_149

Perfect score: 770

Sequence: 1 HPEITLVKVDABDQIGARVG.....MGDHYTRLDWPEELNEALP 149

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	770	100.0	286 2 T51301	beta-lactamase (EC
2	770	100.0	286 2 S47061	beta-lactamase (EC
3	770	100.0	286 4 S41975	beta-lactamase (EC
4	769	99.9	286 1 PNECP	beta-lactamase (EC
5	769	99.9	286 4 I40905	beta-lactamase (EC
6	761	98.8	286 2 S30113	beta-lactamase (EC
7	756	98.2	286 2 S60312	extended spectrum
8	755	98.1	286 2 S60310	extended spectrum
9	755	98.1	286 2 S60311	beta-lactamase (EC
10	755	98.1	286 2 JQ1546	Bla protein - Salm
11	552	71.7	286 2 S16146	beta-lactamase (EC
12	552	71.7	286 2 A60679	beta-lactamase (EC
13	548	71.2	265 2 S00464	beta-lactamase (EC
14	548	71.2	265 2 S02434	beta-lactamase (EC
15	548	71.2	265 2 A60448	beta-lactamase (EC
16	548	71.2	286 1 A44998	beta-lactamase (EC
17	548	71.2	286 2 A60632	beta-lactamase (EC
18	548	71.2	286 2 A37200	beta-lactamase (EC
19	542	70.4	287 1 A44996	beta-lactamase (EC
20	527	68.4	279 1 A24469	beta-lactamase (EC
21	508	66.0	286 1 A44958	beta-lactamase (EC
22	406	52.7	298 2 A41381	beta-lactamase (EC
23	340.5	44.2	23 S06967	beta-lactamase (EC
24	335.5	43.6	306 1 B45822	beta-lactamase (EC
25	332	43.1	281 2 D93395	probable Beta lact
26	330.5	42.9	302 2 S36188	beta-lactamase (EC
27	330.5	42.9	306 2 G69674	beta-lactamase (EC
28	322.5	41.9	311 2 JN0520	beta-lactamase (EC
29	318.5	41.4	306 2 S47330	penicillinase - Ba

30	316.5	41.1	305 1 C45822	beta-lactamase (EC
31	312	40.5	305 2 A61156	beta-lactamase (EC
32	312	40.5	305 2 A57002	beta-lactamase (EC
33	312	40.5	305 2 A60680	beta-lactamase (EC
34	311	40.4	314 1 PMSMU	beta-lactamase (EC
35	309.5	40.2	311 1 S02714	beta-lactamase (EC
36	308.5	40.1	294 2 S16553	beta-lactamase (EC
37	307	39.9	293 2 S04649	beta-lactamase (EC
38	305.5	39.7	307 1 PMSLU	beta-lactamase (EC
39	304.5	39.5	263 2 A54543	beta-lactamase (EC
40	301.5	39.2	291 2 S42075	beta-lactamase (EC
41	301.5	39.2	306 1 PMS5B	beta-lactamase (EC
42	296.5	38.5	306 1 PMSU	beta-lactamase (EC
43	296.5	38.5	306 2 S03167	beta-lactamase (EC
44	294	38.2	294 2 S44080	beta-lactamase (EC
45	293	38.1	310 2 JI0091	beta-lactamase (EC

ALIGNMENTS

RESULT 1
T51301
beta-lactamase (EC 3.5.2.6) - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C:Accession: T51301
R:WACH, A.; BRACHAT, A.; ALBERTSSEGUT, C.; REBISCHUNG, C.; PHILIPSEN, P.
Yeast 13, 1065-1075, 1997
A>Title: Heterologous His3 marker and GFP reporter modules for PCR-targeting in Saccharon
A:Reference number: 209587
A:Accession: T51301
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-286 <MAC>
A:Cross-references: EMBL:AJ002683; PIDN:CAA05686.1
C:Genetics:
A:Gene: bla
C:Superfamily: beta-lactamase I
C:Keywords: hydrolase

Query Match 100.0%; Score 770; DB 2; Length 286;
Best local similarity 100.0%; Pred. No. 1.9e-66;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDABDQIGARVGYLELDLNSGKILSEPRPERPPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKVDABDQIGARVGYLELDLNSGKILSEPRPERPPMSTFVLLCGAVLSRID 83

QY 61 AGQEQIGRRHYSONDLYEVSPTVEKHLTDGNTVRELCSAATWSDNTAAILLTITIGP 120
DB 84 AGQEQIGRRHYSONDLYEVSPTVEKHLTDGNTVRELCSAATWSDNTAAILLTITIGP 143

QY 121 KETLTAFLNMGDHYTRLDWPEELNEALP 149
DB 144 KETLTAFLNMGDHYTRLDWPEELNEALP 172

RESULT 2
S47061
beta-lactamase (EC 3.5.2.6) - phage phi-X174
C:Species: phage phi-X174
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S47061
R:Henrich, B.; Schmidberger, B.
Submitted to the EMBL Data Library, July 1994
A:Description: A variant of phiX174 gene E-based positive selection vectors with enhanced
A:Reference number: S47060
A:Accession: S47061
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-286 <HEN>
A:Cross-references: UNIPROT:Q38058; EMBL:Z35638; NID:g520996; PIDN:CAA84692.1; PID:g52095;

[illegible]

```

RESULT 10
Q01546
Bla protein - Salmonella typhimurium plasmid NTP16
N:Alternate names: beta lactamase homolog
C:Species: Salmonella typhimurium
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: Q01546
R:Canon, P.W.; Scribner, P.
Plasmid 27, 220-230, 1992
A:Title: Complete nucleotide sequence and gene organization of plasmid NTP16.
A:Reference number: Q01538; MUID:92383313; PMID:1325061
A:Accession: Q01546
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <CAN>
A:Cross-references: UNIPROT:Q8L2F9
C:Genetics:
C:Genome: plasmid
C:Superfamily: beta-lactamase I

Query Match          98.1%; Score 755; DB 2; Length 286;
Beat Local Similarity 98.0%; Pred. No. 5.2e-65;
Matches 146; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1  HPELTVKVKQADDEDLGARVGITIELDLSNGKLTGFRPERPRPMSTFRTLGCAGVLSRID 60
DB      24  HPELTVKVKQADEDLGDRVGITIELDLSNGKLTGFRPERPRPMSTFRTLGCAGVLSRVD 83

QY      61  AGGOLGRRHYSONDVEYSPYTEKHLTDGATVRELCSAIIWSDWTAANLLTTIGGP 120
DB      84  AGGOLGRRHIISSNDLVEYSPYTEKHLTDGATVRELCSAIIWSDWTAANLLTTIGGP 143

QY      121 KELTAFLLNMGDHYTRLDRWPEELNEAIP 149
DB      144 KELTAFLLNMGDHYTRLDRWPEELNEAIP 172

RESULT 11
S16146
beta-lactamase (EC 3.5.2.6) 2A precursor - Klebsiella pneumoniae plasmids
N:Alternate names: beta-lactamase SHV2A
C:Species: Klebsiella pneumoniae
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 15-Oct-1999
C:Accession: S16146; A35395; S18767
R:Podbielski, A.; Schoenling, U.; Melzer, B.; Wernatz, K.; Leusch, H.G.
J. Gen. Microbiol. 137, 569-578, 1991
A:Title: Molecular characterization of a new plasmid-encoded SHV-type beta-lactamase (SHV-2)
A:Reference number: S16146; MUID:91237320; PMID:2033379
A:Accession: S16146

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A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <ROD>
A:Cross-references: EMBL:X53817, NID:g43795; PIDD:CAA37813.1, PID:g43796
A:Experimental source: plasmid pGMP1
R:Lee, K.Y.; Hopkins, J.D.; Syvonen, M.
J. Bacteriol. 172, 3229-3236, 1990
A:Title: Direct involvement of 1826 in an antibiotic resistance operon.
A:Reference number: A35395; NCID:90264317; PMID:2160941
A:Accession: A35395
A:Molecule type: DNA
A:Residues: 1-30, 'L', 32-286 <IEB>
A:Cross-references: GB:X62115, NID:g48988; PIDD:CAA44025.1, PID:g48990
A:Experimental source: plasmid BWH77
C:Genetics:
A:Gene: blaS2A
A:Genome: plasmid
C:Superfamily: beta-lactamase I
C:Keywords: antibiotic resistance; hydrolase

[illegible]

RESULT 12
A60679
beta-lactamase (EC 3.5.2.6) SHV-2 precursor - *Salmonella typhimurium* plasmid pHT1
C:Species: *Salmonella typhimurium*
C:Date: 14-May-1991 #sequence_revision 14-May-1993 #text_change 16-Aug-2004
C:Accession: A60679
R:Garbary-Chenon, A.; Godard, V.; Labie, R.; Nicolaie, J.C.
A:Title: Nucleotide sequence of SHV-2 beta-lactamase gene.
A:Reference number: A60679; MUID:90351141; PMID:2201259
A:Accession: A60679
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-286 <GAR>
A:Cross-references: GB:LA7119; NID:g972890; PIDD:AA75015.1; PUD:g972891
C:Genetics:
A:Genome: plasmid
C:Superfamily: Beta-lactamase I
K:Keywords: antibiotic resistance; hydrolase
F:1-21/Domains: signal sequence #status predicted <SIG>

	Query Match	71.7%;	Score 552;	DB 2;	Length 286;
	Best Local Similarity	70.3%;	Pred. No. 1.7e-45;		
	Matches 104;	Conservative 21;	Mismatch 23;	Indels 0;	Gaps 0;
Qy	2 PETLVKVDADBDQAGRVGYIELDNSGKLIESPRPERPFMMSTFKVLLCGAVLSRIDA 61	:	:	:	:
Dd	23 PQLPEQIKOSSQSGLSGRGVMTEMLDASGRITLTARADERPFMMSTFKVLLCGAVLARDA 82	:	:	:	:
Qy	62 GQEOLGRIIRHSQNDLVEYSPVTSEKHLLTDGMTVELCSAATMSDNTANILLTTGGPK 121	:	:	:	:
Dd	83 GDEQLERKIHRQQDLVDYSPVSSEKHLLADGMTVELCPAAITMSDNSANILLTLVGSPA 142	:	:	:	:
Qy	122 ELTAFILNMGDHVRTRLDRMPEELNEALP 149	:	:	:	:
Dd	143 GLTAFLEHQIGDNVTRLDRMTELNEALP 170	:	:	:	:

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:36:31 ; Search time 17.6347 Seconds
(without alignments)
728.091 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_172

Perfect score: 885
Sequence: 1 HPEITLVKXKADQLGARVG.....RDTMPVAMATTLAKLTGE 172

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
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4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTCUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	885	100.0	286	1	US-07-721-775A-2
2	885	100.0	286	1	US-08-339-658-2
3	885	100.0	286	3	US-09-263-933-7
4	885	100.0	286	3	US-09-263-933-14
5	885	100.0	286	3	US-09-263-933-21
6	885	100.0	286	3	US-09-025-769B-265
7	885	100.0	286	3	US-09-025-769B-362
8	885	100.0	286	4	US-09-919-901-7
9	885	100.0	286	4	US-09-919-901-14
10	885	100.0	286	4	US-09-919-901-21
11	885	100.0	286	4	US-09-490-070A-265
12	885	100.0	286	4	US-09-490-070A-362
13	885	100.0	286	4	US-09-490-153-265
14	885	100.0	286	4	US-09-490-153-362
15	885	100.0	286	4	US-10-191-966-7
16	885	100.0	286	4	US-10-191-966-14
17	885	100.0	286	4	US-10-191-966-21
18	885	100.0	286	4	US-09-490-324-265
19	885	100.0	286	4	US-09-490-324-362
20	885	100.0	299	3	US-09-025-769B-285
21	885	100.0	299	3	US-09-025-769B-298
22	885	100.0	299	3	US-09-025-769B-300
23	885	100.0	299	4	US-09-490-070A-285
24	885	100.0	299	4	US-09-490-070A-298
25	885	100.0	299	4	US-09-490-070A-300
26	885	100.0	299	4	US-09-490-153-285
27	885	100.0	299	4	US-09-490-153-298

28	885	100.0	299	4	US-09-490-153-300	Sequence 300, App
29	885	100.0	299	4	US-09-490-324-285	Sequence 285, App
30	885	100.0	299	4	US-09-490-324-298	Sequence 298, App
31	885	100.0	299	4	US-09-490-324-300	Sequence 300, App
32	885	100.0	2307	3	US-09-263-933-2	Sequence 2, Appl1
33	885	100.0	2307	3	US-09-263-933-9	Sequence 9, Appl1
34	885	100.0	2307	3	US-09-263-933-16	Sequence 16, Appl1
35	885	100.0	2307	4	US-09-919-901-2	Sequence 2, Appl1
36	885	100.0	2307	4	US-09-919-901-9	Sequence 9, Appl1
37	885	100.0	2307	4	US-09-919-901-16	Sequence 16, Appl1
38	885	100.0	2307	4	US-10-191-966-2	Sequence 2, Appl1
39	885	100.0	2307	4	US-10-191-966-9	Sequence 9, Appl1
40	885	100.0	2307	4	US-10-191-966-16	Sequence 16, Appl1
41	884	99.9	286	4	US-09-555-510B-9	Sequence 9, Appl1
42	884	99.9	286	4	US-10-231-013-9	Sequence 9, Appl1
43	884	99.9	1293	4	US-09-170-436D-292	Sequence 292, App
44	884	99.9	1293	4	US-09-364-425B-57	Sequence 57, Appl1
45	880	99.4	263	1	US-08-407-544-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-07-721-775A-2

Sequence 2, Application US/07721775A

Patent No. 5180666

GENERAL INFORMATION:

APPLICANT: States, J. Christopher

APPLICANT: Hines, Ronald N.

APPLICANT: No. 5180666ak, Raymond P.

TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING

TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESSES:

ADDRESS: Reising, Ethnington, Barnard, Perry & Milton

STREET: P.O. Box 4390

CITY: Troy

STATE: Michigan

COUNTRY: U.S.A.

ZIP: 48099

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07721,775A

FILING DATE: 19910627

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Kohn, Kenneth I.

REGISTRATION NUMBER: 30,955

REFERENCE/DOCKET NUMBER: P-321WSU

TELECOMMUNICATION INFORMATION:

TELEPHONE: (313) 689-3554

TELEFAX: (313) 689-4071

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 286 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-721-775A-2

Query Match 100.0%; Score 885; DB 1; Length 286;

Best Local Similarity 100.0%; Pred. No. 3.7e-96;

Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPEITLVKXKADQLGARVGITIEDLNSGKTLSPREPRPMSTFVLLCGAVLSRID 60
Db 24 HPEITLVKXKADQLGARVGITIEDLNSGKTLSPREPRPMSTFVLLCGAVLSRID 83

QY 61 AGGOLGRRIHYSNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTGGP 120
DB 84 AGGOLGRRIHYSNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTGGP 143
QY 121 KETLAFLLHNMGDHVTRLDRWEPELNEAIPNDERDTMPVMAATTLRKLLTGE 172
DB 144 KETLAFLLHNMGDHVTRLDRWEPELNEAIPNDERDTMPVMAATTLRKLLTGE 195

RESULT 2

US-08-339-658-2
Sequence 2, Application US/08339658
Patent No. 5525482
GENERAL INFORMATION:
APPLICANT: States, J. Christopher
APPLICANT: Hines, Ronald N.
APPLICANT: No. 5525482ak, Raymond F.
TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reising, Ethington, Barnard, Perry & Milton
STREET: P.O. Box 4390
CITY: Troy
STATE: Michigan
COUNTRY: U.S.A.
ZIP: 48099
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,658
FILING DATE: 15-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,295
FILING DATE: 09-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: P-321WSU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 689-3554
TELEFAX: (313) 689-4071
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-339-658-2

Query Match 100.0%; Score 885; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.7e-96;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEFLVVKDAEDQLGARVGIETDLSNGKILSFRRPEFRPPMSTFKVLLCGAVLSRID 60
DB 24 HPEFLVVKDAEDQLGARVGIETDLSNGKILSFRRPEFRPPMSTFKVLLCGAVLSRID 83
QY 61 AGGOLGRRIHYSNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTGGP 120
DB 84 AGGOLGRRIHYSNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTGGP 143
QY 121 KETLAFLLHNMGDHVTRLDRWEPELNEAIPNDERDTMPVMAATTLRKLLTGE 172
DB 144 KETLAFLLHNMGDHVTRLDRWEPELNEAIPNDERDTMPVMAATTLRKLLTGE 195

RESULT 3
US-09-263-933-7

Sequence 7, Application US/09263933
Patent No. 6280940
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentn Ver. 2.0
SEQ ID NO 7
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
US-09-263-933-7

Query Match 100.0%; Score 885; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.7e-96;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEFLVVKDAEDQLGARVGIETDLSNGKILSFRRPEFRPPMSTFKVLLCGAVLSRID 60
DB 24 HPEFLVVKDAEDQLGARVGIETDLSNGKILSFRRPEFRPPMSTFKVLLCGAVLSRID 83
QY 61 AGGOLGRRIHYSNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTGGP 120
DB 84 AGGOLGRRIHYSNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTGGP 143
QY 121 KETLAFLLHNMGDHVTRLDRWEPELNEAIPNDERDTMPVMAATTLRKLLTGE 172
DB 144 KETLAFLLHNMGDHVTRLDRWEPELNEAIPNDERDTMPVMAATTLRKLLTGE 195

RESULT 4

US-09-263-933-14
Sequence 14, Application US/09263933
Patent No. 6280940
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentn Ver. 2.0
SEQ ID NO 14
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
US-09-263-933-14

Query Match 100.0%; Score 885; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.7e-96;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEFLVVKDAEDQLGARVGIETDLSNGKILSFRRPEFRPPMSTFKVLLCGAVLSRID 60
DB 24 HPEFLVVKDAEDQLGARVGIETDLSNGKILSFRRPEFRPPMSTFKVLLCGAVLSRID 83
QY 61 AGGOLGRRIHYSNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTGGP 120
DB 84 AGGOLGRRIHYSNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTGGP 143

QY 121 KETLAFILNMGDHTVRLDRWEPELNEAIPNDRDITTPVAMATTIRKLLTGE 172
 DB 144 KETLAFILNMGDHTVRLDRWEPELNEAIPNDRDITTPVAMATTIRKLLTGE 195

RESULT 5

US-09-263-933-21
 ; Sequence 21, Application US/09263933
 ; Patent No. 6280940
 ; GENERAL INFORMATION:
 ; APPLICANT: Potts, Karen E.
 ; APPLICANT: Jackson, Roberta L.
 ; APPLICANT: Patrick, Amy K.
 ; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
 ; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
 ; FILE REFERENCE: 0125-0005A
 ; CURRENT FILING DATE: 1999-03-08
 ; EARLIER APPLICATION NUMBER: 09/129,611
 ; EARLIER FILING DATE: 1998-08-05
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 21
 ; LENGTH: 286
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; US-09-263-933-21

Query Match 100.0%; Score 885; DB 3; Length 286;
 Best Local Similarity 100.0%; Pred. No. 3.7e-96;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKXVDADQIGARVGYIELDLSNGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
 DB 24 HPELVKXVDADQIGARVGYIELDLSNGKILSFRRPFRPMSTFKVLLCGAVLSRID 83
 QY 61 AGQBLGRIHISQNDLVEYSPVTEKHLTDGNTVELCSAALTMSDNTANLLTTIGSP 120
 DB 84 AGQBLGRIHISQNDLVEYSPVTEKHLTDGNTVELCSAALTMSDNTANLLTTIGSP 143
 QY 121 KETLAFILNMGDHTVRLDRWEPELNEAIPNDRDITTPVAMATTIRKLLTGE 172
 DB 144 KETLAFILNMGDHTVRLDRWEPELNEAIPNDRDITTPVAMATTIRKLLTGE 195

RESULT 6

US-09-025-769B-265
 ; Sequence 265, Application US/09025769B
 ; Patent No. 6300064
 ; GENERAL INFORMATION:
 ; APPLICANT: Knappik, Achim
 ; APPLICANT: Pack, Peter
 ; APPLICANT: Illag, Vic
 ; APPLICANT: Ge, Liming
 ; APPLICANT: Moroney, Simon
 ; APPLICANT: Plueckthun, Andreas
 ; TITLE OF INVENTION: Protein/(poly)peptide libraries
 ; NUMBER OF SEQUENCES: 373
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 ; STREET: 1251 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10021
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/025,769B
 ; FILING DATE: 18-FEB-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0
 FILING DATE: 18-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: James F. Haley, Jr., Esq.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: MORPHO/5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 596-9000
 TELEFAX: (212) 596-9090
 ; INFORMATION FOR SEQ ID NO: 265:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 286 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-025-769B-265

Query Match 100.0%; Score 885; DB 3; Length 286;
 Best Local Similarity 100.0%; Pred. No. 3.7e-96;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKXVDADQIGARVGYIELDLSNGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
 DB 24 HPELVKXVDADQIGARVGYIELDLSNGKILSFRRPFRPMSTFKVLLCGAVLSRID 83
 QY 61 AGQBLGRIHISQNDLVEYSPVTEKHLTDGNTVELCSAALTMSDNTANLLTTIGSP 120
 DB 84 AGQBLGRIHISQNDLVEYSPVTEKHLTDGNTVELCSAALTMSDNTANLLTTIGSP 143
 QY 121 KETLAFILNMGDHTVRLDRWEPELNEAIPNDRDITTPVAMATTIRKLLTGE 172
 DB 144 KETLAFILNMGDHTVRLDRWEPELNEAIPNDRDITTPVAMATTIRKLLTGE 195

RESULT 7

US-09-025-769B-362
 ; Sequence 362, Application US/09025769B
 ; Patent No. 6300064
 ; GENERAL INFORMATION:
 ; APPLICANT: Knappik, Achim
 ; APPLICANT: Pack, Peter
 ; APPLICANT: Illag, Vic
 ; APPLICANT: Ge, Liming
 ; APPLICANT: Moroney, Simon
 ; APPLICANT: Plueckthun, Andreas
 ; TITLE OF INVENTION: Protein/(poly)peptide libraries
 ; NUMBER OF SEQUENCES: 373
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 ; STREET: 1251 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10021
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/025,769B
 ; FILING DATE: 18-FEB-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 95 11 3021.0
 ; FILING DATE: 18-AUG-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: James F. Haley, Jr., Esq.
 ; REGISTRATION/DOCKET NUMBER: MORPHO/5
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 596-9000
 ; TELEFAX: (212) 596-9090

;; INFORMATION FOR SEQ ID NO: 362:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 286 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-025-769B-362

Query Match 100.0%; Score 885; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.7e-96;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPELVKVKADADQAGAVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
Db 24 HPELVKVKADADQAGAVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 83
Qy 61 AGQQLGRIRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANILLTTIGSP 120
Db 84 AGQQLGRIRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANILLTTIGSP 143
Qy 121 KELTSFLNMGDVTRLDRWEPELNEAIPNDRDITTMPVAAATTIRKLLTGE 172
Db 144 KELTSFLNMGDVTRLDRWEPELNEAIPNDRDITTMPVAAATTIRKLLTGE 195

RESULT 8
US-09-919-901-7
Sequence 7, Application US/09919901
Patent No. 6599738

;; GENERAL INFORMATION:
;; APPLICANT: Potts, Karen E.
;; APPLICANT: Jackson, Roberta L.
;; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
;; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
;; FILE REFERENCE: 0125-0005A
;; CURRENT APPLICATION NUMBER: US/09/919,901
;; CURRENT FILING DATE: 2001-08-02
;; PRIOR APPLICATION NUMBER: 09/263,933
;; PRIOR FILING DATE: 1999-02-08
;; PRIOR APPLICATION NUMBER: 09/129,611
;; PRIOR FILING DATE: 1998-08-05
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO: 7
;; LENGTH: 286
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: :
US-09-919-901-7

Query Match 100.0%; Score 885; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.7e-96;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPELVKVKADADQAGAVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
Db 24 HPELVKVKADADQAGAVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 83
Qy 61 AGQQLGRIRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANILLTTIGSP 120
Db 84 AGQQLGRIRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANILLTTIGSP 143
Qy 121 KELTSFLNMGDVTRLDRWEPELNEAIPNDRDITTMPVAAATTIRKLLTGE 172
Db 144 KELTSFLNMGDVTRLDRWEPELNEAIPNDRDITTMPVAAATTIRKLLTGE 195

RESULT 9
US-09-919-901-14
Sequence 14, Application US/09919901
Patent No. 6599738

;; GENERAL INFORMATION:
;; APPLICANT: Potts, Karen E.
;; APPLICANT: Jackson, Roberta L.
;; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
;; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
;; FILE REFERENCE: 0125-0005A
;; CURRENT APPLICATION NUMBER: US/09/919,901
;; CURRENT FILING DATE: 2001-08-02
;; PRIOR APPLICATION NUMBER: 09/263,933
;; PRIOR FILING DATE: 1999-02-08
;; PRIOR APPLICATION NUMBER: 09/129,611
;; PRIOR FILING DATE: 1998-08-05
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO: 14
;; LENGTH: 286
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: :
US-09-919-901-14

Query Match 100.0%; Score 885; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.7e-96;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPELVKVKADADQAGAVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
Db 24 HPELVKVKADADQAGAVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 83
Qy 61 AGQQLGRIRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANILLTTIGSP 120
Db 84 AGQQLGRIRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANILLTTIGSP 143
Qy 121 KELTSFLNMGDVTRLDRWEPELNEAIPNDRDITTMPVAAATTIRKLLTGE 172
Db 144 KELTSFLNMGDVTRLDRWEPELNEAIPNDRDITTMPVAAATTIRKLLTGE 195

RESULT 10
US-09-919-901-21
Sequence 21, Application US/09919901
Patent No. 6599738

;; GENERAL INFORMATION:
;; APPLICANT: Potts, Karen E.
;; APPLICANT: Jackson, Roberta L.
;; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
;; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
;; FILE REFERENCE: 0125-0005A
;; CURRENT APPLICATION NUMBER: US/09/919,901
;; CURRENT FILING DATE: 2001-08-02
;; PRIOR APPLICATION NUMBER: 09/263,933
;; PRIOR FILING DATE: 1999-02-08
;; PRIOR APPLICATION NUMBER: 09/129,611
;; PRIOR FILING DATE: 1998-08-05
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO: 21
;; LENGTH: 286
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: :
US-09-919-901-21

Query Match 100.0%; Score 885; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.7e-96;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPELVKVKADADQAGAVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
Db 24 HPELVKVKADADQAGAVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 83
Qy 61 AGQQLGRIRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANILLTTIGSP 120
Db 84 AGQQLGRIRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANILLTTIGSP 143
Qy 121 KELTSFLNMGDVTRLDRWEPELNEAIPNDRDITTMPVAAATTIRKLLTGE 172
Db 144 KELTSFLNMGDVTRLDRWEPELNEAIPNDRDITTMPVAAATTIRKLLTGE 195

DB 24 HPEITLVKVDADQAGARVGYIELDLSNGKILSFPEERFPMMSTFKVLLCGAVLSRID 83
QY 61 AGOEOIGRIHYSQNDLVEYSPTVEKHLTDGMTVRELCSAATMSDNTANLLTTIGGP 120
DB 84 AGOEOIGRIHYSQNDLVEYSPTVEKHLTDGMTVRELCSAATMSDNTANLLTTIGGP 143
QY 121 KELITAFIHNMGDVTRLDRWEPELNEAIPNDRDITTPVAMATTIRKLLTGE 172
DB 144 KELITAFIHNMGDVTRLDRWEPELNEAIPNDRDITTPVAMATTIRKLLTGE 195

RESULT 11
US-09-490-070A-265
; Sequence 265, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Laming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Colin G. Sandercock, Esq. c/o Heller Ehrman
; White & McAlliff
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 265:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-09-490-070A-265

Query Match 100.0%; Score 885; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.7e-96;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGYIELDLSNGKILSFPEERFPMMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKVDADQAGARVGYIELDLSNGKILSFPEERFPMMSTFKVLLCGAVLSRID 83
QY 61 AGOEOIGRIHYSQNDLVEYSPTVEKHLTDGMTVRELCSAATMSDNTANLLTTIGGP 120
DB 84 AGOEOIGRIHYSQNDLVEYSPTVEKHLTDGMTVRELCSAATMSDNTANLLTTIGGP 143
QY 121 KELITAFIHNMGDVTRLDRWEPELNEAIPNDRDITTPVAMATTIRKLLTGE 172
DB 144 KELITAFIHNMGDVTRLDRWEPELNEAIPNDRDITTPVAMATTIRKLLTGE 195

DB 144 KELITAFIHNMGDVTRLDRWEPELNEAIPNDRDITTPVAMATTIRKLLTGE 195

RESULT 12
US-09-490-070A-362
; Sequence 362, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Laming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Colin G. Sandercock, Esq. c/o Heller Ehrman
; White & McAlliff
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 362:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 362:
US-09-490-070A-362

Query Match 100.0%; Score 885; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.7e-96;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGYIELDLSNGKILSFPEERFPMMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKVDADQAGARVGYIELDLSNGKILSFPEERFPMMSTFKVLLCGAVLSRID 83
QY 61 AGOEOIGRIHYSQNDLVEYSPTVEKHLTDGMTVRELCSAATMSDNTANLLTTIGGP 120
DB 84 AGOEOIGRIHYSQNDLVEYSPTVEKHLTDGMTVRELCSAATMSDNTANLLTTIGGP 143
QY 121 KELITAFIHNMGDVTRLDRWEPELNEAIPNDRDITTPVAMATTIRKLLTGE 172
DB 144 KELITAFIHNMGDVTRLDRWEPELNEAIPNDRDITTPVAMATTIRKLLTGE 195

RESULT 13
US-09-490-153-265
; Sequence 265, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:

APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-09-490-153-265
Query Match 100.0%; Score 885; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.7e-96;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPELVKVKYKADBDQAGRVGYIELDLSGKILSFRRPFRPMSFTFVLLCGAVLSRID 60
DB 24 HPELVKVKYKADBDQAGRVGYIELDLSGKILSFRRPFRPMSFTFVLLCGAVLSRID 83
QY 61 AGQEQIGRIHYSQNDLYEYSPVTEKHLTDGNTVRELCSAATIMSDNTAANLLTTIGCP 120
DB 84 AGQEQIGRIHYSQNDLYEYSPVTEKHLTDGNTVRELCSAATIMSDNTAANLLTTIGCP 143
QY 121 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDITTMVAMATTIRKLLTGE 172
DB 144 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDITTMVAMATTIRKLLTGE 195
RESULT 14
US-09-490-153-362
Sequence 362, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 362:
US-09-490-153-362
Query Match 100.0%; Score 885; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.7e-96;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPELVKVKYKADBDQAGRVGYIELDLSGKILSFRRPFRPMSFTFVLLCGAVLSRID 60
DB 24 HPELVKVKYKADBDQAGRVGYIELDLSGKILSFRRPFRPMSFTFVLLCGAVLSRID 83
QY 61 AGQEQIGRIHYSQNDLYEYSPVTEKHLTDGNTVRELCSAATIMSDNTAANLLTTIGCP 120
DB 84 AGQEQIGRIHYSQNDLYEYSPVTEKHLTDGNTVRELCSAATIMSDNTAANLLTTIGCP 143
QY 121 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDITTMVAMATTIRKLLTGE 172
DB 144 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDITTMVAMATTIRKLLTGE 195
RESULT 15
US-10-191-966-7
Sequence 7, Application US/10191966
Patent No. 6790612
GENERAL INFORMATION:
APPLICANT: Potte, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
PRIOR FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 7
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-10-191-966-7

Query Match 100.0%; Score 885; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.7e-96;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	HPETLVKVKDAEDQLGARVGYIELDINSGLKESFRPEERFPMWSTFKYLLGAVLSRID	60
Db	24	HPETLVKVKDAEDQLGARVGYIELDINSGLKESFRPEERFPMWSTFKYLLGAVLSRID	83
Qy	61	AGQEOIGRIIHSQNDLVEYSPVTEKHLTDGMTRELCSAITMSDNTANILLTTIGSP	120
Db	84	AGQEOIGRIIHSQNDLVEYSPVTEKHLTDGMTRELCSAITMSDNTANILLTTIGSP	143
Qy	121	KELTAFLEHMGDHYTRLDRWEPELNEAIPNDERDITMPVAMATTILKLLTGE	172
Db	144	KELTAFLEHMGDHYTRLDRWEPELNEAIPNDERDITMPVAMATTILKLLTGE	195

Search completed: June 10, 2005, 11:01:15
Job time : 18.6347 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:35:06 ; Search time 12.543 Seconds

(without alignments)
1319.408 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_172

Perfect score: 885
Sequence: 1 HPETLVKVKQADBDQAGARVG.....RDTTPVAMATTLRLNGE 172

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	885	100.0	286	2	TS1301
2	885	100.0	286	2	beta-lactamase (EC
3	885	100.0	286	4	beta-lactamase (EC
4	880	99.4	286	1	beta-lactamase (EC
5	880	99.4	286	4	beta-lactamase (EC
6	872	98.5	286	2	beta-lactamase (EC
7	867	98.0	286	2	beta-lactamase (EC
8	866	97.9	286	2	beta-lactamase (EC
9	866	97.9	286	2	beta-lactamase (EC
10	866	97.9	286	2	beta-lactamase (EC
11	868	71.0	286	2	beta-lactamase (EC
12	868	71.0	286	2	beta-lactamase (EC
13	864	70.5	265	2	beta-lactamase (EC
14	864	70.5	265	2	beta-lactamase (EC
15	864	70.5	265	2	beta-lactamase (EC
16	864	70.5	286	1	beta-lactamase (EC
17	864	70.5	286	2	beta-lactamase (EC
18	864	70.5	286	2	beta-lactamase (EC
19	863	68.1	279	2	beta-lactamase (EC
20	599.5	67.7	287	1	beta-lactamase (EC
21	573	64.7	286	1	beta-lactamase (EC
22	482	54.5	288	2	beta-lactamase (EC
23	392.5	44.4	281	2	beta-lactamase (EC
24	382.5	43.2	314	2	beta-lactamase (EC
25	379.5	42.9	294	2	beta-lactamase (EC
26	379.5	42.9	302	2	beta-lactamase (EC
27	378	42.7	293	2	beta-lactamase (EC
28	374.5	42.3	263	2	beta-lactamase (EC
29	371.5	42.0	291	2	beta-lactamase (EC

30	370.5	41.9	306	1	beta-lactamase (EC
31	366.5	41.4	306	2	beta-lactamase (EC
32	366.5	41.4	311	2	beta-lactamase (EC
33	360	40.7	305	2	beta-lactamase (EC
34	360	40.7	305	2	beta-lactamase (EC
35	360	40.7	305	2	beta-lactamase (EC
36	357.5	40.4	306	2	beta-lactamase (EC
37	350.5	39.6	288	2	beta-lactamase (EC
38	350.5	39.6	291	2	beta-lactamase (EC
39	349.5	39.5	305	1	beta-lactamase (EC
40	349	39.4	294	2	beta-lactamase (EC
41	347.5	39.3	263	2	beta-lactamase (EC
42	346.5	39.2	304	2	beta-lactamase (EC
43	346.5	39.2	304	2	beta-lactamase (EC
44	345.5	39.0	311	1	beta-lactamase (EC
45	345	39.0	314	1	beta-lactamase (EC

ALIGNMENTS

RESULT 1
TS1301
beta-lactamase (EC 3.5.2.6) - fission yeast (Schizosaccharomyces pombe)
C.Species: Schizosaccharomyces pombe
C.Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C.Accession: TS1301
R.WACH, A.; BRACHAT, A.; ALBERTSSEGUI, C.; REBISCHUNG, C.; PHILIPPSEN, P.
Yeast 13, 1065-1075, 1997
A.Title: Heterologous His3 marker and GFP reporter modules for PCR-targeting in Saccharon
A.Reference number: 209587
A.Accession: TS1301
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-286 <MAC>
A.Cross-references: EMBL:AJ002683; PIDN:CAA05686.1
C.Genetics:
A.Gene: bla
C.Superfamily: beta-lactamase I
C.Keywords: hydrolase

Query Match 100.0%; Score 885; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 4.1e-74;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPETLVKVKQADBDQAGARVGYLELDNSGKLTIESFRPEPRPMSTFKVLLCGAVLSRID 60
DB 24 HPETLVKVKQADBDQAGARVGYLELDNSGKLTIESFRPEPRPMSTFKVLLCGAVLSRID 83
QY 61 AGQEQIGRRIRYSDNDLVESPVYRKHLTDGMYVRELCSAATWSDNRAVLLTTGGP 120
DB 84 AGQEQIGRRIRYSDNDLVESPVYRKHLTDGMYVRELCSAATWSDNRAVLLTTGGP 143
QY 121 KELTAFILNMGDHVTYRLDRWEPELNEALPNDERDTTPVAMATTLRLKLTIGE 172
DB 144 KELTAFILNMGDHVTYRLDRWEPELNEALPNDERDTTPVAMATTLRLKLTIGE 195

RESULT 2
S47061
beta-lactamase (EC 3.5.2.6) - phage phi-X174
C.Species: phage phi-X174
C.Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C.Accession: S47061
R.Henrich, B.; Schmidtberger, B.
Submitted to the EMBL Data Library, July 1994
A.Description: A variant of phix174 gene B-based positive selection vectors with enhanced
A.Reference number: S47060
A.Accession: S47061
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-286 <HEN>
A.Cross-references: UNIPROT:Q38058; EMBL:Z35638; NID:G520996; PIDN:CAA84692.1; PID:G5209;

C:Superfamily: beta-lactamase I
C:Keywords: hydrolase

Query Match 100.0%; Score 885; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 4.1e-74;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKQADBDQAGAVGYIELDNGSKILIESFRPERPFMMSTFKVLCGAVLSRID 60
DB 24 HPEITLVKQADBDQAGAVGYIELDNGSKILIESFRPERPFMMSTFKVLCGAVLSRID 83
QY 61 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAAILLTITIGP 120
DB 84 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAAILLTITIGP 143
QY 121 KELTFLNMGDHTVRLDRWPELNEALPNDERDITMPVAMATTLTKLITGE 172
DB 144 KELTFLNMGDHTVRLDRWPELNEALPNDERDITMPVAMATTLTKLITGE 195

RESULT 3

S41975
beta-lactamase (EC 3.5.2.6) precursor - synthetic
C:Species: synthetic
C:Date: 25-Dec-1994 #sequence_revision 22-Aug-1996 #text_change 20-Oct-2000
C:Accession: S41975

R:Kaeßter, K.H.; Montcollu, L.; Kern, H.; Thulke, M.; Schütz, G.

Gene 148, 67-70, 1994
A:Title: Universal beta-galactosidase cloning vectors for promoter analysis and gene tar
A:Reference number: A57991; MUID:95011660; PMID:7926839
A:Accession: S41975

A:Status: not compared with conceptual translation
A:Molecule type: DNA

A:Residues: 1-286 <KAB>
A:Cross-references: EMBL:X76682; NID:9453622; PIDN:CAA5104.1; PID:9453623
A:Note: submitted to the EMBL Data Library, December 1993
C:Keywords: hydrolase

Query Match 100.0%; Score 885; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 4.1e-74;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKQADBDQAGAVGYIELDNGSKILIESFRPERPFMMSTFKVLCGAVLSRID 60
DB 24 HPEITLVKQADBDQAGAVGYIELDNGSKILIESFRPERPFMMSTFKVLCGAVLSRID 83
QY 61 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAAILLTITIGP 120
DB 84 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAAILLTITIGP 143
QY 121 KELTFLNMGDHTVRLDRWPELNEALPNDERDITMPVAMATTLTKLITGE 172
DB 144 KELTFLNMGDHTVRLDRWPELNEALPNDERDITMPVAMATTLTKLITGE 195

RESULT 4

PRECEP

beta-lactamase (EC 3.5.2.6) precursor - Escherichia coli plasmid
N:Alternate names: beta-lactamase TEM-6 (for blaT-6 DNA); penicillinase
C:Species: Escherichia coli
C:Date: 30-Nov-1980 #sequence_revision 01-Sep-1981 #text_change 16-Aug-2004
C:Accession: A93821; A93820; A35387; S24415; A01005

R:Sutcliffe, J.G.
Proc. Natl. Acad. Sci. U.S.A. 75, 3737-3741, 1978

A:Title: Nucleotide sequence of the ampicillin resistance gene of Escherichia coli plasm
A:Reference number: A93821; MUID:79012484; PMID:358200
A:Accession: A93821

A:Molecule type: DNA

A:Residues: 1-286 <STU>

A:Cross-references: UNIPROT:P00810; GB:V00613; GB:J01832; NID:943710; PIDN:CAA3086.1; F
A:Experimental source: plasmid pBR322
R:Ambler, R.P.; Scott, G.K.

Proc. Natl. Acad. Sci. U.S.A. 75, 3732-3736, 1978

A:Title: Partial amino acid sequence of penicillinase coded by Escherichia coli plasmid F
A:Reference number: A93820; MUID:79012483; PMID:358199
A:Accession: A93820

A:Molecule type: protein

A:Residues: 24-36, 'K', 38-286 <AMB>

A:Experimental source: plasmid R6K
R:Kornacker, J.A.; Burlage, R.S.; Fagurski, D.H.

J. Bacteriol. 172, 3040-3050, 1990

A:Title: The kil-kor region of broad-host-range plasmid RK2: nucleotide sequence, polype
A:Reference number: A35387; MUID:90264294; PMID:2160936

A:Accession: A35387

A:Molecule type: DNA

A:Residues: 182-286 <KOR>

A:Cross-references: GB:M2794; NID:9152521; PIDN:AAA26408.1; PID:9152522

A:Experimental source: PK2

R:Gunsberg, S.; Sougkoff, W.; Mabilat, C.; Bauernfeind, A.; Courvalin, P.

J. Gen. Microbiol. 137, 2681-2687, 1991

A:Title: An ISI-like element is responsible for high-level synthesis of extended-spectrum
A:Reference number: S24415; MUID:92166702; PMID:1665171

A:Accession: S24415

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-101, 'K', 103-161, 'H', 163-286 <GOU>

A:Cross-references: EMBL:X57972; NID:941816; PIDN:CAA41038.1; PID:941817

A:Experimental source: IS1-like blaT-6 DNA

R:Sutcliffe, J.G.

Cold Spring Harb. Symp. Quant. Biol. 43, 77-90, 1979

A:Title: Complete nucleotide sequence of the Escherichia coli plasmid pBR322.

A:Reference number: A80923; MUID:80002802; PMID:383387

A:Contents: annotation

C:Comment: Like most penicillinases from gram-negative bacteria, this enzyme, coded by a
C:Genetics:

A:Genome: plasmid

C:Superfamily: beta-lactamase I

C:Keywords: antibiotic resistance; hydrolase; membrane protein

F:1-33/Domain: signal sequence #status predicted <SIG>

F:24-286/Product: beta-lactamase #status experimental <MAT>

F:68/Active site: Ser #status predicted

F:75-121/Disulfide bonds: #status predicted

Query Match 99.4%; Score 880; DB 1; Length 286;
Best Local Similarity 98.8%; Pred. No. 1.2e-73;
Matches 170; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPEITLVKQADBDQAGAVGYIELDNGSKILIESFRPERPFMMSTFKVLCGAVLSRID 60
DB 24 HPEITLVKQADBDQAGAVGYIELDNGSKILIESFRPERPFMMSTFKVLCGAVLSRID 83
QY 61 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAAILLTITIGP 120
DB 84 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAAILLTITIGP 143
QY 121 KELTFLNMGDHTVRLDRWPELNEALPNDERDITMPVAMATTLTKLITGE 172
DB 144 KELTFLNMGDHTVRLDRWPELNEALPNDERDITMPVAMATTLTKLITGE 195

RESULT 5

I40905

beta-lactamase (EC 3.5.2.6) - synthetic

C:Species: synthetic

A:Note: Cloning vector pCG1408 engineered and expressed in Clavibacter xyli subsp. cynod

C:Date: 15-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Oct-2000

C:Accession: I40905

R:Taylor, J.; Stearman, R.S.; Uratani, B.B.

Plasmid 29, 241-244, 1993

A:Title: Development of a native plasmid as a cloning vector in Clavibacter xyli subsp. c

A:Reference number: I40904; MUID:93361581; PMID:7689234

A:Accession: I40905

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-286 <RES>
A:Cross-references: EMBL:U21228; NID:9885956; PIDN:AAA70411.1; PID:9885958

A:Residues: 1-32 <TOL>
A:Cross-references: GB:M55547; NID:g155010; PIDN:AAA98408.1; PID:g155016
C:Genetics:
A:Gene: TBM-bla
C:Superfamily: beta-lactamase I
C:Keywords: antibiotic resistance; hydrolase

Query Match 97.9%; Score 866; DB 2; Length 286;
Best Local Similarity 97.1%; Pred. No. 2.3e-72;
Matches 167; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGRVGYIELDLSGKILIESFRPERPMMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKVDADQAGRVGYIELDLSGKILIESFRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGQEQIGRIHYSQNDLVYSPVTEKHLLTDGNTVRELCSAATMSDNTAANLLTTIGGP 120
DB 84 AGQEQIGRIHYSQNDLVYSPVTEKHLLTDGNTVRELCSAATMSDNTAANLLTTIGGP 143
QY 121 KELITAFILNMGGDHVTRLDRWPEELNEALPNDERDITTPMAATTKRLLTGE 172
DB 144 KELITAFILNMGGDHVTRLDRWPEELNEALPNDERDITTPMAATTKRLLTGE 195

RESULT 10
J01546
Bla protein - Salmonella typhimurium plasmid NTP16
N:Alternate names: beta lactamase homolog
C:Species: Salmonella typhimurium
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: J01546
R:Cannon, P. M.; Striike, P.
A:Title: Complete nucleotide sequence and gene organization of plasmid NTP16.
A:Reference number: J01546; MUID:92383313; PMID:1325061
A:Accession: J01546
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <CAN>
A:Cross-references: UNIPROT:08L2F9
A:Genome: plasmid
C:Superfamily: beta-lactamase I

Query Match 97.9%; Score 866; DB 2; Length 286;
Best Local Similarity 97.7%; Pred. No. 2.3e-72;
Matches 168; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGRVGYIELDLSGKILIESFRPERPMMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKVDADQAGRVGYIELDLSGKILIESFRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGQEQIGRIHYSQNDLVYSPVTEKHLLTDGNTVRELCSAATMSDNTAANLLTTIGGP 120
DB 84 AGQEQIGRIHYSQNDLVYSPVTEKHLLTDGNTVRELCSAATMSDNTAANLLTTIGGP 143
QY 121 KELITAFILNMGGDHVTRLDRWPEELNEALPNDERDITTPMAATTKRLLTGE 172
DB 144 KELITAFILNMGGDHVTRLDRWPEELNEALPNDERDITTPMAATTKRLLTGE 195

RESULT 11
S16146
beta-lactamase (EC 3.5.2.6) 2A precursor - Klebsiella pneumoniae plasmids
N:Alternate names: beta-lactamase SHV2A
C:Species: Klebsiella pneumoniae
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 15-Oct-1999
C:Accession: S16146; A35395; S18767
R:Podbielski, A.; Schoenling, J.; Melzer, B.; Warnatz, K.; Leusch, H. G.
J:Gen. Microbiol. 137, 569-578, 1991
A:Title: Molecular characterization of a new plasmid-encoded SHV-type beta-lactamase (SHV-2A)
A:Reference number: S16146; MUID:91237320; PMID:2033379
A:Accession: S16146

A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <POD>
A:Cross-references: EMBL:X53817; NID:g43795; PIDN:CAA37813.1; PID:g43796
A:Experimental source: plasmid pZMP1
R:Lee, K.Y.; Hopkins, J.D.; Svanen, M.
J: Bacteriol. 172, 3229-3236, 1990
A:Title: Direct involvement of IS26 in an antibiotic resistance operon.
A:Reference number: A35395; MUID:90264317; PMID:2160941
A:Accession: A35395
A:Molecule type: DNA
A:Residues: 1-30, 'L', 32-286 <LEE>
A:Cross-references: GB:X62115; NID:g48988; PIDN:CAA44025.1; PID:g48990
A:Experimental source: plasmid BWH7
C:Genetics:
A:Gene: bla2A
C:Superfamily: beta-lactamase I
C:Keywords: antibiotic resistance; hydrolase

Query Match 71.0%; Score 628; DB 2; Length 286;
Best Local Similarity 69.6%; Pred. No. 2.1e-50;
Matches 119; Conservative 23; Mismatches 29; Indels 0; Gaps 0;

QY 2 PETTVKVDADQAGRVGYIELDLSGKILIESFRPERPMMSTFKVLLCGAVLSRID 61
DB 23 PQLPEQIKQSQSQSGRVGMIEMDLASGRITLTAWRADRFPMSTFKVLLCGAVLSRID 82
QY 62 GQEQIGRIHYSQNDLVYSPVTEKHLLTDGNTVRELCSAATMSDNTAANLLTTIGGP 121
DB 83 GQEQIGRIHYSQNDLVYSPVTEKHLLTDGNTVRELCSAATMSDNTAANLLTTIGGP 142
QY 122 ELTAFILNMGGDHVTRLDRWPEELNEALPNDERDITTPMAATTKRLLTGE 172
DB 143 ELTAFILNMGGDHVTRLDRWPEELNEALPNDERDITTPMAATTKRLLTGE 193

RESULT 12
A60679
beta-lactamase (EC 3.5.2.6) SHV-2 precursor - Salmonella typhimurium plasmid pHT1
C:Species: Salmonella typhimurium
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Aug-2004
C:Accession: A60679
R:Garbarg-Chenon, A.; Godard, V.; Labia, R.; Nicolaie, J. C.
A:Title: Agents Chemother. 34, 1444-1446, 1990
A:Title: Nucleotide sequence of SHV-2 beta-lactamase gene.
A:Reference number: A60679; MUID:90351141; PMID:2201259
A:Accession: A60679
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-286 <GAR>
A:Cross-references: GB:I47119; NID:g972890; PIDN:AAA75015.1; PID:g972891
C:Genetics:
A:Gene: plasmid
C:Superfamily: beta-lactamase I
C:Keywords: antibiotic resistance; hydrolase
F:1-21/Domain: signal sequence #status predicted <SIG>

Query Match 71.0%; Score 628; DB 2; Length 286;
Best Local Similarity 69.6%; Pred. No. 2.1e-50;
Matches 119; Conservative 23; Mismatches 29; Indels 0; Gaps 0;

QY 2 PETTVKVDADQAGRVGYIELDLSGKILIESFRPERPMMSTFKVLLCGAVLSRID 61
DB 23 PQLPEQIKQSQSQSGRVGMIEMDLASGRITLTAWRADRFPMSTFKVLLCGAVLSRID 82
QY 62 GQEQIGRIHYSQNDLVYSPVTEKHLLTDGNTVRELCSAATMSDNTAANLLTTIGGP 121
DB 83 GQEQIGRIHYSQNDLVYSPVTEKHLLTDGNTVRELCSAATMSDNTAANLLTTIGGP 142
QY 122 ELTAFILNMGGDHVTRLDRWPEELNEALPNDERDITTPMAATTKRLLTGE 172
DB 143 ELTAFILNMGGDHVTRLDRWPEELNEALPNDERDITTPMAATTKRLLTGE 193

RESULT 13

beta-lactamase (EC 3.5.2.6) class A - *Escherichia coli* plasmid p453
 N/Alternate names: beta-lactamase PIT-2; beta-lactamase SHV-1
 C/Species: *Escherichia coli*
 C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1993
 C/Accession: S00464
 R:Barthelemy, M.; Peduzzi, J.; Labia, R.
 Biochem. J. 251, 73-79, 1988
 A/Title: Complete amino acid sequence of p453-plasmid-mediated PIT-2 beta-lactamase (SHV-1)
 A/Reference number: S00464; MUID:88268817; PMID:3260490
 A/Accession: S00464
 A/Molecule type: protein
 A/Residues: 1-265 <BAR>
 C/Genetics:
 A/Genome: plasmid
 C/Superfamily: beta-lactamase I
 C/Keywords: antibiotic resistance; hydrolase

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OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Hafnia.
 OX NCBI_Taxid=569;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MISC198;
 RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY265886; AAP3844.1; --
 DR HSSP; P00807; IKGE.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 FT NON_TER 1
 FT NON_TER 232
 SQ SEQUENCE 232 AA; 25380 MW; 3D5DFD85582C261 CRC64;

Query Match 100.0%; Score 885; DB 2; Length 232;
 Best Local Similarity 100.0%; Pred. No. 3.7e-69;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HPELVKVKDADQAGARVGYIELDLSGKILSFRRPFRPMSSTFVLLCGAVLSRID 60
 DB 2 HPELVKVKDADQAGARVGYIELDLSGKILSFRRPFRPMSSTFVLLCGAVLSRID 61
 OY 61 AGOBLGRIRIHSQNDLYEYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 120
 DB 62 AGOBLGRIRIHSQNDLYEYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 121
 OY 121 KELTAFLLHMGDHYTRLDRLRMEPELNEAIPNDRDITTMVAMATTLRKLLTGS 172
 DB 122 KELTAFLLHMGDHYTRLDRLRMEPELNEAIPNDRDITTMVAMATTLRKLLTGS 173

RESULT 3
 Q6MWY8 PRELIMINARY; PRT; 241 AA.
 AC Q6MWY8;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Beta-lactamase (Fragment).
 DE Name=biatEM;
 GN Klbsiella pneumoniae.
 OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Klebsiella.
 OX NCBI_Taxid=573;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MISC112;
 RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY265887; AAP3840.1; --
 DR HSSP; P00807; IKGE.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 FT NON_TER 1
 FT NON_TER 241
 SQ SEQUENCE 241 AA; 26407 MW; 38DF2AFDF0C5807D CRC64;

Query Match 100.0%; Score 885; DB 2; Length 241;
 Best Local Similarity 100.0%; Pred. No. 3.8e-69;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HPELVKVKDADQAGARVGYIELDLSGKILSFRRPFRPMSSTFVLLCGAVLSRID 60
 DB 7 HPELVKVKDADQAGARVGYIELDLSGKILSFRRPFRPMSSTFVLLCGAVLSRID 66
 OY 61 AGOBLGRIRIHSQNDLYEYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 120

DB 67 AGOBLGRIRIHSQNDLYEYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 126
 OY 121 KELTAFLLHMGDHYTRLDRLRMEPELNEAIPNDRDITTMVAMATTLRKLLTGS 172
 DB 127 KELTAFLLHMGDHYTRLDRLRMEPELNEAIPNDRDITTMVAMATTLRKLLTGS 178

RESULT 4
 Q6MWY3 PRELIMINARY; PRT; 242 AA.
 AC Q6MWY3;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Beta-lactamase (Fragment).
 DE Name=biatEM;
 GN Escherichia coli.
 OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_Taxid=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TA005;
 RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY265887; AAP3845.1; --
 DR HSSP; P00807; IKGE.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 FT NON_TER 1
 FT NON_TER 242
 SQ SEQUENCE 242 AA; 26554 MW; 38C3DFA8A5A3807D CRC64;

Query Match 100.0%; Score 885; DB 2; Length 242;
 Best Local Similarity 100.0%; Pred. No. 3.8e-69;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HPELVKVKDADQAGARVGYIELDLSGKILSFRRPFRPMSSTFVLLCGAVLSRID 60
 DB 8 HPELVKVKDADQAGARVGYIELDLSGKILSFRRPFRPMSSTFVLLCGAVLSRID 67
 OY 61 AGOBLGRIRIHSQNDLYEYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 120
 DB 68 AGOBLGRIRIHSQNDLYEYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 127
 OY 121 KELTAFLLHMGDHYTRLDRLRMEPELNEAIPNDRDITTMVAMATTLRKLLTGS 172
 DB 128 KELTAFLLHMGDHYTRLDRLRMEPELNEAIPNDRDITTMVAMATTLRKLLTGS 179

RESULT 5
 Q6KB67 PRELIMINARY; PRT; 285 AA.
 AC Q6KB67;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OX NCBI_Taxid=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=First leaf;
 RA Jansen C., Korell M., Beckey C., Biedenkopf D., Kogel K.H.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ717739; CAG30723.1; --
 DR HSSP; P00807; IALQ.

OY 1 HPELVKVKDADQAGARVGYIELDLSGKILSFRRPFRPMSSTFVLLCGAVLSRID 60
 DB 7 HPELVKVKDADQAGARVGYIELDLSGKILSFRRPFRPMSSTFVLLCGAVLSRID 66
 OY 61 AGOBLGRIRIHSQNDLYEYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 120

DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR000871; Beta_lactamase_A.
 DR Pfam: PF00144; Beta_lactamase; 1.
 DR PRINTS: PR00118; BLACTAMASEA.
 DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
 DR Hypothetical protein.
 KW NON_TER 285
 FT SEQUENCE 285 AA; 31371 MW; A2F22753375FA930 CRC64;

Query Match 100.0%; Score 885; DB 2; Length 285;
 Best Local Similarity 100.0%; Pred. No. 4.7e-69;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGYIELDLSGKILSFRRPFRPFMMSTFKVLLCGAVLSRID 60
 DB 24 HPEITLVKVDADQAGARVGYIELDLSGKILSFRRPFRPFMMSTFKVLLCGAVLSRID 83
 QY 61 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTANILLTTTGGP 120
 DB 84 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTANILLTTTGGP 143
 QY 121 KELITAFILNMGDHVTRLDRMBEPLNEAIPNDRDITTMPVAMATTLRKLTGE 172
 DB 144 KELITAFILNMGDHVTRLDRMBEPLNEAIPNDRDITTMPVAMATTLRKLTGE 195

RESULT 6

Q38058 PRELIMINARY; PRT; 286 AA.

AC Q38058;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Beta_lactamase.
 GN Name=bla;
 OS Bacteriophage phi-X174.
 OC Viruses; ssDNA viruses; Microviridae; Microvirinae.
 CX NCBI_TaxID=10847;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=95172401; PubMed=7867948; DOI=10.1016/0378-1119(94)00839-K;
 RA Heinrich B.; Schmidtberger B.;
 RT "A variant of phiX174 gene E-based positive selection vectors with
 enhanced lytic potential.";
 RL Gene 154:51-54 (1995).
 DR EMBL; Z35638; CAA84692.1; -.
 DR PIR; S47061; S47061.
 DR HSSP; Q9R435; 1HTZ.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 DR SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;

Query Match 100.0%; Score 885; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 4.7e-69;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGYIELDLSGKILSFRRPFRPFMMSTFKVLLCGAVLSRID 60
 DB 24 HPEITLVKVDADQAGARVGYIELDLSGKILSFRRPFRPFMMSTFKVLLCGAVLSRID 83
 QY 61 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTANILLTTTGGP 120
 DB 84 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTANILLTTTGGP 143
 QY 121 KELITAFILNMGDHVTRLDRMBEPLNEAIPNDRDITTMPVAMATTLRKLTGE 172
 DB 144 KELITAFILNMGDHVTRLDRMBEPLNEAIPNDRDITTMPVAMATTLRKLTGE 195

RESULT 7

000626

AC 000626 PRELIMINARY; PRT; 286 AA.
 AC 000626; 008022; 008102; 009393; 009396; 009397; 009398; 009399;
 AC 009400; 009401; 009402; 009403; 009404; 009405; 009406; 009407;
 AC 009408; 009481; 009482; 009483; 009490; 057339;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Staphylococcus aureus.
 OS Staphylococcus aureus.
 OG Plasmid J3356/POX7/3, and Plasmid J3356/POX7/1.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 CX NCBI_TaxID=1280;
 [1]
 RN SEQUENCE FROM N.A.
 RP PLASMID=J3356/POX7/3, and J3356/POX7/1;
 RC MEDLINE=9642275; PubMed=8825372; DOI=10.1006/plas.1995.0005;
 RA Needham C.; Noble W.C.; Dyke K.G.;
 RT "The staphylococcal insertion sequence IS257 is active.";
 RL Plasmid 34:198-205 (1995).
 DR EMBL; U36912; AAB39957.1; -.
 DR PIR; U36911; AAB39956.1; -.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 KW Plasmid.
 SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;

Query Match 100.0%; Score 885; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 4.7e-69;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGYIELDLSGKILSFRRPFRPFMMSTFKVLLCGAVLSRID 60
 DB 24 HPEITLVKVDADQAGARVGYIELDLSGKILSFRRPFRPFMMSTFKVLLCGAVLSRID 83
 QY 61 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTANILLTTTGGP 120
 DB 84 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTANILLTTTGGP 143
 QY 121 KELITAFILNMGDHVTRLDRMBEPLNEAIPNDRDITTMPVAMATTLRKLTGE 172
 DB 144 KELITAFILNMGDHVTRLDRMBEPLNEAIPNDRDITTMPVAMATTLRKLTGE 195

RESULT 8

Q79CL6 PRELIMINARY; PRT; 286 AA.

AC Q79CL6;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Beta-lactamase.
 GN Name=bla;
 OS Methylobacillus flagellatum.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Methylobacterales;
 OC Methylobacteriaceae; Methylobacillus.
 CX NCBI_TaxID=405;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=97074643; PubMed=8917070; DOI=10.1016/0378-1119(96)00114-X;
 RA Seebrijski I.G.; Vassin V.M.; Tsyganov Y.D.;
 RT "Two new members of the BioB superfamily: cloning, sequencing and
 expression of bioB genes of Methylobacillus flagellatum and
 Corynebacterium glutamicum.";
 RL Gene 175:15-22 (1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Seebrijski I.; Vassin V.; Tsyganov Y.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U31280; AAC44581.1; -.

DR HSSP; P00807; 1ALQ.
DR InterPro; IPR001466; Beta_lactamase_A.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;

Query Match 100.0%; Score 885; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 4.7e-69;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGRVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
DB HPEITLVKVKADBDQAGRVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
QY 61 AGQELGRRIRHSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANILLTTIGCP 120
DB 84 AGQELGRRIRHSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANILLTTIGCP 143
QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAMATTLRKLLTGE 172
DB 144 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAMATTLRKLLTGE 195

RESULT 9

Q79DR3 PRELIMINARY; PRT; 286 AA.

AC Q79DR3; PRELIMINARY; PRT; 286 AA.
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Mutant extended-spectrum beta-lactamase precursor (EC 3.5.2.6).
GN Name=bla; Synonyms=blatEM-116;
OS Escherichia coli.
OC Plasmid pRP4, and plasmid pCAP8.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;

RA SEQUENCE FROM N.A.
RC STRAIN-K-12;
RA Maneewannakul K., Maneewannakul S., Ippen-Ihler K.,
RL Submitted (Aug-1991) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12; PLASMID=PRP4;
RA Rondot S., Anthony K., Dubel S., Ida N., Beyreuther K., Frost L.,
RA Little M., Breiting F.,
RL Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC PLASMID=PCAP8;
RA MEDLINE=96189310; PubMed=9514792; DOI=10.1006/abio.1997.2558;
RA Schleper D., Von Wilcken-Bergmann B., Schmidt M., Sodek H.,
RA Mueller-Hill B.,
RT "A positive selection vector for cloning of long polymerase chain
RT reaction fragments based on a lethal mutant of the crp gene
RT Escherichia coli.";
RL Anal. Biochem. 257:203-209(1998).

RA SEQUENCE FROM N.A.
RX PubMed=15243036;
RA Jeong S.H., Bae I.K., Lee J.H., Sohn S.G., Kang G.H., Jeon G.J.,
RA Kim Y.H., Jeong B.C., Lee S.H.;
RT "Molecular Characterization of Extended-Spectrum Beta-Lactamases
RT Produced by Clinical Isolates of Klebsiella pneumoniae and Escherichia
RT coli from a Korean Nationwide Survey.";
RL J. Clin. Microbiol. 42:2902-2906(2004).
DR EMBL; M74750; AAA24057.1; -.
DR EMBL; Y12694; CAA73226.1; -.
DR EMBL; AJ001614; CAA04868.1; -.
DR EMBL; AY425988; AAO95605.1; -.

DR HSSP; P00807; 1ALQ.
DR GO; GO:0008800; F:beta-lactamase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
DR Hydrolase; Plasmid; Signal.
FT SIGNAL 1
SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;

Query Match 100.0%; Score 885; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 4.7e-69;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGRVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
DB HPEITLVKVKADBDQAGRVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
QY 61 AGQELGRRIRHSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANILLTTIGCP 120
DB 84 AGQELGRRIRHSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANILLTTIGCP 143
QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAMATTLRKLLTGE 172
DB 144 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAMATTLRKLLTGE 195

RESULT 10

Q38212 PRELIMINARY; PRT; 225 AA.

AC Q38212;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Bacteriophage ϕ -R208 ampicillinase gene mutation. (Fragment).
OS Bacteriophage ϕ 1.
OC Viruses; ssDNA viruses; Inoviridae; Inovirus.
OX NCBI_TaxID=10863;

RA SEQUENCE FROM N.A.
RX MEDLINE=86278026; PubMed=3525535;
RA Topal M.D., Badle J.S., Conrad M.,
RT "O-6-methylguanine mutation and repair is nonuniform: Selection for
RT DNA most interactive with O-6-methylguanine.";
RL J. Biol. Chem. 261:9879-9885(1986).
DR EMBL; M14017; AAA32208.1; -.
DR HSSP; Q9R435; IHTZ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1
SQ SEQUENCE 225 AA; 25022 MW; 009BF841D618BA09 CRC64;

Query Match 99.4%; Score 880; DB 2; Length 225;
Best Local Similarity 98.8%; Pred. No. 9.6e-69;
Matches 170; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGRVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
DB HPEITLVKVKADBDQAGRVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
QY 61 AGQELGRRIRHSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANILLTTIGCP 120
DB 84 AGQELGRRIRHSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANILLTTIGCP 143
QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAMATTLRKLLTGE 172
DB 144 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAMATTLRKLLTGE 195

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RESULT 11
Q6PRU7 PRELIMINARY; PRT; 232 AA.
AC Q6PRU7;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Inhibitor-resistant TEM beta-lactamase (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=03;
RA Ghandili S., Hossaini-Mazinani S.M.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY583761; NAS86427.1; -.
DR HSSP; P00807; IALO.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1
FT NON_TER 232
SQ SEQUENCE 232 AA; 25558 MW; 5791CD285E70B80 CRC64;

Query Match 99.4%; Score 880; DB 2; Length 232;
Best Local Similarity 98.8%; Pred. No. 1e-68;
Matches 170; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGRVGYIELDINSKILSFSPERFPMMSTFKVLLCGAVLSRID 60
DB 15 HPEITLVKVDADQAGRVGYIELDINSKILSFSPERFPMMSTFKVLLCGAVLSRYD 74
QY 61 AGQEQIGRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTANILLTTIGSP 120
DB 75 AGQEQIGRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTANILLTTIGSP 134
QY 121 KELITAFIHNMGDHYTRLDRWEPPELNEAIPNDRDITMPVAMATTLKLTGE 172
DB 135 KELITAFIHNMGDHYTRLDRWEPPELNEAIPNDRDITMPVAMATTLKLTGE 186

RESULT 12
Q84H50 PRELIMINARY; PRT; 255 AA.
AC Q84H50;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE TEM-117 beta-lactamase (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RA Box A.T.A., Pauw A., Leverstein-vanHall M.A.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY130282; AAN05026.1; -.
DR HSSP; Q9R435; IHTZ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PR00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1
FT NON_TER 255
SQ SEQUENCE 255 AA; 27906 MW; DCBB28B5978C3A6 CRC64;
```

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Query Match 99.4%; Score 880; DB 2; Length 255;
Best Local Similarity 98.8%; Pred. No. 1e-68;
Matches 170; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGRVGYIELDINSKILSFSPERFPMMSTFKVLLCGAVLSRID 60
DB 12 HPEITLVKVDADQAGRVGYIELDINSKILSFSPERFPMMSTFKVLLCGAVLSRYD 71
QY 61 AGQEQIGRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTANILLTTIGSP 120
DB 72 AGQEQIGRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTANILLTTIGSP 131
QY 121 KELITAFIHNMGDHYTRLDRWEPPELNEAIPNDRDITMPVAMATTLKLTGE 172
DB 132 KELITAFIHNMGDHYTRLDRWEPPELNEAIPNDRDITMPVAMATTLKLTGE 183

RESULT 13
Q84H49 PRELIMINARY; PRT; 261 AA.
AC Q84H49;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE TEM-110 beta-lactamase (Fragment).
OS Klebsiella oxytoca.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=571;
RN [1]
RP SEQUENCE FROM N.A.
RA Box A.T.A., Pauw A., Leverstein-vanHall M.A., Verhoef J., Fluit A.C.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY130283; AAN05027.1; -.
DR HSSP; Q9R435; IHTZ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PR00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1
FT NON_TER 261
SQ SEQUENCE 261 AA; 28738 MW; 4F748F733A08CB8 CRC64;

Query Match 99.4%; Score 880; DB 2; Length 261;
Best Local Similarity 98.8%; Pred. No. 1e-68;
Matches 170; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGRVGYIELDINSKILSFSPERFPMMSTFKVLLCGAVLSRID 60
DB 12 HPEITLVKVDADQAGRVGYIELDINSKILSFSPERFPMMSTFKVLLCGAVLSRYD 71
QY 61 AGQEQIGRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTANILLTTIGSP 120
DB 72 AGQEQIGRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTANILLTTIGSP 131
QY 121 KELITAFIHNMGDHYTRLDRWEPPELNEAIPNDRDITMPVAMATTLKLTGE 172
DB 132 KELITAFIHNMGDHYTRLDRWEPPELNEAIPNDRDITMPVAMATTLKLTGE 183

RESULT 14
Q6PRU6 PRELIMINARY; PRT; 264 AA.
AC Q6PRU6;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE TEM beta-lactamase (Fragment).
OS Acinetobacter sp. U11.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=269266;
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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=U11;
RA Chanditi S., Hosseini-Mazinani S.M.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY563762; AAS6428.1; -.
DR HSSP; P00807; IALQ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1
SQ SEQUENCE 264 AA; 264 264
      264 MM; AAF071CF7489352C CRC64;

Query Match      99.4%; Score 880; DB 2; Length 264;
Best Local Similarity 98.8%; Pred. No. 1.2e-68;
Matches 170; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HPETLVKVDADQLGARVGYELDLSNGKILSFRRPRPPMSTFKYLICGAVLSRID 60
DB 12 HPETLVKVDADQLGARVGYELDLSNGKILSFRRPRPPMSTFKYLICGAVLSRVD 71

OY 61 AGQQLGRRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATWSDNTPANILLTTIGSP 120
DB 72 AGQQLGRRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATWSDNTPANILLTTIGSP 131

OY 121 KETLTFILNMGDHVTIRLDREWEPELNEAIPNDERDTTPMAVAATTLTKLTGE 172
DB 132 KETLTFILNMGDHVTIRLDREWEPELNEAIPNDERDTTPMAVAATTLTKLTGE 183

RESULT 15
OQOIV0 PRELIMINARY; PRT; 281 AA.
AC Q6QIV0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE TEM-1 beta-lactamase (Fragment).
GN Name=blatEM-1;
OS Serratia marcescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ES-42, ES-46, ES-71, and ES-11;
RA Yatsuyanagi J., Saito S., Harata S., Suzuki N., Amano K.-I.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY538700; AAS46846.1; -.
DR EMBL; AY538701; AAS46847.1; -.
DR EMBL; AY538702; AAS46848.1; -.
DR EMBL; AY538698; AAS46844.1; -.
DR HSSP; P00807; IALQ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 281
SQ SEQUENCE 281 AA; 30837 MW; C8934B9C696057BF CRC64;

Query Match      99.4%; Score 880; DB 2; Length 281;
Best Local Similarity 98.8%; Pred. No. 1.3e-68;
Matches 170; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HPETLVKVDADQLGARVGYELDLSNGKILSFRRPRPPMSTFKYLICGAVLSRID 60
DB 24 HPETLVKVDADQLGARVGYELDLSNGKILSFRRPRPPMSTFKYLICGAVLSRVD 83

OY 61 AGQQLGRRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATWSDNTPANILLTTIGSP 120
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DB 84 AGQQLGRRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATWSDNTPANILLTTIGSP 143
OY 121 KETLTFILNMGDHVTIRLDREWEPELNEAIPNDERDTTPMAVAATTLTKLTGE 172
DB 144 KETLTFILNMGDHVTIRLDREWEPELNEAIPNDERDTTPMAVAATTLTKLTGE 195
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Search completed: June 10, 2005, 10:57:02
Job time : 58.6231 secs

XX (PANO-) PANORAMA RES INC.
PA

XX Balint RF, Her J;
PI

XX WPI: 2001-451857/48.
DR

XX N-PSDB; AAD10411.
XX

PT Interaction-dependent enzyme association systems for detecting
PT interactions between two or three polypeptides, especially in human
PT therapeutics, diagnostics or prognostics, comprise circularly permuted
PT proteins.

PS Claim 38; Fig 2; 104dp; English.

XX The invention relates to new interaction-dependent enzyme association
CC (IdRA) systems that comprise a fusion sequence that encodes for a
CC circularly permuted, interaction-activated proteins that reassemble to
CC form functionally reconstituted marker proteins which produce a
CC detectable signal upon the association of two oligopeptides, or upon
CC simultaneous association of two oligopeptides with a third oligopeptide.
CC The marker protein is preferably a type A beta-lactamase, especially TEM-
CC 1 beta-lactamase of *Escherichia coli*. The oligopeptide is a member of a
CC proteome library selected from single chain antibody Fv fragment library,
CC an antibody light chain variable region library and a peptide library
CC displayed within thioredoxin. The IdRA systems are useful for detecting
CC and identifying interactions between intracellular as well as
CC extracellular proteins, particularly between two or three polypeptides.
CC The systems are also useful in selecting with a single marker protein the
CC incorporation of multiple genetic traits in a host cell. In particular,
CC the systems are useful in many applications in human therapeutics,
CC diagnostics and prognostics, as well as in high-throughput screening
CC systems for the discovery and validation of pharmaceutical targets and
CC drugs. Prior systems (e.g. E. coli Dimer Detection System, yeast two-
CC hybrid system or Selective Infective Phage System) require multiple steps
CC between interaction and phenotype, which cause severe loss of efficiency
CC due to high false positive and false negative rates. The present system
CC is capable of simultaneous detection of multiple interactions between
CC extra-cellular as well as intracellular proteins in a high throughput
CC format. The circularly permuted marker proteins comprising interaction-
CC dependent enzymes find use in cell-based sensors for activation or
CC inhibition of metabolic or signal transduction pathways, in high-
CC throughput mapping of pair-wise protein-protein interactions within and
CC between the proteomes of cells, tissues and pathogenic organisms, and in
CC cell-based screens for high-throughput selection of inhibitors of any
CC protein-protein interaction. The present sequence is *Escherichia coli*
CC mature TEM-1 beta-lactamase enzyme from plasmid pBR322. TEM-1 beta-
CC lactamase is a product of ampicillin resistance gene. The enzyme has two
CC domains, alpha-omega and mu
CC
XX

SQ Sequence 263 AA;

Query Match 100.0%; Score 925; DB 4; Length 263;

Best Local Similarity 100.0%; Pred. No. 2.9e-94;

Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGAVGYIELDLSGKILESFRPERFPMWSTFKVLLCGAVLSRID 60
DB 1 HPEITLVKVDADQAGAVGYIELDLSGKILESFRPERFPMWSTFKVLLCGAVLSRID 60
QY 61 AGQEQLGRRIRHSQNDLVEYSPVTEKHLLTDGTVRELCSAAITMSDNTAANILLTTIGGP 120
DB 61 AGQEQLGRRIRHSQNDLVEYSPVTEKHLLTDGTVRELCSAAITMSDNTAANILLTTIGGP 120
QY 121 KETLAFINMGDGHVRLDRWPELNEALPNDERDTTTPVAAATTIRKLLTGELLTLASRQ 180
DB 121 KETLAFINMGDGHVRLDRWPELNEALPNDERDTTTPVAAATTIRKLLTGELLTLASRQ 180
QY 181 Q 181
DB 181 Q 181

RESULT 2

AAB36692
ID AAB36692 standard; protein; 263 AA.

XX AAB36692;

XX 15-MAR-2001 (first entry)

XX *Escherichia coli* mature TEM-1 beta-lactamase protein sequence.

XX Interaction-activated protein; beta-lactamase; protein interaction.

XX *Escherichia coli*.

XX WO200071702-A1.

XX 30-NOV-2000.

XX 16-MAR-2000; 2000WO-US007108.

XX 25-MAY-1999; 99US-0135926P.

XX 13-JAN-2000; 2000US-0175968P.

XX (PANO-) PANORAMA RES INC.

XX Balint RF, Her J;

XX WPI: 2001-032034/04.

XX N-PSDB; AAC90773.

PT Novel fragment complementation system to identify interactions between
PT polypeptides comprises fragment pairs having first and second members
PT that reassemble into a marker protein which has a directly detectable
PT signal.

PS Disclosure; Fig 2; 94dp; English.

XX The present invention describes a fragment complementation system (I)
XX which comprises a first oligopeptide (OP1) containing an N-terminal
XX fragment with a C-terminal break point and a second oligopeptide (OP2)
XX comprising a C-terminal with a N-terminal breakpoint, in which the C and
XX N terminal fragments are both derived from a marker protein (MP) and
XX reassemble to form a functionally reconstituted MP. Methods from the
XX present invention are used for monitoring the occurrence of protein-
XX protein interactions in a sample, identifying oligopeptide interactions
XX between two different proteomes, identifying epitopes that bind to an
XX immunoglobulin (Ig) variable region, for identifying interactions between
XX an extracellular domain of a transmembrane protein and a polypeptide, for
XX high-throughput identification of compounds that inhibit phosphorylation-
XX regulated signal transducers, forming a enzyme complementation system for
XX selecting simultaneous incorporation of multiple genetic elements into a
XX host cell and for activating a beta-lactam derivative of an antitumour
XX compound in a host who is in need of it. The present sequence represents
XX the *Escherichia coli* mature TEM-1 beta-lactamase, which is used in the
XX exemplification of the present invention

SQ Sequence 263 AA;

Query Match 100.0%; Score 925; DB 4; Length 263;

Best Local Similarity 100.0%; Pred. No. 2.9e-94;

Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGAVGYIELDLSGKILESFRPERFPMWSTFKVLLCGAVLSRID 60
DB 1 HPEITLVKVDADQAGAVGYIELDLSGKILESFRPERFPMWSTFKVLLCGAVLSRID 60
QY 61 AGQEQLGRRIRHSQNDLVEYSPVTEKHLLTDGTVRELCSAAITMSDNTAANILLTTIGGP 120
DB 61 AGQEQLGRRIRHSQNDLVEYSPVTEKHLLTDGTVRELCSAAITMSDNTAANILLTTIGGP 120
QY 121 KETLAFINMGDGHVRLDRWPELNEALPNDERDTTTPVAAATTIRKLLTGELLTLASRQ 180
DB 121 KETLAFINMGDGHVRLDRWPELNEALPNDERDTTTPVAAATTIRKLLTGELLTLASRQ 180

QY 181 Q 181
DB 181 Q 181

RESULT 3

ADJ67709
ID ADJ67709 standard; protein; 263 AA.

XX ADJ67709;

XX 20-MAY-2004 (first entry)

DE Escherichia coli TBM-1 beta-lactamase.

XX fragment complementation system; marker protein;
XX multiple genetic element incorporation; antibiotic resistance;
XX beta-lactam derivative activation; anti-tumour compound;
XX functional reassembly; protein-protein interaction; proteome interaction;
XX immunoglobulin variable region; immune cell protein; CD40;
XX phosphorylation-regulated cell signal transducer; TBM-1 beta-lactamase;
XX enzyme.

OS Escherichia coli.

PN US2004038317-A1.

XX 26-FEB-2004.

PF 22-SEP-2003; 2003US-00668778.

XX 15-MAR-1999; 99US-0124339P.

PR 25-MAY-1999; 99US-0135926P.

PR 13-JAN-2000; 2000US-0175968P.

PR 15-MAR-2000; 2000US-00526106.

XX (KALO-) KALOBIOUS INC.

PI Balint RF, Her J;

XX WPI; 2004-203222/19.

DR N-PSDB; ADJ67708.

XX Fragment complementation system for detecting immunoglobulin epitope, has
XX first oligopeptide containing N-terminal fragment with C-terminal break-
XX point, second oligopeptide containing C-terminal fragment with N-terminal
XX break-point.

PS Disclosure; SEQ ID NO 2; 47pp; English.

XX The invention describes a fragment complementation system (I) comprising
XX a first oligopeptide having an N-terminal fragment with a C-terminal
XX break-point, and a second oligopeptide having a C-terminal fragment with
XX a N-terminal break-point, where the N-terminal fragment and the C-
XX terminal fragment each are derived from a marker protein and reassemble
XX to form a functionally reconstituted marker protein. (I) is useful for
XX selecting simultaneous incorporation of multiple genetic elements into a
XX host cell, and activating a beta-lactam derivative of an anti-tumour
XX compound in a host. The method described is useful for identifying a
XX second oligopeptide to which a first oligopeptide binds, involving co-
XX expressing the first and second oligopeptides. Binding of the first
XX oligopeptide to the second oligopeptide results in the functional
XX reassembly of the marker protein. The method is also useful for
XX monitoring the occurrence of protein-protein interactions in a sample;
XX identifying oligopeptide interactions between two different proteomes;
XX and identifying epitopes that bind to an immunoglobulin variable region.
XX (I) or an expression cassette (II), encoding a selectable N or C-terminal
XX peptide, is useful for identifying interactions between an extra cellular
XX domain of a transmembrane protein and a polypeptide, where the
XX transmembrane protein is an immune cell protein, preferably CD40. (I) or
XX (II) is useful for high-throughput identification of compound that
XX inhibit phosphorylation-regulated cell signal transducers. (I)

CC efficiently detects multiple interaction between extracellular and
CC intracellular protein with high throughput format. This is the amino acid
CC sequence of antibiotic resistance enzyme TBM-1 beta-lactamase that can be
CC used as a selectable gene in the fragment complementation system of the
CC invention.

XX SQ Sequence 263 AA;

Query Match 100.0%; Score 925; DB 8; Length 263;
Best Local Similarity 100.0%; Pred. No. 2.9e-94;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPETLVKVDADPDQARVGYIELDINSKILSPFPERFPFMSTFKYLICGAVLSRID 60
DB 1 HPETLVKVDADPDQARVGYIELDINSKILSPFPERFPFMSTFKYLICGAVLSRID 60

QY 61 AGQEQLGRRIHYSQNDLVESPTVEKHITDGMTVRELCSAATMSDNTANLLITIGGP 120
DB 61 AGQEQLGRRIHYSQNDLVESPTVEKHITDGMTVRELCSAATMSDNTANLLITIGGP 120

QY 121 KETLAFIHMGGHVRRLDPWEPELNEAIPNDRDPTTPVAMATTAKLTGELTLASRO 180
DB 121 KETLAFIHMGGHVRRLDPWEPELNEAIPNDRDPTTPVAMATTAKLTGELTLASRO 180

QY 181 Q 181
DB 181 Q 181

RESULT 4
AAW16634
ID AAW16634 standard; protein; 264 AA.

XX AAW16634;

AC 09-AUG-1997 (first entry)

XX 09-AUG-1997 (first entry)

XX Beta-lactamase (including signal peptide).

XX Gene directed enzyme prodng therapy; GDEPT;

XX HIV; inflammation.

XX Escherichia coli.

XX Key Location/Qualifiers

XX Peptide 1..23

XX /label= Sig_peptide

XX MO9719180-A2.

XX 29-MAY-1997.

XX 19-NOV-1996; 96WO-GB002845.

XX 20-NOV-1995; 95GB-00023703.

XX (GLAXO) GLAXO GROUP LTD.

XX Dev I, Moore JT, Ohmstede C;

XX WPI, 1997-298117/27.

XX N-PSDB; AAT66736.

XX Molecular chimera for gene or virus directed enzyme prodng therapy -

XX useful for treatment of cancer, viral infection or inflammation.

XX Example; Page 28; 38pp; English.

XX Escherichia coli beta-lactamase (AAW16634), including the signal peptide,

XX is the expression product of a molecular chimera, designated pCMV-BL

XX (AAT66737), in which the beta-lactamase gene is under control of the CMV

XX intermediate/early promoter. Vectors consisting of a transcriptional

CC regulatory DNA sequence linked to a beta-lactamase gene can be used for
 CC enzyme prodnug therapy. Expression of the beta-lactamase in a targeted
 CC cell allows conversion of a prodnug into an agent toxic to the cell for
 CC treatment of cancer, viral (e.g. HIV) infection or inflammation.
 CC Secretion of the enzyme has the advantage of increasing neighbouring cell
 CC kill

XX Sequence 264 AA;

Query Match 100.0%; Score 925; DB 2; Length 264;

Best Local Similarity 100.0%; Pred. No. 2.9e-94;

Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGIETLDNSGKILSPRPFRPFPMSTFKVLLCGAVLSRID 60
 DB 2 HPEITLVKVDADQAGARVGIETLDNSGKILSPRPFRPFPMSTFKVLLCGAVLSRID 61
 QY 61 AGOEOLGRIRIHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGSP 120
 DB 62 AGOEOLGRIRIHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGSP 121
 QY 121 KELTSFLHMGDHTRLDRWPELNEALPNDERDTTTPVAMATTIRKLLTGELTLASRQ 180
 DB 122 KELTSFLHMGDHTRLDRWPELNEALPNDERDTTTPVAMATTIRKLLTGELTLASRQ 181
 QY 181 Q 181
 DB 182 Q 182

RESULT 5

AAW18680
 ID AAW18680 standard; protein; 264 AA.

AC AAW18680;

DT 13-AUG-1997 (first entry)

DE Intracellularly-expressed beta-lactamase.

KM Prodnug therapy; gene directed enzyme prodnug therapy; GDEPT;

KW virus directed enzyme prodnug therapy; VDEPT; lung cancer;

KM beta-lactamase; PCMV-delBL.

OS Escherichia coli.

PN W09719183-A2.

PD 29-MAY-1997.

PF 19-NOV-1996; 96WO-GB002846.

PR 20-NOV-1995; 95GB-00023703.

PA (GLAX) GLAXO GROUP LTD.

PI Dev I, Moore JT, Sethna PB;

PT WPI; 1997-298118/27.

DR N-PSDB; AAT70311.

XX DNA construct for gene-directed enzyme prodnug therapy of lung cancer -

XX comprises lung- or neuroendocrine-specific promoter controlling

XX expression of prodnug-converting enzyme.

XX Example 8iii; Page 32-34; 53pp; English.

CC The intracellular form (AAW18680) of TEM beta-lactamase is expressed by
 CC PCMV-delBL (AAT70311) in which a PCR-amplified beta-lactamase coding
 CC sequence, minus the signal sequence, is placed under control of the
 CC intermediate/early promoter of cytomegalovirus. Intracellular beta-
 CC lactamase constructs, placed under control of promoter/enhancer elements
 CC of lung-associated protein or neuroendocrine marker protein genes, can be

CC used in novel chimaeric molecules for use in prodnug therapy of lung
 CC cancer

XX Sequence 264 AA;

Query Match 100.0%; Score 925; DB 2; Length 264;

Best Local Similarity 100.0%; Pred. No. 2.9e-94;

Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGIETLDNSGKILSPRPFRPFPMSTFKVLLCGAVLSRID 60
 DB 2 HPEITLVKVDADQAGARVGIETLDNSGKILSPRPFRPFPMSTFKVLLCGAVLSRID 61
 QY 61 AGOEOLGRIRIHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGSP 120
 DB 62 AGOEOLGRIRIHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGSP 121
 QY 121 KELTSFLHMGDHTRLDRWPELNEALPNDERDTTTPVAMATTIRKLLTGELTLASRQ 180
 DB 122 KELTSFLHMGDHTRLDRWPELNEALPNDERDTTTPVAMATTIRKLLTGELTLASRQ 181
 QY 181 Q 181
 DB 182 Q 182

RESULT 6

AAR31575
 ID AAR31575 standard; protein; 286 AA.

AC AAR31575;

DT 10-MAR-2003 (revised)

DT 04-JUN-1993 (first entry)

DE Ampicillin resistance protein.

KW CYP1A1; PRNH127; PRNH155; xeroderma pigmentosum group A; XPA;

KW xenobiotics; circular; chimeric cytochrome P450IA1.

OS Homo sapiens.

PN US5180666-A.

PD 19-JAN-1993.

PF 27-JUN-1991; 91US-00721775.

PR 27-JUN-1991; 91US-00721775.

PA (UYWA-) UNIV WAYNE STATE.

PI States JC, Hines RN, Novak RF;

PT WPI; 1993-052845/06.

DR N-PSDB; AAQ36498.

XX In vitro method for testing mutagenicity of a chemical - by metabolising

XX PT chemical cell line consisting of transformed fibroblasts having

XX PT detectable cytochrome P450 mixed function oxidase activity and detecting

XX PT gene damage.

XX Disclosure; Col 21-24; 24pp; English.

CC The expression constructs PRNH127 and PRNH155 contain identical sequences

CC but were constructed using different strategies (see AAQ36498). The

CC constructs comprise exons 2-7 of human CYP1A1 gene under the control of

CC the inducible mouse metallothionein (MWT-1) promoter. The constructs also

CC contain an open reading frame in the opposite orientation to the

CC cytochrome P450 exons. This ORF encodes ampicillin resistance. The

CC constructs are suitable for transformation of human fibroblasts derived

CC from the xeroderma pigmentosum group A. Cultures of the transformed

CC fibroblasts can be used to test substances for mutagenicity. The presence

CC of the inducible cytochrome P450 gene allows metabolism of the substance
CC to mutagenic metabolites. (Updated on 10-MAR-2003 to add missing OS
CC field.)
XX

Sequence 286 AA;

Query Match 100.0%; Score 925; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.3e-94;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGYIELDINSKILSFPRPERFPMSTFKVLLCGAVISRID 60
DB 24 HPEITLVKVDADQAGARVGYIELDINSKILSFPRPERFPMSTFKVLLCGAVISRID 83
QY 61 ACOEOLGRRIHYSQNDLVEYSPYTEKHLTDGKTVRELCSAATMSDNTAANLLTTIGSP 120
DB 84 ACOEOLGRRIHYSQNDLVEYSPYTEKHLTDGKTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFIHNMGDHYRLDWEPELNEAIPNDRDITMPVAMATTLLKLTGELLTLASRQ 180
DB 144 KELTAFIHNMGDHYRLDWEPELNEAIPNDRDITMPVAMATTLLKLTGELLTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 7

AAR97619
ID AAR97619 standard; protein; 286 AA.

AC AAR97619;

DT 20-AUG-1996 (first entry)

DE Secretory beta-lactamase.

KM Gene therapy; gene directed enzyme prodng therapy; GDEPT;

KM virus directed enzyme prodng therapy; VDEPT; prodng activation;

KM cytotoxic; cytostatic; cancer; tumour; retrovirus; vector;

KM beta-lactamase; cephalosporin.

OS Synthetic.

PN MO9616179-A1.

PD 30-MAY-1996.

PF 20-NOV-1995; 95WO-GB002716.

PR 18-NOV-1994; 94GB-00023367.

PA (WELL) WELLCOME FOUND LTD.

PI Dev IK, Moore JT, Ohmstede C;

DR WPI; 1996-268615/27.

DR N-PSDB; AAT929220.

XX Molecular chimera for use in enzyme gene therapy - is activated in a

XX target cell to express a secretible enzyme which cleaves a prodng

XX outside the cell into a cytotoxic or cytostatic agent.

XX Example 3; Page 57-58; 73pp; English.

XX A secretory beta-lactamase (AAR97619) is expressed from DNA construct

XX PCMW-BL (AAT929220), in which the beta-lactamase coding sequence is under

XX the control of the intermediate/early cytomegalovirus promoter. Beta-

XX lacamase delivery to mammalian cells confers sensitivity to

XX cephalosporin prodngs. Liposomal DNA/5-fluorouracil prodng combinations

XX resulted in 8.c. tumour regression in mice bearing A549 tumours. Survival

XX of mice bearing human large cell lung H460 intrathoracic (i.t.) tumours

XX was increased upon i.t. injection of the secretory beta-lactamase DNA

CC construct
XX
SQ Sequence 286 AA;

Query Match 100.0%; Score 925; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.3e-94;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGYIELDINSKILSFPRPERFPMSTFKVLLCGAVISRID 60
DB 24 HPEITLVKVDADQAGARVGYIELDINSKILSFPRPERFPMSTFKVLLCGAVISRID 83
QY 61 ACOEOLGRRIHYSQNDLVEYSPYTEKHLTDGKTVRELCSAATMSDNTAANLLTTIGSP 120
DB 84 ACOEOLGRRIHYSQNDLVEYSPYTEKHLTDGKTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFIHNMGDHYRLDWEPELNEAIPNDRDITMPVAMATTLLKLTGELLTLASRQ 180
DB 144 KELTAFIHNMGDHYRLDWEPELNEAIPNDRDITMPVAMATTLLKLTGELLTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 8

AAR96423
ID AAR96423 standard; protein; 286 AA.

AC AAR96423;

DT 25-MAR-2003 (revised)

DT 25-NOV-1996 (first entry)

DE Cytochrome P450 (CYP1A1 construct).

KM cytochrome; P450; metallothionein; mouse; human; cytotoxicity; assay;

KM metabolism.

OS Homo sapiens.

PN US5525482-A.

PD 11-JUN-1996.

PF 15-NOV-1994; 94US-00339658.

PR 27-JUN-1991; 91US-00721775.

PR 09-DEC-1992; 92US-00990295.

PA (UTWA-) UNIT WAYNE STATE.

PI Hines RN, Novak RF, States JC;

DR WPI; 1996-286397/29.

DR N-PSDB; AAT30354.

XX Testing chemicals for cytotoxicity to human by detecting gene damage -

XX using recombinant fibroblasts transformed with cytochrome P450 gene under

XX control of inducible promoter.

XX Disclosure; Col 17-24; 26pp; English.

XX The present sequence is encoded by a chimeric mouse metallothionein-

XX cytochrome P450IAl (CYP1A1) expression construct. Two clones, pRNH127 and

XX pRNH15, were isolated by different methods and which both had the same

XX sequence. The CYP1A1 construct is used in assays to test for cytotoxicity

XX of humans to a chemical. The method comprises exposing human fibroblast

XX cells normally not including any cytochrome P450 activity to potentially

XX toxic chemicals. The cells having been transformed to express cytochrome

XX P450, under the control of a controllable promoter through the CYP1A1

XX gene, upon exposure to the chemical in vitro. The chemical is metabolised

XX intracellularly into a cytochrome metabolite by oxidation within the

CC fibroblasts through the intracellular cytochrome P450 mixed function
CC oxidase enzymes expressed by the cells. Gene damage in the test cells is
CC detected as an indication of cytotoxicity of the chemical. (Updated on 25
CC -MAR-2003 to correct PF field.)

XX Sequence 286 AA;

Query Match 100.0%; Score 925; DB 2; Length 286;

Best Local Similarity 100.0%; Pred. No. 3.3e-94;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVAADQAGARVGYIELDLSGKILSPREPERFPMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKVAADQAGARVGYIELDLSGKILSPREPERFPMSTFKVLLCGAVLSRID 83
QY 61 AGQEQIGRRIRHSQNDLVEYSPVTEKHLTDGMYRELCSAATWSDNTAANLLTTIGSP 120
DB 84 AGQEQIGRRIRHSQNDLVEYSPVTEKHLTDGMYRELCSAATWSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRWEPDELNEAIPNDRDITMPVAAATTLRKLLTGBLLTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWEPDELNEAIPNDRDITMPVAAATTLRKLLTGBLLTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 9

AAW16635
ID AAW16635 standard; protein; 286 AA.

AC AAW16635;

DT 09-AUG-1997 (first entry)

DE Beta-lactamase (no signal peptide).

XX Gene directed enzyme prodng therapy; GDEPT;
KM virus directed enzyme prodng therapy; VDEPT; beta-lactamase; cancer;
KW HIV; inflammation.

OS Escherichia coli.

PN WO9719180-A2.

PD 29-MAY-1997.

PF 19-NOV-1996; 96WO-GB002845.

PR 20-NOV-1995; 95GB-00023703.

PA (GLAXO) GLAXO GROUP LTD.

PI Dev I, Moore JT, Ohmstede C;

DR MPI: 1997-298117/27.

DR N-PSDB; AAT66737.

PT Molecular chimaera for gene or virus directed enzyme prodng therapy -
PT useful for treatment of cancer, viral infection or inflammation.

XX Example; Page 26; 38pp; English.

CC Escherichia coli beta-lactamase (AAW16635), lacking the signal peptide,
CC is the expression product of a molecular chimaera, designated PCMV-delta
CC (AAT66738), in which the beta-lactamase gene is under control of the CMV
CC intermediate/early promoter. Vectors consisting of a transcriptional
CC regulatory DNA sequence linked to a beta-lactamase gene can be used for
CC enzyme prodng therapy. Intracellular expression of the beta-lactamase in
CC a targeted cell allows conversion of a prodng into an agent toxic to
CC the cell for treatment of cancer, viral (e.g. HIV) infection or
CC inflammation

XX Sequence 286 AA;

Query Match 100.0%; Score 925; DB 2; Length 286;

Best Local Similarity 100.0%; Pred. No. 3.3e-94;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVAADQAGARVGYIELDLSGKILSPREPERFPMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKVAADQAGARVGYIELDLSGKILSPREPERFPMSTFKVLLCGAVLSRID 83
QY 61 AGQEQIGRRIRHSQNDLVEYSPVTEKHLTDGMYRELCSAATWSDNTAANLLTTIGSP 120
DB 84 AGQEQIGRRIRHSQNDLVEYSPVTEKHLTDGMYRELCSAATWSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRWEPDELNEAIPNDRDITMPVAAATTLRKLLTGBLLTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWEPDELNEAIPNDRDITMPVAAATTLRKLLTGBLLTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 10

AAW18679
ID AAW18679 standard; protein; 286 AA.

AC AAW18679;

DT 13-AUG-1997 (first entry)

DE Secretory beta-lactamase.

XX Prodng therapy; gene directed enzyme prodng therapy; GDEPT;
KM virus directed enzyme prodng therapy; VDEPT; lung cancer;
KW beta-lactamase; PCMV-BL.

OS Escherichia coli.

PN WO9719183-A2.

PD 29-MAY-1997.

PF 19-NOV-1996; 96WO-GB002846.

PR 20-NOV-1995; 95GB-00023703.

PA (GLAXO) GLAXO GROUP LTD.

PI Dev I, Moore JT, Sethna PB;

DR MPI: 1997-298118/27.

DR N-PSDB; AAT70309.

PT DNA construct for gene-directed enzyme prodng therapy of lung cancer -
PT comprises lung- or neuroendocrine-specific promoter controlling
PT expression of prodng-converting enzyme.

XX Example 81; Page 26-27; 53pp; English.

CC The secreted form (AAW18679) of TBM beta-lactamase is expressed by PCMV-
CC BL (AAT70309) in which a PCR-amplified beta-lactamase coding sequence is
CC placed under control of the intermediate/early promoter of
CC cytomegalovirus. Secretory beta-lactamase constructs, placed under
CC control of promoter/enhancer elements of lung-associated protein or
CC neuroendocrine marker protein genes, can be used in novel chimeric

CC molecules for use in prodrg therapy of lung cancer
XX
SQ Sequence 286 AA;

Query Match 100.0%; Score 925; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.3e-94;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQIGARVGYIELDNGSKILSPRPFRPMMSTFKYLGGAVLSRID 60
DB 24 HPEITLVKVDADQIGARVGYIELDNGSKILSPRPFRPMMSTFKYLGGAVLSRID 83
QY 61 AGQEQGRRIHYSQNDLVEYSPTVEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQEQGRRIHYSQNDLVEYSPTVEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDPTTVPVAAATTIRKLLTGELTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDPTTVPVAAATTIRKLLTGELTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 11

AA08529
ID AA08529 standard; protein; 286 AA.

XX
AC AAY08529;

DT 03-AUG-1999 (first entry)

DE Vector pASK75 beta-la protein.

XX
XX Firefly; luciferase; tetracycline; transcriptional control; Tetr; TetA;
KW tetracycline repressor; tetracycline promoter; luminescence; luxCDABE;
KW insect; Tn10; medicine; dosage; cheese production; antibiotic; foodstuff;
KW allergy.

XX
OS Synthetic.

XX
PN MO9925866-A1.

XX
PD 27-MAY-1999.

XX
PF 11-NOV-1998; 98WO-FI000873.

XX
PR 14-NOV-1997; 97FI-00004235.

XX
PA (KORP/) Korpela M.

XX
PA (KARP/) Karp M.

XX
PA (KURITU/) Kurittu J.

XX
PI Korpela M, Karp M, Kurittu J;

XX
DR WPI; 1999-338015/28.

XX
DR N-PSDB; AAV72418.

XX
PT Assaying for tetracycline using recombinant prokaryotic cells.

XX
PS Disclosure; Page 47-48; 67pp; English.

XX
CC This invention describes a novel tetracycline assay that uses recombinant
CC prokaryotic cells comprising a luciferase gene under the transcriptional
CC control of a tetracycline repressor and tetracycline promoter and
CC involves the detection of luminescence emitted from the cells. The assay
CC can be used to distinguish tetracycline from other microbial agents. The
CC invention also describes a novel plasmid comprising either the luxCDABE
CC genes, a tetracycline repressor (Tetr) and a tetracycline promoter (TetA)
CC from Tn10, or the insect luciferase gene, a tetracycline repressor (Tetr)
CC and a tetracycline promoter (TetA) from Tn10. The tetracycline assay
CC method can be used for the determination of tetracycline in a sample.

CC e.g. to study the dosage and penetration of the medicine. The method can
CC also be used to test cheese production, as cheese making bacteria are not
CC able to work in the presence of tetracycline. The method can also be used
CC to determine the presence or concentration of antibiotics in foodstuffs,
CC e.g. for allergic people. The present assay method does not rely on the
CC growth of microbes as do conventional tests, and so is much more rapid.
CC The present assay is also more sensitive, as even a small amount of
CC luminescence can be detected

XX
SQ Sequence 286 AA;

Query Match 100.0%; Score 925; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.3e-94;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQIGARVGYIELDNGSKILSPRPFRPMMSTFKYLGGAVLSRID 60
DB 24 HPEITLVKVDADQIGARVGYIELDNGSKILSPRPFRPMMSTFKYLGGAVLSRID 83
QY 61 AGQEQGRRIHYSQNDLVEYSPTVEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQEQGRRIHYSQNDLVEYSPTVEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDPTTVPVAAATTIRKLLTGELTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDPTTVPVAAATTIRKLLTGELTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 12

AAB10442
ID AAB10442 standard; protein; 286 AA.

XX
AC AAB10442;

DT 01-DEC-2000 (first entry)

DE Expression vector pSEX15G2 bla protein.

XX
XX Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
KW B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.

XX
OS Synthetic.

XX
PN DEL1990635-A1.

XX
PD 13-JUL-2000.

XX
PF 11-JAN-1999; 99DE-01000635.

XX
PR 11-JAN-1999; 99DE-01000635.

XX
PA (DEKR-) DEUT KRBSFORSCHUNGSZENTRUM.

XX
PI Breiting F, Poustka A, Moldenhauer G;

XX
DR WPI; 2000-499832/45.

XX
DR N-PSDB; AAA71430.

XX
PT Selecting monoclonal antibodies, by expressing them on the surface of
PT hybridomas attached to antibody-binding protein, then reaction with
PT antibody library.

XX
PS Claim 16; Fig 3; 22pp; German.

XX
CC This invention describes a novel method for the selection of monoclonal
CC antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma
CC cells to produce antibody-producing hybridomas such that the antibodies
CC are presented at the surface of the hybridomas by an antibody-binding
CC protein (I); and (ii) binding the antibody to antigens (Ag). The

invention also describes antibody-binding proteins (I) that comprise a combination of the signal peptide of a murine immunoglobulin (Ig) kappa chain or a murine MHC (major histocompatibility complex) Class I K(K) molecule; an antibody-binding site of proteins A, G, L or Ig, and the transmembrane domain of PDGFR (platelet-derived growth factor receptor) or CD53. The method is used to select Mab with specificity for particular antigens. Mab can be selected without separate culture of hybridomas, and selection can be made against many antigens in a library, optionally on the basis of strength of affinity for a particular antigen. Complex mixtures of hybridomas can be used for selection, reducing the time and cost involved in Mab selection. This sequence represents the bla protein contained in the expression vector pSEX11G2 which contains the bla protein, Neo-R and protein G described in the method of the invention

SQ Sequence 286 AA;

Query Match 100.0%; Score 925; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.3e-94;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVAEDQAGRVGYIELDLSNGKILSFRRPERPMMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKVAEDQAGRVGYIELDLSNGKILSFRRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGOEOLGRRIRHSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTTIGSP 120
DB 84 AGOEOLGRRIRHSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTTIGSP 143
QY 121 KELTAFILNMGDHTVRLDRWPELNEAIPNDRDITVPAVATTIRKLLTGELLTLASRQ 180
DB 144 KELTAFILNMGDHTVRLDRWPELNEAIPNDRDITVPAVATTIRKLLTGELLTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 13

AAB10438

ID AAB10438 standard; protein; 286 AA.

AC AAB10438;

DT 01-DEC-2000 (first entry)

DE Expression vector pSEX11L4 bla protein.

XX Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
KW B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.

OS Synthetic.

PN DE19900635-A1.

PD 13-JUL-2000.

PF 11-JAN-1999; 99DE-01000635.

PR 11-JAN-1999; 99DE-01000635.

PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

PI Breitling F, Poustka A, Moldenhauer G;

DR WPI: 2000-499832/45.

DR N-PSDB; AAA71428.

XX Selecting monoclonal antibodies, by expressing them on the surface of
PT hybridomas attached to antibody-binding protein, then reaction with
PT antibody library.

Claim 16; Fig 1; 22pp; German.

This invention describes a novel method for the selection of monoclonal antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma cells to produce antibody-producing hybridomas such that the antibodies are presented at the surface of the hybridomas by an antibody-binding protein (I); and (ii) binding the antibody to antigens (Ag). The invention also describes antibody-binding proteins (I) that comprise a combination of the signal peptide of a murine immunoglobulin (Ig) kappa chain or a murine MHC (major histocompatibility complex) Class I K(K) molecule; an antibody-binding site of proteins A, G, L or Ig, and the transmembrane domain of PDGFR (platelet-derived growth factor receptor) or CD53. The method is used to select Mab with specificity for particular antigens. Mab can be selected without separate culture of hybridomas, and selection can be made against many antigens in a library, optionally on the basis of strength of affinity for a particular antigen. Complex mixtures of hybridomas can be used for selection, reducing the time and cost involved in Mab selection. This sequence represents the Neo-R protein contained in the expression vector pSEX11L4 which contains the bla protein, Neo-R and protein G described in the method of the invention

SQ Sequence 286 AA;

Query Match 100.0%; Score 925; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.3e-94;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVAEDQAGRVGYIELDLSNGKILSFRRPERPMMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKVAEDQAGRVGYIELDLSNGKILSFRRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGOEOLGRRIRHSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTTIGSP 120
DB 84 AGOEOLGRRIRHSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTTIGSP 143
QY 121 KELTAFILNMGDHTVRLDRWPELNEAIPNDRDITVPAVATTIRKLLTGELLTLASRQ 180
DB 144 KELTAFILNMGDHTVRLDRWPELNEAIPNDRDITVPAVATTIRKLLTGELLTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 14

AAB10440

ID AAB10440 standard; protein; 286 AA.

AC AAB10440;

DT 01-DEC-2000 (first entry)

DE Expression vector pSEX11G2 bla protein.

XX Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
KW B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.

OS Synthetic.

PN DE19900635-A1.

PD 13-JUL-2000.

PF 11-JAN-1999; 99DE-01000635.

PR 11-JAN-1999; 99DE-01000635.

PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

PI Breitling F, Poustka A, Moldenhauer G;

DR WPI: 2000-499832/45.

DR N-PSDB; AAA71429.

XX Selecting monoclonal antibodies, by expressing them on the surface of

hybridomas attached to antibody-binding protein, then reaction with antibody library.

Claim 16; Fig 2; 22pp; German.

This invention describes a novel method for the selection of monoclonal antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma cells to produce antibody-producing hybridomas such that the antibodies are presented at the surface of the hybridomas by an antibody-binding protein (I); and (ii) binding the antibody to antigens (Ag). The invention also describes antibody-binding proteins (I) that comprise a combination of the signal peptide of a murine immunoglobulin (Ig) kappa chain or a murine MHC (major histocompatibility complex) Class I K(k) molecule; an antibody-binding site of proteins A, G, I or Ig, and the transmembrane domain of PDGFR (platelet-derived growth factor receptor) or CD52. The method is used to select Mab with specificity for particular antigens. Mab can be selected without separate culture of hybridomas, and selection can be made against many antigens in a library, optionally on the basis of strength of affinity for a particular antigen. Complex mixtures of hybridomas can be used for selection, reducing the time and cost involved in Mab selection. This sequence represents the bla protein contained in the expression vector pSEK11G2 which contains the bla protein, Neo-R and protein G described in the method of the invention

Sequence 286 AA;

Query Match 100.0%; Score 925; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.3e-94;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVDADSDQAGRVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVDADSDQAGRVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
QY 61 ACOEQLGRRIHYSQNDLVEYSPVTEKHLDGKMTVRELCSAAITMSDNTAANLLTTIGSP 120
DB 84 ACOEQLGRRIHYSQNDLVEYSPVTEKHLDGKMTVRELCSAAITMSDNTAANLLTTIGSP 143
QY 121 KELTAFIHNMGDGHVTRLDRWPELNEAIPNDRDITMPVAMATTLLKLTGELLTASRQ 180
DB 144 KELTAFIHNMGDGHVTRLDRWPELNEAIPNDRDITMPVAMATTLLKLTGELLTASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 15

AAB50898
ID AAB50898 standard; protein; 286 AA.

XX AAB50898;

AC AAB50898;

DE Protein encoded by bla resistance marker of integration vector pLO12306.

XX bla resistance marker; recombinant host cell; saccharification;
KW fermentation; polysaccharase; oligosaccharide degradation; celz gene;
KW glucanase; integration vector; pLO12306.

XX Unidentified.

OS WO200071729-A2.

PD 30-NOV-2000.

PF 26-MAY-2000; 2000MO-US014773.

PR 26-MAY-1999; 99US-0136376P.

PA (UYFL) UNIV FLORIDA RES FOUND.

PI Ingram LO, Zhou S;
XX
DR MPI: 2001-032043/04.
DR N-PSDB; AAC91455.

XX Recombinant host cells useful for producing polysaccharase for degrading
PT oligosaccharides, comprises a first heterologous polynucleotide encoding
PS polysaccharase under control of surrogate promoter.

XX Disclosure; Page 82-83; 87pp; English.

XX The present sequence is given in a specification relating to a
CC recombinant host cell suitable for simultaneous saccharification and
CC fermentation. The host cell contains at least one heterologous
CC polynucleotide encoding a polysaccharase under the transcriptional
CC control of a surrogate promoter capable of increasing expression of the
CC polysaccharase. The host cell also contains a second heterologous
CC polynucleotide encoding a secretory polypeptide to facilitate the
CC secretion of the expressed polysaccharase. The recombinant host cell is
CC useful for producing polysaccharase which is useful for enzymatically
CC degrading oligosaccharides such as lignocellulose, hemicellulose,
CC cellulose, pectin or their combinations, and fermenting the product to
CC ethanol, by simultaneous saccharification and fermentation processes. The
CC present sequence is encoded by an integration vector which was introduced
CC into cells to generate recombinant host cells. The vector contains a
CC surrogate promoter from *Zymomonas mobilis*, the celz gene from *Erwinia*
CC chrysanthemi, resistance markers bla and tet, and *Klebsiella oxytoca*
CC target sequence

Sequence 286 AA;

Query Match 100.0%; Score 925; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.3e-94;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVDADSDQAGRVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVDADSDQAGRVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
QY 61 ACOEQLGRRIHYSQNDLVEYSPVTEKHLDGKMTVRELCSAAITMSDNTAANLLTTIGSP 120
DB 84 ACOEQLGRRIHYSQNDLVEYSPVTEKHLDGKMTVRELCSAAITMSDNTAANLLTTIGSP 143
QY 121 KELTAFIHNMGDGHVTRLDRWPELNEAIPNDRDITMPVAMATTLLKLTGELLTASRQ 180
DB 144 KELTAFIHNMGDGHVTRLDRWPELNEAIPNDRDITMPVAMATTLLKLTGELLTASRQ 203
QY 181 Q 181
DB 204 Q 204

Search completed: June 10, 2005, 10:49:10
Job time : 71.1783 secs

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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:36:31 ; Search time 18.5574 Seconds
(without alignments)
728.091 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_181

Perfect score: 925

Sequence: 1 HPELVKVKADMDQAGRVG.....ATTLRKLTGLTGLTLASRQ 181

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/pdata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/pdata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/pdata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/pdata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/pdata/1/1aa/6CTUS_COMB.pep:*
6: /cgn2_6/pdata/1/1aa/6ackfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	925	100.0	286 1 US-07-721-775A-2	Sequence 2, Appl
2	925	100.0	286 1 US-08-339-658-2	Sequence 2, Appl
3	925	100.0	286 3 US-09-263-933-7	Sequence 7, Appl
4	925	100.0	286 3 US-09-263-933-14	Sequence 14, Appl
5	925	100.0	286 3 US-09-263-933-21	Sequence 21, Appl
6	925	100.0	286 3 US-09-025-769B-265	Sequence 265, App
7	925	100.0	286 4 US-09-025-769B-362	Sequence 362, App
8	925	100.0	286 4 US-09-919-901-7	Sequence 7, Appl
9	925	100.0	286 4 US-09-919-901-14	Sequence 14, Appl
10	925	100.0	286 4 US-09-919-901-21	Sequence 21, Appl
11	925	100.0	286 4 US-09-490-070A-265	Sequence 265, App
12	925	100.0	286 4 US-09-490-070A-362	Sequence 362, App
13	925	100.0	286 4 US-09-490-153-265	Sequence 265, App
14	925	100.0	286 4 US-09-490-153-362	Sequence 362, App
15	925	100.0	286 4 US-10-191-966-7	Sequence 7, Appl
16	925	100.0	286 4 US-10-191-966-14	Sequence 14, Appl
17	925	100.0	286 4 US-10-191-966-21	Sequence 21, Appl
18	925	100.0	286 4 US-09-490-324-265	Sequence 265, App
19	925	100.0	286 4 US-09-490-324-362	Sequence 362, App
20	925	100.0	286 3 US-09-025-769B-285	Sequence 285, App
21	925	100.0	286 3 US-09-025-769B-298	Sequence 298, App
22	925	100.0	286 3 US-09-025-769B-300	Sequence 300, App
23	925	100.0	286 4 US-09-490-070A-285	Sequence 285, App
24	925	100.0	286 4 US-09-490-070A-298	Sequence 298, App
25	925	100.0	286 4 US-09-490-070A-300	Sequence 300, App
26	925	100.0	286 4 US-09-490-153-285	Sequence 285, App
27	925	100.0	286 4 US-09-490-153-298	Sequence 298, App

28	925	100.0	299 4 US-09-490-153-300	Sequence 300, App
29	925	100.0	299 4 US-09-490-324-285	Sequence 285, App
30	925	100.0	299 4 US-09-490-324-298	Sequence 298, App
31	925	100.0	299 4 US-09-490-324-300	Sequence 300, App
32	925	100.0	2307 3 US-09-263-933-2	Sequence 2, Appl
33	925	100.0	2307 3 US-09-263-933-9	Sequence 9, Appl
34	925	100.0	2307 3 US-09-263-933-16	Sequence 16, Appl
35	925	100.0	2307 4 US-09-919-901-2	Sequence 2, Appl
36	925	100.0	2307 4 US-09-919-901-9	Sequence 9, Appl
37	925	100.0	2307 4 US-09-919-901-16	Sequence 16, Appl
38	925	100.0	2307 4 US-10-191-966-2	Sequence 2, Appl
39	925	100.0	2307 4 US-10-191-966-9	Sequence 9, Appl
40	925	100.0	2307 4 US-10-191-966-16	Sequence 16, Appl
41	924	99.9	286 4 US-09-555-510B-9	Sequence 9, Appl
42	924	99.9	286 4 US-10-231-013-9	Sequence 9, Appl
43	924	99.9	1293 4 US-09-170-496D-292	Sequence 292, App
44	924	99.9	1293 4 US-09-364-425B-57	Sequence 57, Appl
45	920	99.5	263 1 US-08-407-544-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-07-721-775A-2
Sequence 2, Application US/07721775A
Patent No. 5180666
GENERAL INFORMATION:
APPLICANT: States, J. Christopher
APPLICANT: Hines, Ronald N.
TITLE OF INVENTION: No. 5180666ak, Raymond F.
TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSER: Relating, Echington, Barnard, Perry & Milton
STREET: P.O. Box 4390
CITY: Troy
STATE: Michigan
COUNTRY: U.S.A.
ZIP: 48099
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07721,775A
FILING DATE: 19910627
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: P-321WSU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 689-3554
TELEFAX: (313) 689-4071
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-721-775A-2

Query Match 100.0%; Score 925; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 4,1e-100;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADMDQAGRVGIEIDLSGKILIESRPPRPPMSTFYLLCGAVLSRID 60
DB 24 HPELVKVKADMDQAGRVGIEIDLSGKILIESRPPRPPMSTFYLLCGAVLSRID 83

QY 61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGVTRELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGVTRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KETLAFILHNMGDHVTRLDRWPELNEAIPNDRDPTTVPVAAATTLRKLLTGELTLASRQ 180
DB 144 KETLAFILHNMGDHVTRLDRWPELNEAIPNDRDPTTVPVAAATTLRKLLTGELTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 2

US-08-339-658-2
Sequence 2, Application US/08339658
Patent No. 5525482
GENERAL INFORMATION:
APPLICANT: States, J. Christopher
APPLICANT: Hines, Ronald N.
APPLICANT: No. 5525482ak, Raymond F.
TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Relising, Ethnington, Barnard, Perry & Milton
STREET: P. O. Box 4390
CITY: Troy
STATE: Michigan
COUNTRY: U.S.A.
ZIP: 48099
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,658
FILING DATE: 15-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,295
FILING DATE: 09-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: P-321WSU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 689-3554
TELEFAX: (313) 689-4071
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-339-658-2

Query Match 100.0%; Score 925; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 4.1e-100; Mismatches 0; Indels 0; Gaps 0;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEITVKYKADBDQAGARVGYELDINSKILSPRPERPMMSTFKVLLCGAVLSRID 60
DB 24 HPEITVKYKADBDQAGARVGYELDINSKILSPRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGVTRELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGVTRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KETLAFILHNMGDHVTRLDRWPELNEAIPNDRDPTTVPVAAATTLRKLLTGELTLASRQ 180
DB 144 KETLAFILHNMGDHVTRLDRWPELNEAIPNDRDPTTVPVAAATTLRKLLTGELTLASRQ 203

QY 181 Q 181
DB 204 Q 204

RESULT 3

US-09-263-933-7
Sequence 7, Application US/09263933
Patent No. 6280940
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
US-09-263-933-7

Query Match 100.0%; Score 925; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 4.1e-100; Mismatches 0; Indels 0; Gaps 0;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITVKYKADBDQAGARVGYELDINSKILSPRPERPMMSTFKVLLCGAVLSRID 60
DB 24 HPEITVKYKADBDQAGARVGYELDINSKILSPRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGVTRELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGVTRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KETLAFILHNMGDHVTRLDRWPELNEAIPNDRDPTTVPVAAATTLRKLLTGELTLASRQ 180
DB 144 KETLAFILHNMGDHVTRLDRWPELNEAIPNDRDPTTVPVAAATTLRKLLTGELTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 4

US-09-263-933-14
Sequence 14, Application US/09263933
Patent No. 6280940
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
US-09-263-933-14

Query Match 100.0%; Score 925; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 4.1e-100;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKTVKADADQAGVGYIELDLSGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
DB 24 HPELVKTVKADADQAGVGYIELDLSGKILSFRRPFRPMSTFKVLLCGAVLSRID 83
QY 61 AGQEQGLRRIRHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQEQGLRRIRHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFLLNMGDHTRLDRWPELNEAIPNDRDITMPVAAATTIRKLLTGELITLASRQ 180
DB 144 KELTAFLLNMGDHTRLDRWPELNEAIPNDRDITMPVAAATTIRKLLTGELITLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 5

US-09-263-933-21
; Sequence 21, Application US/09263933
; Patent No. 6280940
; GENERAL INFORMATION:
; APPLICANT: Potte, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/263,933
; EARLIER FILING DATE: 1999-03-08
; EARLIER APPLICATION NUMBER: 09/129,611
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO: 21
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-09-263-933-21

Query Match 100.0%; Score 925; DB 3; Length 286;

Best Local Similarity 100.0%; Pred. No. 4.1e-100;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKTVKADADQAGVGYIELDLSGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
DB 24 HPELVKTVKADADQAGVGYIELDLSGKILSFRRPFRPMSTFKVLLCGAVLSRID 83
QY 61 AGQEQGLRRIRHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQEQGLRRIRHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFLLNMGDHTRLDRWPELNEAIPNDRDITMPVAAATTIRKLLTGELITLASRQ 180
DB 144 KELTAFLLNMGDHTRLDRWPELNEAIPNDRDITMPVAAATTIRKLLTGELITLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 6

US-09-025-769B-265
; Sequence 265, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic

APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 265:

SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-265

Query Match 100.0%; Score 925; DB 3; Length 286;

Best Local Similarity 100.0%; Pred. No. 4.1e-100;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKTVKADADQAGVGYIELDLSGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
DB 24 HPELVKTVKADADQAGVGYIELDLSGKILSFRRPFRPMSTFKVLLCGAVLSRID 83
QY 61 AGQEQGLRRIRHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQEQGLRRIRHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFLLNMGDHTRLDRWPELNEAIPNDRDITMPVAAATTIRKLLTGELITLASRQ 180
DB 144 KELTAFLLNMGDHTRLDRWPELNEAIPNDRDITMPVAAATTIRKLLTGELITLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 7

US-09-025-769B-362
; Sequence 362, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 362:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-362

Query Match 100.0%; Score 925; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 4.1e-100; Indels 0; Gaps 0;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEITLVKKAEDDQAGAVGYIELDLSGKILIESPRPERPPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKKAEDDQAGAVGYIELDLSGKILIESPRPERPPMSTFVLLCGAVLSRID 83
QY 61 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGSP 120
DB 84 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGSP 143
QY 121 KELTAFILNMGDHYTRLDRWEPELNEALPNDERDTMPVAAATTLRKLLTGSELLTLASRQ 180
DB 144 KELTAFILNMGDHYTRLDRWEPELNEALPNDERDTMPVAAATTLRKLLTGSELLTLASRQ 203
QY 181 Q 181
DB 204 Q 204
RESULT 8
US-09-919-901-7
Sequence 7, Application US/09919901
Patent No. 6599738
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 7

LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-09-919-901-7

Query Match 100.0%; Score 925; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 4.1e-100; Indels 0; Gaps 0;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEITLVKKAEDDQAGAVGYIELDLSGKILIESPRPERPPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKKAEDDQAGAVGYIELDLSGKILIESPRPERPPMSTFVLLCGAVLSRID 83
QY 61 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGSP 120
DB 84 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGSP 143
QY 121 KELTAFILNMGDHYTRLDRWEPELNEALPNDERDTMPVAAATTLRKLLTGSELLTLASRQ 180
DB 144 KELTAFILNMGDHYTRLDRWEPELNEALPNDERDTMPVAAATTLRKLLTGSELLTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 9
US-09-919-901-14
Sequence 14, Application US/09919901
Patent No. 6599738
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 14
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-09-919-901-14

Query Match 100.0%; Score 925; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 4.1e-100; Indels 0; Gaps 0;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEITLVKKAEDDQAGAVGYIELDLSGKILIESPRPERPPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKKAEDDQAGAVGYIELDLSGKILIESPRPERPPMSTFVLLCGAVLSRID 83
QY 61 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGSP 120
DB 84 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGSP 143
QY 121 KELTAFILNMGDHYTRLDRWEPELNEALPNDERDTMPVAAATTLRKLLTGSELLTLASRQ 180
DB 144 KELTAFILNMGDHYTRLDRWEPELNEALPNDERDTMPVAAATTLRKLLTGSELLTLASRQ 203
QY 181 Q 181

Db 204 Q 204

RESULT 10

US-09-919-901-21

Sequence 21, Application US/09919901

Patent No. 6599738

GENERAL INFORMATION:

APPLICANT: Potts, Karen E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patrick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT

TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/09/919,901

CURRENT FILING DATE: 2001-08-02

PRIOR APPLICATION NUMBER: 09/263,933

PRIOR FILING DATE: 1999-02-08

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 21

LENGTH: 286

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURES:

OTHER INFORMATION:

US-09-919-901-21

Query Match 100.0%; Score 925; DB 4; Length 286;

Best Local Similarity 100.0%; Pred. No. 4,1e-100; Mismatches 0; Indels 0; Gaps 0;

Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	HPETLVKVDADQAGARVGYIELDNLSGKILSPRPERFPMSTFKYLICGAVLSRID	60
DB	24	HPETLVKVDADQAGARVGYIELDNLSGKILSPRPERFPMSTFKYLICGAVLSRID	83
QY	61	AGQEQGRRIHNSQNDLVESPVTEKHLTDGTVRELCSAATMSDNTANILTTIGSP	120
DB	84	AGQEQGRRIHNSQNDLVESPVTEKHLTDGTVRELCSAATMSDNTANILTTIGSP	143
QY	121	KELTAFINMGDHTVRLDRWPELNEAIPNDRDITMPVAMATTIRKLTGELLTASRQ	180
DB	144	KELTAFINMGDHTVRLDRWPELNEAIPNDRDITMPVAMATTIRKLTGELLTASRQ	203
QY	181	Q 181	
DB	204	Q 204	

RESULT 11

US-09-490-070A-265

Sequence 265, Application US/09490070A

Patent No. 6696248

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

APPLICANT: Pack, Peter

APPLICANT: Ilag, Vic

APPLICANT: Ge, Liming

APPLICANT: Moroney, Simon

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSER: Colin G. Sandercock, Esq. c/o Heller Ehrman

White & Mcauliffe

STREET: 1666 K Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,070A

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Colin G. Sandercock, Esq.

REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 37629-0005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 912-2000

TELEFAX: (202) 912-2020

INFORMATION FOR SEQ ID NO: 265:

SEQUENCE CHARACTERISTICS:

LENGTH: 286 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 265:

US-09-490-070A-265

Query Match 100.0%; Score 925; DB 4; Length 286;

Best Local Similarity 100.0%; Pred. No. 4,1e-100; Mismatches 0; Indels 0; Gaps 0;

Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	HPETLVKVDADQAGARVGYIELDNLSGKILSPRPERFPMSTFKYLICGAVLSRID	60
DB	24	HPETLVKVDADQAGARVGYIELDNLSGKILSPRPERFPMSTFKYLICGAVLSRID	83
QY	61	AGQEQGRRIHNSQNDLVESPVTEKHLTDGTVRELCSAATMSDNTANILTTIGSP	120
DB	84	AGQEQGRRIHNSQNDLVESPVTEKHLTDGTVRELCSAATMSDNTANILTTIGSP	143
QY	121	KELTAFINMGDHTVRLDRWPELNEAIPNDRDITMPVAMATTIRKLTGELLTASRQ	180
DB	144	KELTAFINMGDHTVRLDRWPELNEAIPNDRDITMPVAMATTIRKLTGELLTASRQ	203
QY	181	Q 181	
DB	204	Q 204	

RESULT 12

US-09-490-070A-362

Sequence 362, Application US/09490070A

Patent No. 6696248

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

APPLICANT: Pack, Peter

APPLICANT: Ilag, Vic

APPLICANT: Ge, Liming

APPLICANT: Moroney, Simon

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSER: Colin G. Sandercock, Esq. c/o Heller Ehrman

White & Mcauliffe

STREET: 1666 K Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 362:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 362:
US-09-490-070A-362

Query Match 100.0%; Score 925; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 4,1e-100;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKDAEDQAGRVGTYIEDLNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVKDAEDQAGRVGTYIEDLNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 83
QY 61 AGQQLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAITSNDNTAAILTTIGCP 120
DB 84 AGQQLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAITSNDNTAAILTTIGCP 143
QY 121 KETLAFILNMGDHYTRLDRWEPELNEAIPNDRDITMVPVAMATTLRKLLTGELLTLASRQ 180
DB 144 KETLAFILNMGDHYTRLDRWEPELNEAIPNDRDITMVPVAMATTLRKLLTGELLTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 13
US-09-490-153-265
Sequence 265, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Moroney, Simon
Pineckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-09-490-153-265

Query Match 100.0%; Score 925; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 4,1e-100;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKDAEDQAGRVGTYIEDLNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVKDAEDQAGRVGTYIEDLNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 83
QY 61 AGQQLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAITSNDNTAAILTTIGCP 120
DB 84 AGQQLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAITSNDNTAAILTTIGCP 143
QY 121 KETLAFILNMGDHYTRLDRWEPELNEAIPNDRDITMVPVAMATTLRKLLTGELLTLASRQ 180
DB 144 KETLAFILNMGDHYTRLDRWEPELNEAIPNDRDITMVPVAMATTLRKLLTGELLTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 14
US-09-490-153-362
Sequence 362, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Moroney, Simon
Pineckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Reg.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 362:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 362:
US-09-490-153-362

Query Match 100.0%; Score 925; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 4.1e-100;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADSDQAGARVGYIELDLSGKILSPRPERFPMSTFKYLICGAVLSRID 60
DB 24 HPEITLVKVDADSDQAGARVGYIELDLSGKILSPRPERFPMSTFKYLICGAVLSRID 83
QY 61 AGQEQIGRRIRHYSQNDLVESPVTEKHLTDGNTVRELCSAITMSDNTANILLTTIGSP 120
DB 84 AGQEQIGRRIRHYSQNDLVESPVTEKHLTDGNTVRELCSAITMSDNTANILLTTIGSP 143
QY 121 KELITAFLNMGDHTRLDRWPELNEAIPNDERDTTMPVAMATTIRKLLTGELITLASRQ 180
DB 144 KELITAFLNMGDHTRLDRWPELNEAIPNDERDTTMPVAMATTIRKLLTGELITLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 15

US-10-191-966-7
Sequence 7, Application US/10191966
Patent No. 6790612
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-10-191-966-7

Query Match 100.0%; Score 925; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 4.1e-100;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADSDQAGARVGYIELDLSGKILSPRPERFPMSTFKYLICGAVLSRID 60
DB 24 HPEITLVKVDADSDQAGARVGYIELDLSGKILSPRPERFPMSTFKYLICGAVLSRID 83
QY 61 AGQEQIGRRIRHYSQNDLVESPVTEKHLTDGNTVRELCSAITMSDNTANILLTTIGSP 120

DB 84 AGQEQIGRRIRHYSQNDLVESPVTEKHLTDGNTVRELCSAITMSDNTANILLTTIGSP 143
QY 121 KELITAFLNMGDHTRLDRWPELNEAIPNDERDTTMPVAMATTIRKLLTGELITLASRQ 180
DB 144 KELITAFLNMGDHTRLDRWPELNEAIPNDERDTTMPVAMATTIRKLLTGELITLASRQ 203
QY 181 Q 181
DB 204 Q 204

Search completed: June 10, 2005, 11:01:14
Job time : 19.5574 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2005, 10:35:06 ; Search time 13.1993 Seconds
(without alignments)
1319.408 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_181

Perfect score: 925
Sequence: 1 HPEITLVKVKDABDQIGARVGV.....ATTLRKLTGELLTLASRQ 181

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	925	100.0	286	2 TS1301	beta-lactamase (EC
2	925	100.0	286	2 S47061	beta-lactamase (EC
3	925	100.0	286	4 S41975	beta-lactamase (EC
4	920	99.5	286	1 PNECP	beta-lactamase (EC
5	920	99.5	286	4 P40905	beta-lactamase (EC
6	912	98.6	286	2 S30113	beta-lactamase (EC
7	907	98.1	286	2 S60312	extended spectrum
8	906	97.9	286	2 S60310	extended spectrum
9	906	97.9	286	2 S60311	beta-lactamase (EC
10	906	97.9	286	2 J01546	Bla protein - Salim
11	640	69.2	286	2 S16146	beta-lactamase (EC
12	640	69.2	286	2 A60679	beta-lactamase (EC
13	636	68.8	265	2 S00464	beta-lactamase (EC
14	636	68.8	265	2 S02434	beta-lactamase (EC
15	636	68.8	286	1 A44998	beta-lactamase (EC
16	636	68.8	286	2 A60632	beta-lactamase (EC
17	633	68.4	265	2 A60448	beta-lactamase (EC
18	633	68.4	286	2 A37200	beta-lactamase (EC
19	618	66.8	279	2 A24469	beta-lactamase (EC
20	611.5	66.1	287	1 A44996	beta-lactamase (EC
21	585	63.2	286	1 A44958	beta-lactamase (EC
22	506	54.7	298	2 A41381	beta-lactamase (EC
23	410.5	44.4	281	2 D95395	probable Beta lact
24	395.5	42.8	314	2 S06967	beta-lactamase (EC
25	392.5	42.4	294	2 S16553	beta-lactamase (EC
26	386	41.7	293	3 S04649	beta-lactamase (EC
27	383.5	41.5	306	1 S45822	beta-lactamase (EC
28	382.5	41.4	302	2 S36188	beta-lactamase (EC
29	380.5	41.1	263	2 A54543	beta-lactamase (EC

30	377.5	40.8	291	2 S42075	beta-lactamase (EC
31	372.5	40.3	306	2 G69674	beta-lactamase (EC
32	371.5	40.2	311	2 JN0520	beta-lactamase (EC
33	368	39.8	305	2 A61156	beta-lactamase (EC
34	368	39.8	305	2 A57002	beta-lactamase (EC
35	368	39.8	305	2 A60680	beta-lactamase (EC
36	367.5	39.7	306	2 S47330	penicillinase - Ba
37	359.5	38.9	291	2 JP0074	beta-lactamase (EC
38	357	38.6	310	2 J10091	beta-lactamase (EC
39	356.5	38.5	305	1 C45822	beta-lactamase (EC
40	354.5	38.3	263	2 S23929	beta-lactamase (EC
41	354.5	38.3	288	2 UQ1136	beta-lactamase (EC
42	354	38.3	294	2 S04080	beta-lactamase (EC
43	353.5	38.2	311	1 S02714	beta-lactamase (EC
44	350.5	37.9	304	2 A49789	beta-lactamase (EC
45	350.5	37.9	304	2 A35001	beta-lactamase (EC

ALIGNMENTS

RESULT 1
TS1301
beta-lactamase (EC 3.5.2.6) - fission yeast (Schizosaccharomyces pombe)
C1:Species: Schizosaccharomyces pombe
C1:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C1:Accession: TS1301
R1:WACH, A.; BRACHAT, A.; ALBERTISSEGUI, C.; REBISCHUNG, C.; PHILIPSEN, P.
Yeast 13, 1065-1075, 1997
A1:Title: Heterologous His3 marker and GFP reporter modules for PCR-targeting in Saccharon
A1:Reference number: Z09587
A1:Accession: TS1301
A1>Status: preliminary; translated from GB/EMBL/DBJ
A1:Molecule type: DNA
A1:Residues: 1-286 <MAC>
A1:Cross-references: EMBL:AJ002683; PIDN:CAA05686.1
C1:Genetics:
A1:Gene: bla
C1:Superfamily: beta-lactamase I
C1:Keywords: hydrolase

Query Match 100.0%; Score 925; DB 2; Length 286;
Best local similarity 100.0%; Pred. No. 2.5e-76;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	HPEITLVKVKDABDQIGARVGYIELDNGKIIIESRPERPFPMSTFKYLICGAVLSRID	60
DB	24	HPEITLVKVKDABDQIGARVGYIELDNGKIIIESRPERPFPMSTFKYLICGAVLSRID	83
QY	61	AGOEOLGRRIHYSQNDIVESPVTEKHLTDGWTVELCSAATIMSDNTPAANLLTTIGSP	120
DB	84	AGOEOLGRRIHYSQNDIVESPVTEKHLTDGWTVELCSAATIMSDNTPAANLLTTIGSP	143
QY	121	KELTAFILNMGDHYTRLDREBELNEAIPNDRDITMPVAMATTIRKLTGELLTLASRQ	180
DB	144	KELTAFILNMGDHYTRLDREBELNEAIPNDRDITMPVAMATTIRKLTGELLTLASRQ	203
QY	181	Q 181	
DB	204	Q 204	

RESULT 2
S47061
beta-lactamase (EC 3.5.2.6) - phage phi-X174
C1:Species: phage phi-X174
C1:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C1:Accession: S47061
R1:Heinrich, B.; Schmidtberger, B.
submitted to the EMBL Data Library, July 1994
A1:Description: A variant of phix174 gene B-based positive selection vectors with enhanced
A1:Reference number: S47060
A1:Accession: S47061

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-286 <HEV>
 A:Cross-references: UNIPROT:Q38058; EMBL:Z35638; NID:g520996; PIDN:CAA84692.1; PID:g5209
 C:Superfamily: beta-lactamase I
 C:Keywords: hydrolase

Query Match 100.0%; Score 925; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 2.5e-76;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGYIELDLSGKILSFRRPFRPMSSTPKVLLCGAVLSRID 60
 DB HPEITLVKVDADQAGARVGYIELDLSGKILSFRRPFRPMSSTPKVLLCGAVLSRID 83
 QY 61 AGQEQIGRRIRHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGP 120
 DB AGQEQIGRRIRHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGP 143
 QY 121 KELTAFILNMGDHYTRLDRWPELNEAIPNDRDITTPVAAATTIRKLLTGELLTLASRQ 180
 DB KELTAFILNMGDHYTRLDRWPELNEAIPNDRDITTPVAAATTIRKLLTGELLTLASRQ 203
 QY 181 Q 181
 DB 204 Q 204

RESULT 3
 S11975
 beta-lactamase (EC 3.5.2.6) precursor - synthetic
 C:Species: synthetic
 C:Date: 25-Dec-1994 #sequence_revision 22-Aug-1996 #text_change 20-Oct-2000
 R:Accession: S41975
 R:Kaestner, K.H.; Montoliu, L.; Kern, H.; Thulke, M.; Schutz, G.
 Gene 148, 67-70, 1994
 A:Title: Universal beta-galactosidase cloning vectors for promoter analysis and gene tar
 A:Reference number: A57991; MUID:95011660; PMID:7926839
 A:Accession: S41975
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-286 <KAB>
 A:Cross-references: EMBL:X76682; NID:g453622; PIDN:CAA54104.1; PID:g453623
 A:Note: submitted to the EMBL Data Library, December 1993
 C:Keywords: hydrolase

Query Match 100.0%; Score 925; DB 4; Length 286;
 Best Local Similarity 100.0%; Pred. No. 2.5e-76;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGYIELDLSGKILSFRRPFRPMSSTPKVLLCGAVLSRID 60
 DB HPEITLVKVDADQAGARVGYIELDLSGKILSFRRPFRPMSSTPKVLLCGAVLSRID 83
 QY 61 AGQEQIGRRIRHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGP 120
 DB AGQEQIGRRIRHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGP 143
 QY 121 KELTAFILNMGDHYTRLDRWPELNEAIPNDRDITTPVAAATTIRKLLTGELLTLASRQ 180
 DB KELTAFILNMGDHYTRLDRWPELNEAIPNDRDITTPVAAATTIRKLLTGELLTLASRQ 203
 QY 181 Q 181
 DB 204 Q 204

RESULT 4
 PNECP
 beta-lactamase (EC 3.5.2.6) precursor - Escherichia coli plasmids
 N:Alternate names: beta-lactamase TEM-6 (for blaT-6 DNA); penicillinase
 C:Species: Escherichia coli
 C:Date: 30-Nov-1980 #sequence_revision 01-Sep-1981 #text_change 16-Aug-2004

C:Accession: A93821; A93820; A35387; S24415; A01005
 R:Sutcliffe, J.G.
 Proc. Natl. Acad. Sci. U.S.A. 75, 3737-3741, 1978
 A:Title: Nucleotide sequence of the ampicillin resistance gene of Escherichia coli plasmid
 A:Reference number: A93821; MUID:79012484; PMID:358200
 A:Accession: A93821
 A:Molecule type: DNA
 A:Residues: 1-286 <STU>
 A:Cross-references: UNIPROT:P00810; GB:V00613; GB:J01832; NID:g43710; PIDN:CAA23886.1; P1

A:Accession: A93820
 A:Molecule type: protein
 A:Residues: 24-36, 'K', 38-286 <AMB>
 A:Experimental source: plasmid R6K
 R:Kornacki, J.A.; Burlage, R.S.; Figurski, D.H.
 J. Bacteriol. 172, 3040-3050, 1990
 A:Title: The *kil*-kor region of broad-host-range plasmid RK2: nucleotide sequence, polype
 A:Reference number: A35387; MUID:90264294; PMID:2160936
 A:Accession: A35387

A:Molecule type: DNA
 A:Residues: 182-286 <KOR>
 A:Cross-references: GB:M32794; NID:g152521; PIDN:AAA26408.1; PID:g152522
 A:Experimental source: PK2
 R:Goussard, S.; Sougkoff, W.; Mabilat, C.; Baumenfeind, A.; Courvalin, P.
 U. Gen. Microbiol. 137, 2681-2687, 1991
 A:Title: An ISI-like element is responsible for high-level synthesis of extended-spectrum
 A:Reference number: S24415; MUID:92166702; PMID:1665171
 A:Accession: S24415
 A:Status: translation not shown

A:Molecule type: DNA
 A:Residues: 1-101, 'K', 103-161, 'H', 163-286 <GOU>
 A:Cross-references: EMBL:X57972; NID:g41816; PIDN:CAA41038.1; PID:g41817
 A:Experimental source: ISI-like blaT-6 DNA
 R:Sutcliffe, J.G.
 Cold Spring Harb. Symp. Quant. Biol. 43, 77-90, 1979

A:Title: Complete nucleotide sequence of the Escherichia coli plasmid pBR322.
 A:Reference number: A90923; MUID:80002802; PMID:383387
 A:Contents: annotation
 C:Comment: like most penicillinases from gram-negative bacteria, this enzyme, coded by a
 C:Genetics:
 A:Genome: plasmid
 C:Superfamily: Beta-lactamase I
 C:Keywords: antibiotic resistance; hydrolase; membrane protein
 F:1-23/Domains: signal sequence #status predicted <SIG>
 F:24-286/Product: beta-lactamase #status experimental <MAT>
 F:68/Active site: Ser #status predicted
 F:75-121/Diulfide bonds: #status predicted

Query Match 99.5%; Score 920; DB 1; Length 286;
 Best Local Similarity 98.9%; Pred. No. 7.2e-76;
 Matches 179; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGYIELDLSGKILSFRRPFRPMSSTPKVLLCGAVLSRID 60
 DB HPEITLVKVDADQAGARVGYIELDLSGKILSFRRPFRPMSSTPKVLLCGAVLSRID 83
 QY 61 AGQEQIGRRIRHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGP 120
 DB AGQEQIGRRIRHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGP 143
 QY 121 KELTAFILNMGDHYTRLDRWPELNEAIPNDRDITTPVAAATTIRKLLTGELLTLASRQ 180
 DB KELTAFILNMGDHYTRLDRWPELNEAIPNDRDITTPVAAATTIRKLLTGELLTLASRQ 203
 QY 181 Q 181
 DB 204 Q 204

RESULT 5

140905
beta-lactamase (EC 3.5.2.6) - synthetic
C:Species: synthetic
A:Note: Cloning vector pCG1408 engineered and expressed in *Clavibacter xyli* subsp. *cynod*
C:Date: 15-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Oct-2000
C:Accession: I40905
R:Taylor, J.; Stearman, R.S.; Uratani, B.B.
Plasmid 29, 241-244, 1993
A:Title: Development of a native plasmid as a cloning vector in *Clavibacter xyli* subsp.
A:Reference number: 140904; MUID:93361581; PMID:7689234
A:Accession: I40905
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1286 <RES>
A:Cross-references: EMBL:U21228; NID:9885956; PIDD:AAA70411.1; PID:9885958
C:Keywords: hydrolase

Query Match 99.5%; Score 920; DB 4; Length 286;
Best Local Similarity 98.9%; Pred. No. 7, 2e-76;
Matches 179; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPELVKXADQAGVGYIELDLSGKILSFRRPFRPMSFPKVLGAVLSRD 60
DB 24 HPELVKXADQAGVGYIELDLSGKILSFRRPFRPMSFPKVLGAVLSRD 83
QY 61 AGQOLGRRIRHSQNDLVYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQOLGRRIRHSQNDLVYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFLLNMGDHYTRLDRWPELNEALPNDERDITMPAAMATTLRKLLTGELTLASRQ 180
DB 144 KELTAFLLNMGDHYTRLDRWPELNEALPNDERDITMPAAMATTLRKLLTGELTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 6

S30113
beta-lactamase (EC 3.5.2.6) TEM-3 - *Klebsiella pneumoniae* plasmid pCF04
C:Species: *Klebsiella pneumoniae*
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: S30113
R:Mabilat, C.; Lourenco-Vital, J.; Goussard, S.; Courvalin, P.
Mol. Gen. Genet. 235, 113-121, 1992
A:Title: A new example of physical linkage between *Tn1* and *Tn21*: the antibiotic multiple
A:Reference number: S30112; MUID:93062798; PMID:1331747
A:Accession: S30113
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <MA>
A:Cross-references: UNIPROT:P00810; EMBL:X64523; NID:943797; PIDD:CAA45828.1; PID:943798
C:Genetics:
A:Gene: bla(TEM-3)
A:Genome: plasmid
C:Superfamily: beta-lactamase I
C:Keywords: antibiotic resistance; hydrolase

Query Match 98.6%; Score 912; DB 2; Length 286;
Best Local Similarity 97.8%; Pred. No. 3, 8e-75;
Matches 177; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPELVKXADQAGVGYIELDLSGKILSFRRPFRPMSFPKVLGAVLSRD 60
DB 24 HPELVKXADQAGVGYIELDLSGKILSFRRPFRPMSFPKVLGAVLSRD 83
QY 61 AGQOLGRRIRHSQNDLVYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQOLGRRIRHSQNDLVYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFLLNMGDHYTRLDRWPELNEALPNDERDITMPAAMATTLRKLLTGELTLASRQ 180

DB 144 KELTAFLLNMGDHYTRLDRWPELNEALPNDERDITMPAAMATTLRKLLTGELTLASRQ 203

QY 181 Q 181
DB 204 Q 204

RESULT 7

S60312
extended spectrum beta-lactamase CAZ-7 - *Klebsiella pneumoniae*
C:Species: *Klebsiella pneumoniae*
C:Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 22-Jun-1999
C:Accession: S60312
R:Chanal, C.; Poupart, M.C.; Strot, D.; Labia, R.; Strot, J.; Cluzel, R.
Antimicrob. Agents Chemother. 36, 1817-1820, 1992
A:Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.
A:Reference number: S60310; MUID:93037315; PMID:1416873
A:Accession: S60312
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <CHA>
A:Cross-references: EMBL:X65254; NID:9296955; PIDD:CAA46346.1; PID:9296956
C:Superfamily: beta-lactamase I

Query Match 98.1%; Score 907; DB 2; Length 286;
Best Local Similarity 97.2%; Pred. No. 1, 1e-74;
Matches 176; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPELVKXADQAGVGYIELDLSGKILSFRRPFRPMSFPKVLGAVLSRD 60
DB 24 HPELVKXADQAGVGYIELDLSGKILSFRRPFRPMSFPKVLGAVLSRD 83
QY 61 AGQOLGRRIRHSQNDLVYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQOLGRRIRHSQNDLVYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFLLNMGDHYTRLDRWPELNEALPNDERDITMPAAMATTLRKLLTGELTLASRQ 180
DB 144 KELTAFLLNMGDHYTRLDRWPELNEALPNDERDITMPAAMATTLRKLLTGELTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 8

S60310
extended spectrum beta-lactamase CAZ-2 - *Klebsiella pneumoniae*
C:Species: *Klebsiella pneumoniae*
C:Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 22-Jun-1999
C:Accession: S60310
R:Chanal, C.; Poupart, M.C.; Strot, D.; Labia, R.; Strot, J.; Cluzel, R.
Antimicrob. Agents Chemother. 36, 1817-1820, 1992
A:Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.
A:Reference number: S60310; MUID:93037315; PMID:1416873
A:Accession: S60310
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <CHA>
A:Cross-references: EMBL:X65252; NID:9296951; PIDD:CAA46344.1; PID:9296952
C:Superfamily: beta-lactamase I

Query Match 97.9%; Score 906; DB 2; Length 286;
Best Local Similarity 97.2%; Pred. No. 1, 3e-74;
Matches 176; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPELVKXADQAGVGYIELDLSGKILSFRRPFRPMSFPKVLGAVLSRD 60
DB 24 HPELVKXADQAGVGYIELDLSGKILSFRRPFRPMSFPKVLGAVLSRD 83
QY 61 AGQOLGRRIRHSQNDLVYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 120

Db 84 AGOEOLGRRIRHYSQNDLVKSPVTEKHLLTDGWTVELCSAAITMSDNTAANILLTTIGCP 143
QY 121 KETLAFILNMGDHVTRLDRWPELNEALPNDERDITMPVAMATTIRKLLTGELLTLASRQ 180
Db 144 KETLAFILNMGDHVTRLDRWPELNEALPNDERDITMPVAMATTIRKLLTGELLTLASRQ 203
QY 181 Q 181
Db 204 Q 204

RESULT 9

S60311
beta-lactamase (EC 3.5.2.6) TEM-1 - Klebsiella pneumoniae transposon Tn1331
C:Species: Klebsiella pneumoniae
C:Date: 12-Apr-1996 #sequence revision 19-Apr-1996 #text_change 09-Jul-2004
C:Accession: S60311; F37392; F00498
R:Chanal, C.; Foupert, M.C.; Siroc, D.; Labia, R.; Siroc, J.; Cluzel, R.
AntiMicrob. Agents Chemother. 36, 1817-1820, 1992
A:Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.
A:Reference number: S60310; MUID:93037315; PMID:1416873
A:Accession: S60311
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <CAN>
A:Cross-references: UNIPROT:Q99224; EMBL:X65253; NID:g296953; PIDN:CAA46345.1; PID:g2969

R:Toimasky, M.E.
plasmid 24, 218-226, 1990
A:Title: Sequencing and expression of aadA, bla, and tnpR from the multiresistance trans
A:Reference number: A57392; MUID:91172904; PMID:1963948
A:Accession: F37392
A:Molecule type: DNA
A:Residues: 1-32 <TOL>
A:Cross-references: GB:M55547; NID:g155010; PIDN:AAA98408.1; PID:g155016
C:Genetics:
A:Gene: TEM-bla
C:Superfamily: beta-lactamase I
C:Keywords: antibiotic resistance; hydrolase

Query Match 97.9%; Score 906; DB 2; Length 286;
Best Local Similarity 97.2%; Pred. No. 1.3e-74;
Matches 176; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITLVKXDAEDQAGAVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
Db 24 HPEITLVKXDAEDQAGAVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
QY 61 AGOEOLGRRIRHYSQNDLVKSPVTEKHLLTDGWTVELCSAAITMSDNTAANILLTTIGCP 120
Db 84 AGOEOLGRRIRHYSQNDLVKSPVTEKHLLTDGWTVELCSAAITMSDNTAANILLTTIGCP 143
QY 121 KETLAFILNMGDHVTRLDRWPELNEALPNDERDITMPVAMATTIRKLLTGELLTLASRQ 180
Db 144 KETLAFILNMGDHVTRLDRWPELNEALPNDERDITMPVAMATTIRKLLTGELLTLASRQ 203
QY 181 Q 181
Db 204 Q 204

RESULT 10

QJ0156
Bla protease - Salmonella typhimurium plasmid NTP16
N:Alternate names: beta lactamase homolog
C:Species: Salmonella typhimurium
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: J01546
R:Canon, P.M.; Strife, P.
Plasmid 27, 220-230, 1992
A:Title: Complete nucleotide sequence and gene organization of plasmid NTP16.
A:Reference number: J01548; MUID:92383313; PMID:1325061
A:Accession: J01546
A:Status: translation not shown

A:Molecule type: DNA
A:Residues: 1-286 <CAN>
A:Cross-references: UNIPROT:Q8L2F9
C:Genetics:
A:Genome: plasmid
C:Superfamily: beta-lactamase I

Query Match 97.9%; Score 906; DB 2; Length 286;
Best Local Similarity 97.8%; Pred. No. 1.3e-74;
Matches 177; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HPEITLVKXDAEDQAGAVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
Db 24 HPEITLVKXDAEDQAGAVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
QY 61 AGOEOLGRRIRHYSQNDLVKSPVTEKHLLTDGWTVELCSAAITMSDNTAANILLTTIGCP 120
Db 84 AGOEOLGRRIRHYSQNDLVKSPVTEKHLLTDGWTVELCSAAITMSDNTAANILLTTIGCP 143
QY 121 KETLAFILNMGDHVTRLDRWPELNEALPNDERDITMPVAMATTIRKLLTGELLTLASRQ 180
Db 144 KETLAFILNMGDHVTRLDRWPELNEALPNDERDITMPVAMATTIRKLLTGELLTLASRQ 203
QY 181 Q 181
Db 204 Q 204

RESULT 11

S16146
beta-lactamase (EC 3.5.2.6) 2A precursor - Klebsiella pneumoniae plasmids
N:Alternate names: beta-lactamase SHV2A
C:Species: Klebsiella pneumoniae
C:Date: 21-Nov-1993 #sequence revision 10-Nov-1995 #text_change 15-Oct-1999
C:Accession: S16146; A53395; S18767
R:Podbielski, A.; Schoenling, J.; Melzer, B.; Wamatz, K.; Leusch, H.G.
J. Gen. Microbiol. 137, 569-578, 1991
A:Title: Molecular characterization of a new plasmid-encoded SHV-type beta-lactamase (SHV

A:Reference number: S16146; MUID:91237320; PMID:2033379
A:Accession: S16146
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <POD>
A:Cross-references: EMBL:X53817; NID:g43795; PIDN:CAA37813.1; PID:g43796
A:Experimental source: plasmid pZMP1
R:Lee, K.Y.; Hopkins, J.D.; Syvonen, M.
J. Bacteriol. 172, 3229-3236, 1990
A:Title: Direct involvement of IS26 in an antibiotic resistance operon.
A:Reference number: A53395; MUID:90264317; PMID:2160941
A:Molecule type: DNA
A:Residues: 1-30, 'L', 32-286 <LBE>
A:Cross-references: GB:X62115; NID:g48988; PIDN:CAA44025.1; PID:g48990
A:Experimental source: plasmid BW77
C:Genetics:
A:Gene: blaS2A
A:Genome: plasmid
C:Superfamily: beta-lactamase I
C:Keywords: antibiotic resistance; hydrolase

Query Match 69.2%; Score 640; DB 2; Length 286;
Best Local Similarity 67.8%; Pred. No. 1.7e-50;
Matches 122; Conservative 26; Mismatches 32; Indels 0; Gaps 0;

QY 2 PETLVKXDAEDQAGAVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 61
Db 23 PETLVKXDAEDQAGAVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 82
QY 62 AGOEOLGRRIRHYSQNDLVKSPVTEKHLLTDGWTVELCSAAITMSDNTAANILLTTIGCP 121
Db 83 AGOEOLGRRIRHYSQNDLVKSPVTEKHLLTDGWTVELCSAAITMSDNTAANILLTTIGCP 142
QY 122 ELTAFILNMGDHVTRLDRWPELNEALPNDERDITMPVAMATTIRKLLTGELLTLASRQ 181


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Db      23  P Q P L E Q I K L S E S Q L S G R V G M I E M D L A S G R T L T A M R A D E R F P M M S T F K V V L C G A V L A R Y D A      82
Qy      62  G O E O L G R R I H Y S O N D L V E Y S P V T E K H L T D G M T V R E L C S A I T M S D N T A N L L T T I G P K      121
Db      83  G B E O L E R K I H R Q O D L V D Y S P V S E K H L A D G M T V G E L C A A I T M S D N S A N L L L A T V G G P A      142
Qy      122 E L T A F L H N M G D H V T R L D R W E P E L N E A I P N D E R D T T M P V A M A T T L R K L L T G B L L T L A S R Q      181
Db      143 G L T A F L R Q I G D N V T R L D R W E T E L N E A L P O D A R D T T P A S M A T L R K L L T S Q R L S A R S Q R Q      202

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Search completed: June 10, 2005, 10:58:45
 Job time : 14.193 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:23:36 ; Search time 60.6383 Seconds
(without alignments)
1528.512 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_181
Perfect score: 925
Sequence: 1 HPEITLVKVKDABDQIGARVG.....ATTLRKLTGELLTLASRQ 181

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*\n1: uniprot_sprot:*\n2: uniprot_trernbl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	925	100.0	229	2	Q6WY5 Klebsiella
2	925	100.0	232	2	Q6WY4 Klebsiella
3	925	100.0	241	2	Q6WY8 Klebsiella
4	925	100.0	242	2	Q6WY3 Klebsiella
5	925	100.0	285	2	Q6KB67 hordeum val
6	925	100.0	286	2	Q38058 bacterioph
7	925	100.0	286	2	Q00626 staphylococ
8	925	100.0	286	2	Q79C16 methylobact
9	925	100.0	286	2	Q79DR3 Klebsiella
10	920	99.5	225	2	Q38212 bacterioph
11	920	99.5	232	2	Q6PRU7 Klebsiella
12	920	99.5	255	2	Q84H50 Klebsiella
13	920	99.5	261	2	Q84H49 Klebsiella
14	920	99.5	264	2	Q6PRU6 Klebsiella
15	920	99.5	281	2	Q6QIV0 Klebsiella
16	920	99.5	282	2	Q6QIV1 Klebsiella
17	920	99.5	286	1	BLAT_ECOLI
18	920	99.5	286	1	BLAT_SALTI
19	920	99.5	286	2	Q53043 Klebsiella
20	920	99.5	286	2	Q8KSD3 Klebsiella
21	920	99.5	286	2	Q8VP43 Klebsiella
22	920	99.5	286	2	Q93328 Klebsiella
23	920	99.5	286	2	Q934D7 Klebsiella
24	920	99.5	286	2	Q93A77 Klebsiella
25	920	99.5	286	2	Q93G13 Klebsiella
26	920	99.5	286	2	Q6A253 Klebsiella
27	920	99.5	286	2	Q6LBN9 Klebsiella
28	920	99.5	286	2	Q6LBN9 Klebsiella
29	920	99.5	286	2	Q6LBN9 Klebsiella
30	920	99.5	286	2	Q6LBN9 Klebsiella
31	920	99.5	286	2	Q6WJ74 Klebsiella

32	920	99.5	286	2	Q6WJ1 Klebsiella
33	920	99.5	286	2	Q6WY2 Klebsiella
34	920	99.5	286	2	Q6WY4 Klebsiella
35	920	99.5	286	2	Q7B3X5 Klebsiella
36	920	99.5	286	2	Q7B899 Klebsiella
37	920	99.5	286	2	Q7B957 Klebsiella
38	920	99.5	286	2	Q7BR75 Klebsiella
39	920	99.5	286	2	Q7DFY3 Klebsiella
40	920	99.5	286	2	Q7DHD3 Klebsiella
41	920	99.5	286	2	Q844X1 Klebsiella
42	920	99.5	286	2	Q8GAB5 Klebsiella
43	920	99.5	286	2	Q9EYX1 Klebsiella
44	920	99.5	286	2	Q9K582 Klebsiella
45	920	99.5	286	2	Q9R770 Klebsiella

ALIGNMENTS

RESULT 1	PRELIMINARY	PRT	229 AA
Q6WY5			
ID Q6WY5			
AC Q6WY5			
DT 05-JUL-2004 (TRENBLrel. 27, Created)			
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)			
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)			
DE Beta-lactamase (Fragment).			
GN Name=BLATEM;			
OS Klebsiella oxytoca.			
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC Enterobacteriaceae; Klebsiella.			
OX NCBI_TaxID=571;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=MISC126;			
RA Ober C.A., Goldstone C.M., Gordon D.M., Riley M.A.;			
RL Submitted (Apr-2004) to the EMBL/Genbank/DBJ databases.			
DR EMBL; AY265885; AAP93843.1; ..			
DR HSRP; P00807; 1KGE.			
DR InterPro; IPR000871; Beta_lactamase_A.			
DR PRINTS; PR00118; BLACTAMASEA.			
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.			
FT NON_TER 1 1			
FT NON_TER 229 229			
SQ SEQUENCE 229 AA; 25067 MW; C85582C2617F4467 CRC64;			
Query Match 100.0%; Score 925; DB 2; Length 229;			
Best Local Similarity 100.0%; Pred. No. 1.7e-71;			
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY 1 HPEITLVKVKDABDQIGARVGITIEDLNSGKILSFRRPFRPMSTFVLLCGAVLSRID 60			
DB 2 HPEITLVKVKDABDQIGARVGITIEDLNSGKILSFRRPFRPMSTFVLLCGAVLSRID 61			
QY 61 AGQEQGRIRHSQNDLVESPVTEKHLTDGVTVEISAAITMSDNPANLLTTIGSP 120			
DB 62 AGQEQGRIRHSQNDLVESPVTEKHLTDGVTVEISAAITMSDNPANLLTTIGSP 121			
QY 121 KETLTFILNMGDHYTRLDREWEPELNEALPNDERDTTMEVAAATTLTKLTLTGELTLASRQ 180			
DB 122 KETLTFILNMGDHYTRLDREWEPELNEALPNDERDTTMEVAAATTLTKLTLTGELTLASRQ 181			
QY 181 Q 181			
DB 182 Q 182			
RESULT 2			
Q6WY4			
ID Q6WY4			
AC Q6WY4			
DT 05-JUL-2004 (TRENBLrel. 27, Created)			
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)			

DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Beta-lactamase (Fragment).
 GN Name=blatEM;
 OS Hafnia alvei.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Hafnia.
 OX NCBI_TaxID=569;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MISC198;
 RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
 RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY265886; AAP93844.1; -.
 DR HSSP; P00807; IKGE.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 FT NON_TER 1
 FT NON_TER 232
 SQ SEQUENCE 232 AA; 25380 MW; 3D5DFD85582C261 CRC64;

Query Match 100.0%; Score 925; DB 2; Length 232;
 Best Local Similarity 100.0%; Pred. No. 1.7e-71;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGAVGYIEIDLSGKILSFRRPERPMMSTFVLLCGAVLSRID 60
 DB 2 HPEITLVKVDADQAGAVGYIEIDLSGKILSFRRPERPMMSTFVLLCGAVLSRID 61
 QY 61 AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTIGP 120
 DB 62 AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTIGP 121
 QY 121 KELTAFILNMGDHVTRLDRWPEPELNEAIPNDRDITMPVAAATTLRKLLTGBLLTLASRQ 180
 DB 122 KELTAFILNMGDHVTRLDRWPEPELNEAIPNDRDITMPVAAATTLRKLLTGBLLTLASRQ 181
 QY 181 Q 181
 DB 182 Q 182

RESULT 3

Q6MWY8 PRELIMINARY; PRT; 241 AA.
 AC O6MWY8;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE Beta-lactamase (Fragment).
 GN Name=blatEM;
 OS Klebsiella pneumoniae.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Klebsiella.
 OX NCBI_TaxID=573;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MISC112;
 RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
 RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY265882; AAP93840.1; -.
 DR HSSP; P00807; IKGE.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 FT NON_TER 1
 FT NON_TER 241
 SQ SEQUENCE 241 AA; 26407 MW; 38DF2AFDF0C5807D CRC64;

Query Match 100.0%; Score 925; DB 2; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.8e-71;

Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HPEITLVKVDADQAGAVGYIEIDLSGKILSFRRPERPMMSTFVLLCGAVLSRID 60
 DB 7 HPEITLVKVDADQAGAVGYIEIDLSGKILSFRRPERPMMSTFVLLCGAVLSRID 66
 QY 61 AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTIGP 120
 DB 67 AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTIGP 126
 QY 121 KELTAFILNMGDHVTRLDRWPEPELNEAIPNDRDITMPVAAATTLRKLLTGBLLTLASRQ 180
 DB 127 KELTAFILNMGDHVTRLDRWPEPELNEAIPNDRDITMPVAAATTLRKLLTGBLLTLASRQ 186
 QY 181 Q 181
 DB 187 Q 187

RESULT 4

Q6MWY3 PRELIMINARY; PRT; 242 AA.
 AC O6MWY3;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE Beta-lactamase (Fragment).
 GN Name=blatEM;
 OS Escherichia coli.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TA005;
 RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
 RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY265887; AAP93845.1; -.
 DR HSSP; P00807; IKGE.
 DR InterPro; IPR001466; Beta_lactamase.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 FT NON_TER 1
 FT NON_TER 242
 SQ SEQUENCE 242 AA; 26554 MW; 38C3DFA8A5A3807D CRC64;

Query Match 100.0%; Score 925; DB 2; Length 242;
 Best Local Similarity 100.0%; Pred. No. 1.8e-71;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGAVGYIEIDLSGKILSFRRPERPMMSTFVLLCGAVLSRID 60
 DB 8 HPEITLVKVDADQAGAVGYIEIDLSGKILSFRRPERPMMSTFVLLCGAVLSRID 67
 QY 61 AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTIGP 120
 DB 68 AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTIGP 127
 QY 121 KELTAFILNMGDHVTRLDRWPEPELNEAIPNDRDITMPVAAATTLRKLLTGBLLTLASRQ 180
 DB 128 KELTAFILNMGDHVTRLDRWPEPELNEAIPNDRDITMPVAAATTLRKLLTGBLLTLASRQ 187
 QY 181 Q 181
 DB 188 Q 188

RESULT 5

Q6KB67 PRELIMINARY; PRT; 285 AA.
 AC Q6KB67;

DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Triticeae; Hordeum.
 OC NCBI_Taxid=4513;
 RX SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RA Jansen C., Korell M., Rckey C., Biedenkopf D., Kogel K.H.;
 RL Submitted (May-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ171739; CAG30723.1; -.
 DR HSP; P00807; IAUO.
 DR InterPro; IPR001466; Beta_lactamase.
 DR Pfam; PF00144; Beta_lactamase_A.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 KM Hypothetical protein.
 FT NON_TER 285
 SQ SEQUENCE 285 AA; 31371 MW; A2F22753375FA930 CRC64;
 Query Match 100.0%; Score 925; DB 2; Length 285;
 Best Local Similarity 100.0%; Pred. No. 2.2e-71;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HPEITLVKVDADQAGRVGYIELDLSGKILSFPRPERPFPMSTFKVLLCGAVLSRID 60
 DB 24 HPEITLVKVDADQAGRVGYIELDLSGKILSFPRPERPFPMSTFKVLLCGAVLSRID 83
 QY 61 AGQEQLGRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANILLTTIGP 120
 DB 84 AGQEQLGRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANILLTTIGP 143
 QY 121 KELITAFILNMGDHTVRLDRWPELNEALPNDERDITMPVAMATTIRKLLTGELLTLASRQ 180
 DB 144 KELITAFILNMGDHTVRLDRWPELNEALPNDERDITMPVAMATTIRKLLTGELLTLASRQ 203
 QY 181 Q 181
 DB 204 Q 204
 RESULT 6
 ID Q38058 PRELIMINARY; PRT; 286 AA.
 AC Q38058;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Beta lactamase.
 GN Name=bla;
 OS Bacteriophage phi-X174.
 OC Viruses; ssDNA viruses; Microviridae; Microvirus.
 OC NCBI_Taxid=10847;
 RX SEQUENCE FROM N.A.
 RP MEDLINE=95172401; PubMed=7867948; DOI=10.1016/0378-1119(94)00839-K;
 RA Henrich B., Schmitzberger B.;
 RT "A variant of phiX174 gene B-based positive selection vectors with
 RT enhanced lytic potential.";
 RL Gene 154:51-54(1995).
 DR EMBL; Z35638; CAA84692.1; -.
 DR PIR; S47061; S47061.
 DR HSP; Q9R435; 1HTZ.
 DR InterPro; IPR001466; Beta_lactamase.
 DR Pfam; PF00144; Beta_lactamase_A.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.

SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;
 Query Match 100.0%; Score 925; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 2.2e-71;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HPEITLVKVDADQAGRVGYIELDLSGKILSFPRPERPFPMSTFKVLLCGAVLSRID 60
 DB 24 HPEITLVKVDADQAGRVGYIELDLSGKILSFPRPERPFPMSTFKVLLCGAVLSRID 83
 QY 61 AGQEQLGRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANILLTTIGP 120
 DB 84 AGQEQLGRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANILLTTIGP 143
 QY 121 KELITAFILNMGDHTVRLDRWPELNEALPNDERDITMPVAMATTIRKLLTGELLTLASRQ 180
 DB 144 KELITAFILNMGDHTVRLDRWPELNEALPNDERDITMPVAMATTIRKLLTGELLTLASRQ 203
 QY 181 Q 181
 DB 204 Q 204
 RESULT 7
 ID Q00626 PRELIMINARY; PRT; 286 AA.
 AC Q00626; O08022; O08102; O09393; O09397; O09398; O09399;
 AC O09400; O09401; O09402; O09403; O09404; O09405; O09406; O09407;
 AC O09408; O09481; O09482; O09483; O09490; Q57339;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Beta-lactamase.
 OS Staphylococcus aureus.
 OG Plasmid J3356/POX7/3, and Plasmid J3356/POX7/1.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OC NCBI_Taxid=1280;
 RX SEQUENCE FROM N.A.
 RC PLASMID=J3356/POX7/3, and J3356/POX7/1;
 RX MEDLINE=96422755; PubMed=8825372; DOI=10.1006/plas.1995.0005;
 RA Needham C., Noble W.C., Dyke K.G.;
 RT "The staphylococcal insertion sequence IS257 is active.";
 RL Plasmid 34:198-205(1995).
 DR EMBL; U36912; AAB39957.1; -.
 DR EMBL; U36911; AAB39956.1; -.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 KW Plasmid.
 SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;
 Query Match 100.0%; Score 925; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 2.2e-71;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HPEITLVKVDADQAGRVGYIELDLSGKILSFPRPERPFPMSTFKVLLCGAVLSRID 60
 DB 24 HPEITLVKVDADQAGRVGYIELDLSGKILSFPRPERPFPMSTFKVLLCGAVLSRID 83
 QY 61 AGQEQLGRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANILLTTIGP 120
 DB 84 AGQEQLGRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANILLTTIGP 143
 QY 121 KELITAFILNMGDHTVRLDRWPELNEALPNDERDITMPVAMATTIRKLLTGELLTLASRQ 180
 DB 144 KELITAFILNMGDHTVRLDRWPELNEALPNDERDITMPVAMATTIRKLLTGELLTLASRQ 203
 QY 181 Q 181
 DB 204 Q 204

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RESULT 8
ID Q79CL6 PRELIMINARY; PRT: 286 AA.
AC Q79CL6;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Beta-lactamase.
GN Name=bla;
OS Methylobacillus flagellatum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Methylobacterales;
OC Methylobacterales; Methylobacillus.
OX NCBI_TaxID=405;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97074643; PubMed=8917070; DOI=10.1016/0378-1119(96)00114-X;
RA Serebrjtski I.G., Vassin V.M., Tsygankov Y.D.;
RT "Two new members of the B108 superfamily: cloning, sequencing and
RT expression of b108 genes of Methylobacillus flagellatum and
RT Corynebacterium glutamicum.";
RN Gene 175:15-22(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Serebrjtski I., Vassin V., Tsygankov Y.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U1280; AAC44581.1; -.
DR HSSP; P00807; IALQ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
SQ SEQUENCE 286 AA; 31557 MW; 5EB2F2275375FA9 CRC64;

Query Match 100.0%; Score 925; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.2e-71;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGARVGYIEIDLSGKILSFRRPFRPMMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKVKADBDQAGARVGYIEIDLSGKILSFRRPFRPMMSTFVLLCGAVLSRID 83
QY 61 AGQQLGRRIHYSQNDLVEYSPTVEKHLTDGWTVEILCSAITSNDTANALLTTIGSP 120
DB 84 AGQQLGRRIHYSQNDLVEYSPTVEKHLTDGWTVEILCSAITSNDTANALLTTIGSP 143
QY 121 KETLAFILNMGDHYTRLDREWEPELNEAIPNDRDITPMVANAATTLRKLLTGELLTLASRQ 180
DB 144 KETLAFILNMGDHYTRLDREWEPELNEAIPNDRDITPMVANAATTLRKLLTGELLTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 9
ID Q79DR3 PRELIMINARY; PRT: 286 AA.
AC Q79DR3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Mutant extended-spectrum beta-lactamase precursor (EC 3.5.2.6).
GN Name=bla; Synonyms=blatEM-116;
OS Escherichia coli.
OG Plasmid pBP4, and plasmid pCAPs.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN-K-12;
RA Manewannakul K., Manewannakul S., Ippen-Ihler K.;
RL Submitted (AUG-1991) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12; PLASMID=PRP4;
RA Rondot S., Anthony K., Dubel S., Ida N., Beyreuther K., Frost L.,
RA Little M., Breilting F.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC PLASMID=PCAPS;
RX MEDLINE=98189310; PubMed=9514792; DOI=10.1006/abio.1997.2558;
RA Schlieper D., Von Wilcken-Bergmann B., Schmidt M., Sobek H.,
RA Mueller-Hill B.;
RT "A positive selection vector for cloning of long polymerase chain
RT reaction fragments based on a lethal mutant of the csp gene
RT Escherichia coli.";
RL Anal. Biochem. 257:203-209(1998).
RN [4]
RP SEQUENCE FROM N.A.
RX PubMed=15243036;
RA Jeong S.H., Bae I.K., Lee J.H., Sohn S.G., Kang G.H., Jeon G.J.,
RA Kim Y.H., Jeong B.C., Lee S.H.;
RT "Molecular Characterization of Extended-Spectrum Beta-Lactamases
RT Produced by Clinical Isolates of Klebsiella pneumoniae and Escherichia
RT coli from a Korean Nationwide Survey.";
RL J. Clin. Microbiol. 42:2902-2906(2004).
DR EMBL; M74750; AAA24057.1; -.
DR EMBL; AJ001614; CAA73226.1; -.
DR EMBL; AY425988; AAG95605.1; -.
DR HSSP; P00807; IALQ.
DR GO; GO:000800; F:beta-lactamase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW Hydrolase; Plasmid; Signal.
FT SIGNAL 1 23 Potential.
SQ SEQUENCE 286 AA; 31557 MW; 5EB2F2275375FA9 CRC64;

Query Match 100.0%; Score 925; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.2e-71;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGARVGYIEIDLSGKILSFRRPFRPMMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKVKADBDQAGARVGYIEIDLSGKILSFRRPFRPMMSTFVLLCGAVLSRID 83
QY 61 AGQQLGRRIHYSQNDLVEYSPTVEKHLTDGWTVEILCSAITSNDTANALLTTIGSP 120
DB 84 AGQQLGRRIHYSQNDLVEYSPTVEKHLTDGWTVEILCSAITSNDTANALLTTIGSP 143
QY 121 KETLAFILNMGDHYTRLDREWEPELNEAIPNDRDITPMVANAATTLRKLLTGELLTLASRQ 180
DB 144 KETLAFILNMGDHYTRLDREWEPELNEAIPNDRDITPMVANAATTLRKLLTGELLTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 10
ID Q38212 PRELIMINARY; PRT: 225 AA.
AC Q38212;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Bacteriophage f1-R208 amplicillinase gene mutation. (Fragment).

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OS Bacteriophage f1.
 OC Viruses; ssDNA viruses; Inoviridae; Inovirus.
 OX NCBI_TaxID=10863;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86278026; PubMed=3525535;
 RA Topal M.D., Badie J.S., Conrad M.;
 RT "O-6-methylguanine mutation and repair is nonuniform: Selection for
 DNA most interactive with O-6-methylguanine.";
 RL J. Biol. Chem. 261:9879-9885(1986).
 DR HSSP; M14017; AAA32208.1; -.
 DR HSSP; Q9R435; 1HTZ.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 FT NON_TER
 SQ SEQUENCE 225 AA; 25022 MW; 009BF841D618A09 CRC64;

Query Match 99.5%; Score 920; DB 2; Length 225;
 Best Local Similarity 98.9%; Pred. No. 4.5e-71;
 Matches 179; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HPETLVKVDADQLGARVGYIELDLSGKILESFRPERFPMMSTFKYLLCGAVLSRID 60
 |||||
 DB 24 HPETLVKVDADQLGARVGYIELDLSGKILESFRPERFPMMSTFKYLLCGAVLSRD 83
 |||||
 OY 61 AGQEQIGRRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTNANILLTTIGSP 120
 |||||
 DB 84 AGQEQIGRRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTNANILLTTIGSP 143
 |||||
 OY 121 KELLTAFLHMGDHVTRLDRWEPELNEAIPNDRDITMPAAMATTIRKLLTGELTLASRQ 180
 |||||
 DB 144 KELLTAFLHMGDHVTRLDRWEPELNEAIPNDRDITMPAAMATTIRKLLTGELTLASRQ 203
 |||||
 OY 181 Q 181
 |||||
 DB 204 Q 204
 |||||

RESULT 11
 O6PRU7 PRELIMINARY; PRT; 232 AA.
 AC O6PRU7; 05-JUN-2004 (TrEMBLrel. 27, Created)
 DT 05-JUN-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUN-2004 (TrEMBLrel. 27, Last annotation update)
 DE Inhibitor-resistant TEM beta-lactamase (Fragment).
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=U3;
 RA Chandil S., Hoessein-Mazinani S.M.;
 RL Submitted (Mar-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY583761; AAS86427.1; -.
 DR HSSP; P00807; 1ALQ.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 FT NON_TER
 SQ SEQUENCE 232 AA; 25558 MW; 5791CD285E70DB0 CRC64;

Query Match 99.5%; Score 920; DB 2; Length 232;
 Best Local Similarity 98.9%; Pred. No. 4.6e-71;
 Matches 179; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HPETLVKVDADQLGARVGYIELDLSGKILESFRPERFPMMSTFKYLLCGAVLSRID 60
 |||||
 DB 15 HPETLVKVDADQLGARVGYIELDLSGKILESFRPERFPMMSTFKYLLCGAVLSRD 74
 |||||
 OY 61 AGQEQIGRRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTNANILLTTIGSP 120
 |||||
 DB 75 AGQEQIGRRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTNANILLTTIGSP 134
 |||||
 OY 121 KELLTAFLHMGDHVTRLDRWEPELNEAIPNDRDITMPAAMATTIRKLLTGELTLASRQ 180
 |||||
 DB 135 KELLTAFLHMGDHVTRLDRWEPELNEAIPNDRDITMPAAMATTIRKLLTGELTLASRQ 194
 |||||
 OY 181 Q 181
 |||||
 DB 195 Q 195
 |||||

RESULT 12
 O84H50 PRELIMINARY; PRT; 255 AA.
 AC O84H50;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE TEM-117 beta-lactamase (Fragment).
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Box A.T.A., Paauw A., Laverstein-van Hall M.A.;
 RL Submitted (Jul-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF130282; AAN05026.1; -.
 DR HSSP; Q9R435; 1HTZ.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 255 AA; 27906 MW; DCBB28B65978C3A6 CRC64;

Query Match 99.5%; Score 920; DB 2; Length 255;
 Best Local Similarity 98.9%; Pred. No. 5.2e-71;
 Matches 179; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HPETLVKVDADQLGARVGYIELDLSGKILESFRPERFPMMSTFKYLLCGAVLSRID 60
 |||||
 DB 12 HPETLVKVDADQLGARVGYIELDLSGKILESFRPERFPMMSTFKYLLCGAVLSRD 71
 |||||
 OY 61 AGQEQIGRRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTNANILLTTIGSP 120
 |||||
 DB 72 AGQEQIGRRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTNANILLTTIGSP 131
 |||||
 OY 121 KELLTAFLHMGDHVTRLDRWEPELNEAIPNDRDITMPAAMATTIRKLLTGELTLASRQ 180
 |||||
 DB 133 KELLTAFLHMGDHVTRLDRWEPELNEAIPNDRDITMPAAMATTIRKLLTGELTLASRQ 191
 |||||
 OY 181 Q 181
 |||||
 DB 192 Q 192
 |||||

RESULT 13
 O84H49 PRELIMINARY; PRT; 261 AA.
 AC O84H49;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE TEM-110 beta-lactamase (Fragment).
 FT NON_TER

OS Klebsiella oxytoca.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Klebsiella.
 OX NCBI_TaxID=571;
 RN
 RP SEQUENCE FROM N.A.
 RA Box A.T.A., Pauw A., Leverstein-Vanhal M.A., Verhoef J., Fluit A.C.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY130283; AAN05027.1; -
 DR HSSP: Q9R435; 1HTZ.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR000871; Beta_lactamase_A.
 DR Pfam: PF00144; Beta_lactamase; 1.
 DR PRINTS: PR00118; BLACTAMASEA.
 DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
 FT NON TER 1
 FT NON TER 261
 SQ SEQUENCE 261 AA; 28738 MW; 4F748F773A08CBB CRC64;

Query Match 99.5%; Score 920; DB 2; Length 261;
 Best Local Similarity 98.9%; Pred. No. 5.3e-71;
 Matches 179; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HPEITLVKVKADQDQAGVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
 DB 12 HPEITLVKVKADQDQAGVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 71
 OY 61 AGOELGRIRHYSONDLVEYSPVTEKHLTDGMTVRELCSAATWSDNTAANLLTTIGSP 120
 DB 72 AGOELGRIRHYSONDLVEYSPVTEKHLTDGMTVRELCSAATWSDNTAANLLTTIGSP 131
 OY 121 KELTAFLLNMGDHYTRLDRWPEPELNEAIPNDRDPTMPVAMATTLRKLLTGELLTLASRQ 180
 DB 132 KELTAFLLNMGDHYTRLDRWPEPELNEAIPNDRDPTMPVAMATTLRKLLTGELLTLASRQ 191
 OY 181 Q 181
 DB 192 Q 192

RESULT 14
 Q6PRU6 PRELIMINARY; PRT; 264 AA.
 ID Q6PRU6
 AC Q6PRU6
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE TEM beta-lactamase (Fragment).
 DE Acinetobacter sp. U1.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Moraxellaceae; Acinetobacter.
 OX NCBI_TaxID=269266;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=U1;
 RA Chandali S., Hoeselini-Mazinani S.M.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY583762; AAS6428.1; -
 DR HSSP: P00807; 1ALQ.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR000871; Beta_lactamase_A.
 DR Pfam: PF00144; Beta_lactamase; 1.
 DR PRINTS: PR00118; BLACTAMASEA.
 DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
 FT NON TER 1
 FT NON TER 264
 SQ SEQUENCE 264 AA; 28986 MW; AAF071CF7489352C CRC64;

Query Match 99.5%; Score 920; DB 2; Length 264;
 Best Local Similarity 98.9%; Pred. No. 5.4e-71;
 Matches 179; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HPEITLVKVKADQDQAGVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60

DB 12 HPEITLVKVKADQDQAGVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 71
 OY 61 AGOELGRIRHYSONDLVEYSPVTEKHLTDGMTVRELCSAATWSDNTAANLLTTIGSP 120
 DB 72 AGOELGRIRHYSONDLVEYSPVTEKHLTDGMTVRELCSAATWSDNTAANLLTTIGSP 131
 OY 121 KELTAFLLNMGDHYTRLDRWPEPELNEAIPNDRDPTMPVAMATTLRKLLTGELLTLASRQ 180
 DB 132 KELTAFLLNMGDHYTRLDRWPEPELNEAIPNDRDPTMPVAMATTLRKLLTGELLTLASRQ 191
 OY 181 Q 181
 DB 192 Q 192

RESULT 15
 Q6QIV0 PRELIMINARY; PRT; 281 AA.
 ID Q6QIV0
 AC Q6QIV0
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE TEM-1 beta-lactamase (Fragment).
 GN Name=blatEM-1;
 OS Serratia marcescens.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Serratia.
 OX NCBI_TaxID=615;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=ES-42, ES-46, ES-71, and ES-11;
 RA Yacuyuanagi J., Saito S., Harata S., Suzuki N., Amano K.-I.;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY538700; AAS46846.1; -
 DR EMBL: AY538701; AAS46847.1; -
 DR EMBL: AY538702; AAS46848.1; -
 DR EMBL: AY538698; AAS46844.1; -
 DR HSSP: P00807; 1ALQ.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR000871; Beta_lactamase_A.
 DR Pfam: PF00144; Beta_lactamase; 1.
 DR PRINTS: PR00118; BLACTAMASEA.
 DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
 FT NON TER 281
 FT NON TER 281
 SQ SEQUENCE 281 AA; 30837 MW; C6934B9C696057BP CRC64;

Query Match 99.5%; Score 920; DB 2; Length 281;
 Best Local Similarity 98.9%; Pred. No. 5.8e-71;
 Matches 179; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HPEITLVKVKADQDQAGVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
 DB 24 HPEITLVKVKADQDQAGVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
 OY 61 AGOELGRIRHYSONDLVEYSPVTEKHLTDGMTVRELCSAATWSDNTAANLLTTIGSP 120
 DB 84 AGOELGRIRHYSONDLVEYSPVTEKHLTDGMTVRELCSAATWSDNTAANLLTTIGSP 143
 OY 121 KELTAFLLNMGDHYTRLDRWPEPELNEAIPNDRDPTMPVAMATTLRKLLTGELLTLASRQ 180
 DB 144 KELTAFLLNMGDHYTRLDRWPEPELNEAIPNDRDPTMPVAMATTLRKLLTGELLTLASRQ 203
 OY 181 Q 181
 DB 204 Q 204

Search completed: June 10, 2005, 10:57:00
 Job time : 61.6383 secs

XX (PANO-) PANORAMA RES INC.
PA
XX

XX Balint RF, Her J;
PI
XX

XX WPI: 2001-451857/48.
DR
XX N-PSDB; AAD10411.
DR

XX Interaction-dependent enzyme association systems for detecting
PT interactions between two or three polypeptides, especially in human
PT therapeutics, diagnostics or prognostics, comprise circularly permuted
PT proteins.

XX Claim 38; Fig 2; 104bp; English.
PS
XX

XX The invention relates to new interaction-dependent enzyme association
CC (IdRA) systems that comprise a fusion sequence that encodes for a
CC circularly permuted, interaction-activated proteins that reassemble to
CC form functionally reconstituted marker proteins which produce a
CC detectable signal upon the association of two oligopeptides, or upon
CC simultaneous association of two oligopeptides with a third oligopeptide.
CC The marker protein is preferably a type A beta-lactamase, especially TEM-
CC 1 beta-lactamase of *Escherichia coli*. The oligopeptide is a member of a
CC proteome library selected from single chain antibody Fv fragment library,
CC an antibody light chain variable region library and a peptide library
CC displayed within thioredoxin. The IdRA systems are useful for detecting
CC and identifying interactions between intracellular as well as
CC extracellular proteins, particularly between two or three polypeptides.
CC The systems are also useful in selecting with a single marker protein the
CC incorporation of multiple genetic traits in a host cell. In particular,
CC the systems are useful in many applications in human therapeutics,
CC diagnostics and prognostics, as well as in high-throughput screening
CC systems for the discovery and validation of pharmaceutical targets and
CC drugs. Prior systems (e.g. E. coli Dimer Detection System, Yeast two-
CC hybrid system or Selective Infective Phage System) require multiple steps
CC between interaction and phenotype, which cause severe loss of efficiency
CC due to high false positive and false negative rates. The present system
CC is capable of simultaneous detection of multiple interactions between
CC extra-cellular as well as intracellular proteins in a high throughput
CC format. The circularly permuted marker proteins comprising interaction-
CC dependent enzymes find use in cell-based sensors for activation or
CC inhibition of metabolic or signal transduction pathways, in high-
CC throughput mapping of pair-wise protein-protein interactions within and
CC between the proteomes of cells, tissues and pathogenic organisms, and in
CC cell-based screens for high-throughput selection of inhibitors of any
CC protein-protein interaction. The present sequence is *Escherichia coli*
CC mature TEM-1 beta-lactamase enzyme from plasmid pBR322. TEM-1 beta-
CC lactamase is a product of ampicillin resistance gene. The enzyme has two
CC domains, alpha-omega and mu
XX
XX

XX Sequence 263 AA;

XX Query Match 100.0%; Score 975; DB 4; Length 263;
XX Best Local Similarity 100.0%; Pred. No. 6.6e-98;

XX Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADDOAGARVGYIELDINSKILLESFRPERPMMSTFFKVLGCAVLSRID 60
DB 1 HPEITLVKVDADDOAGARVGYIELDINSKILLESFRPERPMMSTFFKVLGCAVLSRID 60
QY 61 AGOEOLGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANILLTTIGCP 120
DB 61 AGOEOLGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANILLTTIGCP 120
QY 121 KELTAFILNMGDHYTRLDRWPELNEALPNDERDITPMVAAATTIRKLLTGELLTLASRQ 180
DB 121 KELTAFILNMGDHYTRLDRWPELNEALPNDERDITPMVAAATTIRKLLTGELLTLASRQ 180
QY 181 QLIIDWMEADK 190
DB 181 QLIIDWMEADK 190

RESULT 2
AAB36692
ID AAB36692 standard; protein; 263 AA.
XX

XX AAB36692;
AC
XX

XX 15-MAR-2001 (first entry)
DT
XX

XX *Escherichia coli* mature TEM-1 beta-lactamase protein sequence.
DE

XX Interaction-activated protein; beta-lactamase; protein interaction.
KW

XX *Escherichia coli*.
OS

XX WO200071702-A1.
PN

XX 30-NOV-2000.
PD

XX 16-MAR-2000; 2000WO-US007108.
PF

XX 25-MAY-1999; 99US-0135926P.
PR

XX 13-JAN-2000; 2000US-0175968P.
PR

XX (PANO-) PANORAMA RES INC.
PA

XX Balint RF, Her J;
PI

XX WPI: 2001-032034/04.
DR

XX N-PSDB; AAC90773.
DR

XX Novel fragment complementation system to identify interactions between
PT polypeptides comprises fragment pairs having first and second members
PT that reassemble into a marker protein which has a directly detectable
PT signal.

XX Disclosure: Fig 2; 94bp; English.
PS

XX The present invention describes a fragment complementation system (I)
CC which comprises a first oligopeptide (OP1) containing an N-terminal
CC fragment with a C-terminal break point and a second oligopeptide (OP2)
CC comprising a C-terminal with a N-terminal breakpoint, in which the C and
CC N terminal fragments are both derived from a marker protein (MP) and
CC reassemble to form a functionally reconstituted MP. Methods from the
CC present invention are used for monitoring the occurrence of protein-
CC protein interactions in a sample, identifying oligopeptide interactions
CC between two different proteomes, identifying epitopes that bind to an
CC immunoglobulin (Ig) variable region, for identifying interactions between
CC an extracellular domain of a transmembrane protein and a polypeptide, for
CC high-throughput identification of compounds that inhibit phosphorylation/
CC regulated signal transducers, forming a enzyme complementation system for
CC selecting simultaneous incorporation of multiple genetic elements into a
CC host cell and for activating a beta-lactam derivative of an antitumor
CC compound in a host who is in need of it. The present sequence represents
CC the *Escherichia coli* mature TEM-1 beta-lactamase, which is used in the
CC exemplification of the present invention
XX
XX

XX Sequence 263 AA;

XX Query Match 100.0%; Score 975; DB 4; Length 263;
XX Best Local Similarity 100.0%; Pred. No. 6.6e-98;

XX Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADDOAGARVGYIELDINSKILLESFRPERPMMSTFFKVLGCAVLSRID 60
DB 1 HPEITLVKVDADDOAGARVGYIELDINSKILLESFRPERPMMSTFFKVLGCAVLSRID 60
QY 61 AGOEOLGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANILLTTIGCP 120
DB 61 AGOEOLGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANILLTTIGCP 120
QY 121 KELTAFILNMGDHYTRLDRWPELNEALPNDERDITPMVAAATTIRKLLTGELLTLASRQ 180
DB 121 KELTAFILNMGDHYTRLDRWPELNEALPNDERDITPMVAAATTIRKLLTGELLTLASRQ 180

Qy 181 QLIDWMEADK 190
 Db 181 QLIDWMEADK 190

RESULT 3
 ADJ67709
 ID ADJ67709 standard; protein; 263 AA.
 XX
 AC ADJ67709;
 DT 20-MAY-2004 (first entry)
 XX
 DE Escherichia coli TEM-1 beta-lactamase.

fragment complementation system; marker protein;
 multiple genetic element incorporation; antibiotic resistance;
 beta-lactam derivative activation; anti-tumour compound;
 functional assembly; protein-protein interaction; proteome interaction;
 immunoglobulin variable region; immune cell protein; CD40;
 immunophorlation-regulated cell signal transducer; TEM-1 beta-lactamase;
 enzyme.
 KM Escherichia coli.
 XX
 OS US2004038317-A1.
 XX
 PN 26-FEB-2004.
 XX
 PD 22-SEP-2003; 2003US-00668778.
 XX
 PF 15-MAR-1999; 99US-0124339P.
 XX
 PR 25-MAY-1999; 99US-0135826P.
 XX
 PR 13-JAN-2000; 2000US-0175968P.
 XX
 PR 15-MAR-2000; 2000US-00526106.
 XX
 PA (KALO-) KALOBIOS INC.
 XX
 PI Balint RF, Her J;
 XX
 DR WPI; 2004-203222/19.
 XX
 DR N-PSDB; ADJ67708.
 XX
 PT
 PT
 PT

Fragment complementation system for detecting immunoglobulin epitope, has
 first oligopeptide containing N-terminal fragment with C-terminal break-
 point, second oligopeptide containing C-terminal fragment with N-terminal
 break-point.
 PS Disclosure; SEQ ID NO 2; 47pp; English.

The invention describes a fragment complementation system (I) comprising
 a first oligopeptide having an N-terminal fragment with a C-terminal
 break-point, and a second oligopeptide having a C-terminal fragment with
 a N-terminal break-point, where the N-terminal fragment and the C-
 terminal fragment each are derived from a marker protein and the C-
 terminal fragment is functionally reconstituted marker protein. (I) is useful for
 selecting simultaneous incorporation of multiple genetic elements into a
 host cell, and activating a beta-lactam derivative of an anti-tumour
 compound in a host. The method described is useful for identifying a
 second oligopeptide to which a first oligopeptide binds, involving co-
 expressing the first and second oligopeptides. Binding of the first
 oligopeptide to the second oligopeptide results in the functional
 reassembly of the marker protein. The method is also useful for
 monitoring the occurrence of protein-protein interactions in a sample;
 identifying oligopeptide interactions between two different proteomes;
 and identifying epitopes that bind to an immunoglobulin variable region.
 (I) or an expression cassette (II), encoding a selectable N or C-terminal
 peptide, is useful for identifying interactions between an extra cellular
 domain of a transmembrane protein and a polypeptide, where the
 transmembrane protein is an immune cell protein, preferably CD40. (I) or
 (II) is useful for high-throughput identification of compound that
 inhibit phosphorylation-regulated cell signal transducers. (I)

CC efficiently detects multiple interaction between extracellular and
 CC intracellular protein with high throughput format. This is the amino acid
 CC sequence of antibiotic resistance enzyme TEM-1 beta-lactamase that can be
 CC used as a selectable gene in the fragment complementation system of the
 CC invention.
 XX
 XX

Sequence 263 AA;

Query Match 100.0%; Score 975; DB 8; Length 263;
 Best Local Similarity 100.0%; Pred. No. 6,66-98;
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPETLVKVDADQLGARVGYIELDLNSGKILESFRPERFPMSSTFKYLLCGAVLSRID 60
 Db 1 HPETLVKVDADQLGARVGYIELDLNSGKILESFRPERFPMSSTFKYLLCGAVLSRID 60
 Qy 61 ACOEQLGRRIHYSQNDLVESPYTEKHLTDGMTVRELCSAATITMSDNTNANILLTTIGSP 120
 Db 61 ACOEQLGRRIHYSQNDLVESPYTEKHLTDGMTVRELCSAATITMSDNTNANILLTTIGSP 120
 Qy 121 KELLTAFLHMGDHYTRLDRWEPELNEAIPNDSRDITMPVAMATTLRKLLTGEELTLASRQ 180
 Db 121 KELLTAFLHMGDHYTRLDRWEPELNEAIPNDSRDITMPVAMATTLRKLLTGEELTLASRQ 180
 Qy 181 QLIDWMEADK 190
 Db 181 QLIDWMEADK 190

RESULT 4
 AAM16634
 ID AAM16634 standard; protein; 264 AA.
 XX
 AC AAM16634;
 XX
 DT 09-AUG-1997 (first entry)
 XX
 XX
 DE Beta-lactamase (including signal peptide).
 XX
 KM Gene directed enzyme prodnug therapy; GDSPT;
 KM virus directed enzyme prodnug therapy; VDSPT; beta-lactamase; cancer;
 KM HIV; inflammation.
 XX
 OS Escherichia coli.
 XX
 FH Key
 FT Peptide
 FT 1..23
 XX
 XX //label= Sig_peptide

MO9719180-A2.
 XX
 PD 29-MAY-1997.
 XX
 PF 19-NOV-1996; 96WO-GB002845.
 XX
 PR 20-NOV-1995; 95GB-00023703.
 XX
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Dev I, Moore JT, Ohmstede C;
 XX
 DR WPI; 1997-298117/27.
 XX
 DR N-PSDB; AAT66736.
 XX
 XX Molecular chimera for gene or virus directed enzyme prodnug therapy -
 PT useful for treatment of cancer, viral infection or inflammation.
 PT
 XX Example; Page 28; 38pp; English.
 PS Escherichia coli beta-lactamase (AAM16634), including the signal peptide,
 CC is the expression product of a molecular chimera, designated pCMV-BL
 CC (AAT66737), in which the beta-lactamase gene is under control of the
 CC intermediate/early promoter. Vectors consisting of a transcriptional

CC regulatory DNA sequence linked to a beta-lactamase gene can be used for
 CC enzyme producing therapy. Expression of the beta-lactamase in a targeted
 CC cell allows conversion of a producing into an agent toxic to the cell for
 CC treatment of cancer, viral (e.g. HIV) infection or inflammation.
 CC Secretion of the enzyme has the advantage of increasing neighbouring cell
 CC kill

XX Sequence 264 AA;

Query Match 100.0%; Score 975; DB 2; Length 264;
 Best Local Similarity 100.0%; Pred. No. 6,6e-98;
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGARVGYIELDNSGKILLESFRPERPFPMSSTFKVLLCGAVLSRID 60

DB 2 HPEITLVKVKADBDQAGARVGYIELDNSGKILLESFRPERPFPMSSTFKVLLCGAVLSRID 61

QY 61 AGGEGGRRIRHYSQNDLVEYSPTTEKHLTDGMYRELCSAATWSDNTAANILLTTIGCP 120

DB 62 AGGEGGRRIRHYSQNDLVEYSPTTEKHLTDGMYRELCSAATWSDNTAANILLTTIGCP 121

QY 121 KELTAFILNMGDHYTRLDRWPELNEALPNDERDITMPVAAATTLTKLLTSELTLASRQ 180

DB 122 KELTAFILNMGDHYTRLDRWPELNEALPNDERDITMPVAAATTLTKLLTSELTLASRQ 181

QY 181 QLIDWMEADK 190

DB 182 QLIDWMEADK 191

RESULT 5
 AAM18680
 ID AAM18680 standard; protein; 264 AA.

XX AAM18680;

DT 13-AUG-1997 (first entry)

XX Intracellularly-expressed beta-lactamase.

XX Producing therapy; gene directed enzyme producing therapy; GDEPT;

KM virus directed enzyme producing therapy; VDEPT; lung cancer;

XX beta-lactamase; PCMV-delBL.

OS Escherichia coli.

PN W09719183-A2.

PD 29-MAY-1997.

XX 19-NOV-1996; 96WO-GB002846.

PR 20-NOV-1995; 95GB-00023703.

PA (GLAX) GLAXO GROUP LTD.

PI Dev I, Moore JT, Sethna PB;

DR WPI, 1997-298118/27.

XX N-PSDB; AAT70311.

PT DNA construct for gene-directed enzyme producing therapy of lung cancer -

PS comprises lung- or neuroendocrine-specific promoter controlling

PT expression of producing-converting enzyme.

XX Example 811; Page 32-34; 53pp; English.

CC The intracellular form (AAM18680) of TEM beta-lactamase is expressed by
 CC PCMV-delBL (AAT70311) in which a PCR-amplified beta-lactamase coding
 CC sequence, minus the signal sequence, is placed under control of the
 CC intermediate/early promoter of cytomegalovirus. Intracellular beta-
 CC lactamase constructs, placed under control of promoter/enhancer elements
 CC of lung-associated protein or neuroendocrine marker protein genes, can be

CC used in novel chimaeric molecules for use in producing therapy of lung
 CC cancer

XX Sequence 264 AA;

XX Sequence 264 AA;

Query Match 100.0%; Score 975; DB 2; Length 264;
 Best Local Similarity 100.0%; Pred. No. 6,6e-98;
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGARVGYIELDNSGKILLESFRPERPFPMSSTFKVLLCGAVLSRID 60

DB 2 HPEITLVKVKADBDQAGARVGYIELDNSGKILLESFRPERPFPMSSTFKVLLCGAVLSRID 61

QY 61 AGGEGGRRIRHYSQNDLVEYSPTTEKHLTDGMYRELCSAATWSDNTAANILLTTIGCP 120

DB 62 AGGEGGRRIRHYSQNDLVEYSPTTEKHLTDGMYRELCSAATWSDNTAANILLTTIGCP 121

QY 121 KELTAFILNMGDHYTRLDRWPELNEALPNDERDITMPVAAATTLTKLLTSELTLASRQ 180

DB 122 KELTAFILNMGDHYTRLDRWPELNEALPNDERDITMPVAAATTLTKLLTSELTLASRQ 181

QY 181 QLIDWMEADK 190

DB 182 QLIDWMEADK 191

RESULT 6
 AAR31575
 ID AAR31575 standard; protein; 286 AA.

XX AAR31575;

DT 10-MAR-2003 (revised)

XX 04-JUN-1993 (first entry)

XX Ampicillin resistance protein.

XX CYP1A1; PRNH127; PRNH155; xeroderma pigmentosum group A; XPA;

KM xenobiotics; circular; chimeric cytochrome P4501A1.

XX Homo sapiens.

PN US5180666-A.

PD 19-JAN-1993.

XX 27-JUN-1991; 91US-00721775.

PR 27-JUN-1991; 91US-00721775.

PA (UYWA-) UNIV WAYNE STATE.

PI States JC, Hines RN, Novak RF;

DR WPI, 1993-052845/06.

XX N-PSDB; AAQ36498.

PT In vitro method for testing mutagenicity of a chemical - by metabolising

PS chemical cell line consisting of transformed fibroblasts having

PT detectable cytochrome P450 mixed function oxidase activity and detecting

XX gene damage.

XX Disclosure; Col 21-24; 24pp; English.

CC The expression constructs PRNH127 and PRNH155 contain identical sequences
 CC but were constructed using different strategies (see AAQ36498). The
 CC constructs comprise exons 2-7 of human CYP1A1 gene under the control of
 CC the inducible mouse metallothionein (MT-1) promoter. The constructs also
 CC contain an open reading frame in the opposite orientation to the
 CC cytochrome P450 exons. This ORF encodes ampicillin resistance. The
 CC constructs are suitable for transformation of human fibroblasts derived
 CC from the xeroderma pigmentosum group A. Cultures of the transformed
 CC fibroblasts can be used to test substances for mutagenicity. The presence

CC of the inducible cytochrome P450 gene allows metabolism of the substance
CC to mutagenic metabolites. (Updated on 10-MAR-2003 to add missing OS
CC field.)
XX
SQ Sequence 286 AA;
Query Match 100.0%; Score 975; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 7.4e-98;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEITLVKVDADQAGARVGYIELDLSGKILSPRPERFPMWSTFKVLLCGAVLSRD 60
DB 24 HPEITLVKVDADQAGARVGYIELDLSGKILSPRPERFPMWSTFKVLLCGAVLSRD 83
QY 61 AGQEQLGRIIRHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQEQLGRIIRHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILHMGDVTRLDRWEPDELNEAIPNDRDITMPVAMATTLLKLTGELLTLASRQ 180
DB 144 KELTAFILHMGDVTRLDRWEPDELNEAIPNDRDITMPVAMATTLLKLTGELLTLASRQ 203
QY 181 QLIIDWMEADK 190
DB 204 QLIIDWMEADK 213
RESULT 7
AAR97619
ID AAR97619 standard; protein; 286 AA.
XX
AC AAR97619;
XX
DT 20-AUG-1996 (first entry)
XX
DE Secretory beta-lactamase.
XX
KW Gene therapy; gene directed enzyme prodnrg therapy; GDEPT;
KW virus directed enzyme prodnrg therapy; VDEPT; prodnrg activation;
KW cytotoxic; cytostatic; cancer; tumour; retrovirus; vector;
KW beta-lactamase; cephalosporin.
XX
OS Synthetic.
XX
FN W09616179-A1.
XX
PD 30-MAY-1996.
XX
PF 20-NOV-1995; 95WO-GB002716.
XX
PR 18-NOV-1994; 94GB-00023367.
XX
PA (WEILL) WEILLCOMB FOUND LTD.
XX
PI Dev IK, Moore JT, Ohmstede C;
XX
DR WPI; 1996-268615/27.
XX
DR N-PSDB; AAT92920.
XX
PT Molecular chimera for use in enzyme gene therapy - is activated in a
PT target cell to express a secretable enzyme which cleaves a prodnrg
PT outside the cell into a cytotoxic or cytostatic agent.
XX
PS Example 3; Page 57-58; 73pp; English.
XX
CC A secretory beta-lactamase (AAR97619) is expressed from DNA construct
CC PCMW-BL (AAT92920), in which the beta-lactamase coding sequence is under
CC the control of the intermediate/early cytomagalovirus promoter. Beta-
CC lactamase delivery to mammalian cells confers sensitivity to
CC cephalosporin prodnrgs. Liposomal DNA/5-fluorouracil prodnrg combinations
CC resulted in s.c. tumour regression in mice bearing A549 tumours. Survival
CC of mice bearing human large cell lung H460 intrathoracic (i.t.) tumours
CC was increased upon i.t. injection of the secretory beta-lactamase DNA

CC construct
XX
SQ Sequence 286 AA;
Query Match 100.0%; Score 975; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 7.4e-98;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEITLVKVDADQAGARVGYIELDLSGKILSPRPERFPMWSTFKVLLCGAVLSRD 60
DB 24 HPEITLVKVDADQAGARVGYIELDLSGKILSPRPERFPMWSTFKVLLCGAVLSRD 83
QY 61 AGQEQLGRIIRHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQEQLGRIIRHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILHMGDVTRLDRWEPDELNEAIPNDRDITMPVAMATTLLKLTGELLTLASRQ 180
DB 144 KELTAFILHMGDVTRLDRWEPDELNEAIPNDRDITMPVAMATTLLKLTGELLTLASRQ 203
QY 181 QLIIDWMEADK 190
DB 204 QLIIDWMEADK 213
RESULT 8
AAR96423
ID AAR96423 standard; protein; 286 AA.
XX
AC AAR96423;
XX
DT 25-MAR-2003 (revised)
DT 25-NOV-1996 (first entry)
XX
DB Cytochrome P450 (CYP1A1 construct).
XX
KW cytochrome; P450; metallothionein; mouse; human; cytotoxicity; assay;
KW metabolism.
XX
OS Homo sapiens.
XX
PN US5525482-A.
XX
PD 11-JUN-1996.
XX
PF 15-NOV-1994; 94US-00339658.
XX
PR 27-JUN-1991; 91US-00721775.
XX
PR 09-DEC-1992; 92US-00990295.
XX
PA (UYMA-) UNITV WAYNE STATE.
XX
PI Hines RN, Novak RF, States JC;
XX
DR WPI; 1996-286397/29.
XX
DR N-PSDB; AAT30354.
XX
PT Testing chemicals for cytotoxicity to human by detecting gene damage -
PT using recombinant fibroblasts transformed with cytochrome P450 gene under
PT control of inducible promoter.
XX
PS Disclosure; Col 17-24; 26pp; English.
XX
CC The present sequence is encoded by a chimeric mouse metallothionein-
CC cytochrome P450Ia1 (CYP1A1) expression construct. Two clones, pRNH127 and
CC pRNH15, were isolated by different methods and which both had the same
CC sequence. The CYP1A1 construct is used in assays to test for cytotoxicity
CC of humans to a chemical. The method comprises exposing human fibroblast
CC cells normally not including any cytochrome P450 activity to potentially
CC toxic chemicals. The cells having been transformed to express cytochrome
CC P450, under the control of a controllable promoter through the CYP1A1
CC gene, upon exposure to the chemical in vitro. The chemical is metabolised
CC intracellularly into a cytochrome metabolite by oxidation within the

CC fibroblasts through the intracellular cytochrome P450 mixed function
 CC oxidase enzymes expressed by the cells. Gene damage in the test cells is
 CC detected as an indication of cytotoxicity of the chemical. (Updated on 25
 CC -MAR-2003 to correct PF field.)

XX Sequence 286 AA;

Query Match 100.0%; Score 975; DB 2; Length 286;

Best Local Similarity 100.0%; Pred. No. 7.4e-98;
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 HPEITLVKVKDAEDQAGAVGYIELDLSGKILIESFRPERPPMSTFVLLCGAVLSRID 60
   |||||
DB 24 HPEITLVKVKDAEDQAGAVGYIELDLSGKILIESFRPERPPMSTFVLLCGAVLSRID 83
   |||||
QY 61 AGOBLGRRIHSQNDLVEYSPVTEKHLTDGWTVELCSAATWSNDTNAALLTTIGSP 120
   |||||
DB 84 AGOBLGRRIHSQNDLVEYSPVTEKHLTDGWTVELCSAATWSNDTNAALLTTIGSP 143
   |||||
QY 121 KELTAFILNMGDHVTRLDRMBEPELNEALPNDERDTTPVAAATTLRKLLTGELTLASRQ 180
   |||||
DB 144 KELTAFILNMGDHVTRLDRMBEPELNEALPNDERDTTPVAAATTLRKLLTGELTLASRQ 203
   |||||
QY 181 QLIDWMEADK 190
   |||||
DB 204 QLIDWMEADK 213
   |||||

```

RESULT 9

AAW16635
 ID AAW16635 standard; protein; 286 AA.

XX AAW16635;

DT 09-AUG-1997 (first entry)

DE Beta-lactamase (no signal peptide).

XX Gene directed enzyme prodnrg therapy; GDEPT;
 KW virus directed enzyme prodnrg therapy; VDEPT; beta-lactamase; cancer;
 KW HIV; inflammation.

XX Escherichia coli.

OS Escherichia coli.

XX WO9719180-A2.

XX 29-MAY-1997.

XX 19-NOV-1996; 96WO-GB002845.

XX 20-NOV-1995; 95GB-00023703.

XX (GLAXO) GLAXO GROUP LTD.

PA Dev I, Moore JT, Ohmstede C;

XX WPI; 1997-298117/27.

XX N-PSDB; AAT66737.

PT Molecular chimera for gene or virus directed enzyme prodnrg therapy -
 PT useful for treatment of cancer, viral infection or inflammation.

XX Example; Page 26; 38pp; English.

XX Escherichia coli beta-lactamase (AAW16635), lacking the signal peptide,
 CC is the expression product of a molecular chimera, designated pCMV-delBL
 CC (AAT66738), in which the beta-lactamase gene is under control of the CMV
 CC intermediate/early promoter. Vectors consisting of a transcriptional
 CC regulatory DNA sequence linked to a beta-lactamase gene can be used for
 CC enzyme prodnrg therapy. Intracellular expression of the beta-lactamase in
 CC a targeted cell allows conversion of a prodnrg into an agent toxic to
 CC the cell for treatment of cancer, viral (e.g. HIV) infection or
 CC inflammation

XX Sequence 286 AA;

Query Match 100.0%; Score 975; DB 2; Length 286;

Best Local Similarity 100.0%; Pred. No. 7.4e-98;
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 HPEITLVKVKDAEDQAGAVGYIELDLSGKILIESFRPERPPMSTFVLLCGAVLSRID 60
   |||||
DB 24 HPEITLVKVKDAEDQAGAVGYIELDLSGKILIESFRPERPPMSTFVLLCGAVLSRID 83
   |||||
QY 61 AGOBLGRRIHSQNDLVEYSPVTEKHLTDGWTVELCSAATWSNDTNAALLTTIGSP 120
   |||||
DB 84 AGOBLGRRIHSQNDLVEYSPVTEKHLTDGWTVELCSAATWSNDTNAALLTTIGSP 143
   |||||
QY 121 KELTAFILNMGDHVTRLDRMBEPELNEALPNDERDTTPVAAATTLRKLLTGELTLASRQ 180
   |||||
DB 144 KELTAFILNMGDHVTRLDRMBEPELNEALPNDERDTTPVAAATTLRKLLTGELTLASRQ 203
   |||||
QY 181 QLIDWMEADK 190
   |||||
DB 204 QLIDWMEADK 213
   |||||

```

RESULT 10

AAW18679
 ID AAW18679 standard; protein; 286 AA.

XX AAW18679;

DT 13-AUG-1997 (first entry)

DE Secretory beta-lactamase.

XX Prodnrg therapy; gene directed enzyme prodnrg therapy; GDEPT;
 KW virus directed enzyme prodnrg therapy; VDEPT; lung cancer;
 KW beta-lactamase; pCMV-BL.

XX Escherichia coli.

OS Escherichia coli.

XX Key Location/Qualifiers

XX Peptide 1..23

XX Protein 24..286

XX /label= Mat_protein

XX WO9719183-A2.

XX 29-MAY-1997.

XX 19-NOV-1996; 96WO-GB002846.

XX 20-NOV-1995; 95GB-00023703.

XX (GLAXO) GLAXO GROUP LTD.

XX Dev I, Moore JT, Sethna PB;

XX WPI; 1997-298118/27.

XX N-PSDB; AAT70309.

PT DNA construct for gene-directed enzyme prodnrg therapy of lung cancer -
 PT comprises lung- or neuroendocrine-specific promoter controlling
 PT expression of prodnrg-converting enzyme.

XX Example 8ii; Page 26-27; 53pp; English.

XX The secreted form (AAW18679) of TEM beta-lactamase is expressed by pCMV-
 CC BL (AAT70309) in which a PCR-amplified beta-lactamase coding sequence is
 CC placed under control of the intermediate/early promoter of
 CC cytomagalovirus. Secretory beta-lactamase constructs, placed under
 CC control of promoter/enhancer elements of lung-associated protein or
 CC neuroendocrine marker protein genes, can be used in novel chimeric

CC molecules for use in prodnug therapy of lung cancer
 XX Sequence 286 AA;
 SQ Query Match 100.0%; Score 975; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 7.4e-98;
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HETLVKVDADQAGRVGYIELDNSGKILSPRPSPRPMSFPKVLICGAVLSRID 60
 DB 24 HETLVKVDADQAGRVGYIELDNSGKILSPRPSPRPMSFPKVLICGAVLSRID 83
 QY 61 AGOEOLGRRIRHSQNDLVESPVTEKHLTDGVTRELCSAATMSDNTANLLTTIGSP 120
 DB 84 AGOEOLGRRIRHSQNDLVESPVTEKHLTDGVTRELCSAATMSDNTANLLTTIGSP 143
 QY 121 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDITTPVMAATTIRKLLTGELTLASRQ 180
 DB 144 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDITTPVMAATTIRKLLTGELTLASRQ 203
 QY 181 OLIDWMEADK 190
 DB 204 OLIDWMEADK 213

RESULT 11
 AAY08529
 ID AAY08529 standard; protein; 286 AA.
 AC AAY08529;
 DT 03-AUG-1999 (first entry)
 DE Vector pASK75 beta-1a protein.
 XX Firefly; luciferase; tetracycline; transcriptional control; TetR; TetA;
 KW tetracycline repressor; tetracycline promoter; luminescence; luxCDABE;
 KW insect; Tn10; medicine; dosage; cheese production; antibiotic; foodstuff;
 KW allergy.
 OS Synthetic.
 XX MO9925866-A1.
 XX 27-MAY-1999.
 XX 11-NOV-1998; 98WO-FI000873.
 XX 14-NOV-1997; 97FI-00004235.
 XX (KORP/) KORPELA M.
 XX (KARP/) KARP M.
 XX (KURI/) KURITTU J.
 XX Korpele M, Karp M, Kurittu J;
 XX WPI; 1999-338015/28.
 XX N-PSDB; AAV72418.
 XX Assaying for tetracycline using recombinant prokaryotic cells.
 XX Disclosure; Page 47-48; 67pp; English.

CC This invention describes a novel tetracycline assay that uses recombinant
 CC prokaryotic cells comprising a luciferase gene under the transcriptional
 CC control of a tetracycline repressor and tetracycline promoter and
 CC involves the detection of luminescence emitted from the cells. The assay
 CC can be used to distinguish tetracycline from other microbial agents. The
 CC invention also describes a novel plasmid comprising either the luxCDABE
 CC genes, a tetracycline repressor (TetR) and a tetracycline promoter (TetA)
 CC from Tn10, or the insect luciferase gene, a tetracycline repressor (TetR)
 CC and a tetracycline promoter (TetA) from Tn10. The tetracycline assay
 CC method can be used for the determination of tetracycline in a sample,

CC e.g. to study the dosage and penetration of the medicine. The method can
 CC also be used to test cheese production, as cheese making bacteria are not
 CC able to work in the presence of tetracycline. The method can also be used
 CC to determine the presence or concentration of antibiotics in foodstuffs,
 CC e.g. for allergic people. The present assay method does not rely on the
 CC growth of microbes as do conventional tests, and so is much more rapid.
 CC The present assay is also more sensitive, as even a small amount of
 CC luminescence can be detected

XX Sequence 286 AA;
 SQ Query Match 100.0%; Score 975; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 7.4e-98;
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HETLVKVDADQAGRVGYIELDNSGKILSPRPSPRPMSFPKVLICGAVLSRID 60
 DB 24 HETLVKVDADQAGRVGYIELDNSGKILSPRPSPRPMSFPKVLICGAVLSRID 83
 QY 61 AGOEOLGRRIRHSQNDLVESPVTEKHLTDGVTRELCSAATMSDNTANLLTTIGSP 120
 DB 84 AGOEOLGRRIRHSQNDLVESPVTEKHLTDGVTRELCSAATMSDNTANLLTTIGSP 143
 QY 121 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDITTPVMAATTIRKLLTGELTLASRQ 180
 DB 144 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDITTPVMAATTIRKLLTGELTLASRQ 203
 QY 181 OLIDWMEADK 190
 DB 204 OLIDWMEADK 213

RESULT 12
 AAB10442
 ID AAB10442 standard; protein; 286 AA.
 AC AAB10442;
 DT 01-DEC-2000 (first entry)
 DE Expression vector pSEX15G2 bla protein.
 XX Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
 KW B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.
 OS Synthetic.
 XX DE19900635-A1.
 XX 13-JUL-2000.
 XX 11-JAN-1999; 99DE-01000635.
 XX 11-JAN-1999; 99DE-01000635.
 XX (DEKR-) DEUT FORSCHUNGSZENTRUM.
 XX Breilting F, Poustka A, Moldenhauer G;
 XX WPI; 2000-499832/45.
 XX N-PSDB; AAA71430.
 XX Selecting monoclonal antibodies, by expressing them on the surface of
 XX hybridomas attached to antibody-binding protein, then reaction with
 XX antibody library.
 XX Claim 16; Fig 3; 22pp; German.

CC This invention describes a novel method for the selection of monoclonal
 CC antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma
 CC cells to produce antibody-producing hybridomas such that the antibodies
 CC are presented at the surface of the hybridomas by an antibody-binding
 CC protein (I); and (ii) binding the antibody to antigens (Ag). The

CC invention also describes antibody-binding proteins (I) that comprise a
CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa
CC chain or a murine MHC (major histocompatibility complex) Class I K(K)
CC molecule; an antibody-binding site of proteins A, G, I or Ig, and the
CC transmembrane domain of PDGFR (platelet-derived growth factor receptor)
CC or CD52. The method is used to select Mab with specificity for particular
CC antigens. Mab can be selected without separate culture of hybridomas, and
CC selection can be made against many antigens in a library, optionally on
CC the basis of strength of affinity for a particular antigen. Complex
CC mixtures of hybridomas can be used for selection, reducing the time and
CC cost involved in Mab selection. This sequence represents the bla protein
CC protein contained in the expression vector pSEX11G2 which contains the
CC bla protein, Neo-R and protein G described in the method of the invention
XX
XX

Query Match 100.0%; Score 975; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 7.4e-98;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 286 AA;

1 HPETLVKVKDAEDQLGARVGYIELDLSGKILSFRRPEERPFPMSTFKVLLCGAVLSRID 60
24 HPETLVKVKDAEDQLGARVGYIELDLSGKILSFRRPEERPFPMSTFKVLLCGAVLSRID 83
61 AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATWMSDNTAANLLTTIGSP 120
84 AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATWMSDNTAANLLTTIGSP 143
121 KETLFAFLNMGDHTRLDRWEPELNEAIPNDERDTTPVAAATTIRKLLTGELLTLASRQ 180
144 KETLFAFLNMGDHTRLDRWEPELNEAIPNDERDTTPVAAATTIRKLLTGELLTLASRQ 203
181 QLIIDWMEADK 190
204 QLIIDWMEADK 213

RESULT 13

AAB10438
ID AAB10438 standard; protein; 286 AA.

AC AAB10438;

DT 01-DEC-2000 (first entry)

XX Expression vector pSEX11L4 bla protein.

XX Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
KM B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.

XX Synthetic.

PN DE19900635-A1.

PD 13-JUL-2000.

PF 11-JAN-1999; 99DE-01000635.

PR 11-JAN-1999; 99DE-01000635.

PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

PI Breitling F, Poustka A, Moldenhauer G;

DR MPI: 2000-499832/45.

XX N-PSDB; AAA71428.

XX Selecting monoclonal antibodies, by expressing them on the surface of
PT hybridomas attached to antibody-binding protein, then reaction with
PT antibody library.

XX Claim 16; Fig 1; 22pp; German.

CC This invention describes a novel method for the selection of monoclonal
CC antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma
CC cells to produce antibody-producing hybridomas such that the antibodies
CC are presented at the surface of the hybridomas by an antibody-binding
CC protein (I); and (ii) binding the antibody to antigens (Ag). The
CC invention also describes antibody-binding proteins (I) that comprise a
CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa
CC chain or a murine MHC (major histocompatibility complex) Class I K(K)
CC molecule; an antibody-binding site of proteins A, G, I or Ig, and the
CC transmembrane domain of PDGFR (platelet-derived growth factor receptor)
CC or CD52. The method is used to select Mab with specificity for particular
CC antigens. Mab can be selected without separate culture of hybridomas, and
CC selection can be made against many antigens in a library, optionally on
CC the basis of strength of affinity for a particular antigen. Complex
CC mixtures of hybridomas can be used for selection, reducing the time and
CC cost involved in Mab selection. This sequence represents the Neo-R
CC protein contained in the expression vector pSEX11L4 which contains the
CC bla protein, Neo-R and protein G described in the method of the invention
XX
XX

Sequence 286 AA;

Query Match 100.0%; Score 975; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 7.4e-98;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 HPETLVKVKDAEDQLGARVGYIELDLSGKILSFRRPEERPFPMSTFKVLLCGAVLSRID 60
24 HPETLVKVKDAEDQLGARVGYIELDLSGKILSFRRPEERPFPMSTFKVLLCGAVLSRID 83
61 AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATWMSDNTAANLLTTIGSP 120
84 AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATWMSDNTAANLLTTIGSP 143
121 KETLFAFLNMGDHTRLDRWEPELNEAIPNDERDTTPVAAATTIRKLLTGELLTLASRQ 180
144 KETLFAFLNMGDHTRLDRWEPELNEAIPNDERDTTPVAAATTIRKLLTGELLTLASRQ 203
181 QLIIDWMEADK 190
204 QLIIDWMEADK 213

RESULT 14

AAB10440
ID AAB10440 standard; protein; 286 AA.

AC AAB10440;

DT 01-DEC-2000 (first entry)

XX Expression vector pSEX11G2 bla protein.

XX Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
KM B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.

XX Synthetic.

PN DE19900635-A1.

PD 13-JUL-2000.

PF 11-JAN-1999; 99DE-01000635.

PR 11-JAN-1999; 99DE-01000635.

PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

PI Breitling F, Poustka A, Moldenhauer G;

DR MPI: 2000-499832/45.

XX N-PSDB; AAA71429.

XX Selecting monoclonal antibodies, by expressing them on the surface of
PT

PT hybridomas attached to antibody-binding protein, then reaction with
PT antibody library.

PS Claim 16; Fig 2; 22pp; German.

CC This invention describes a novel method for the selection of monoclonal
CC antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma
CC cells to produce antibody-producing hybridomas such that the antibodies
CC are presented at the surface of the hybridomas by an antibody-binding
CC protein (I); and (ii) binding the antibody to antigens (Ag). The
CC invention also describes antibody-binding proteins (I) that comprise a
CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa
CC chain or a murine MHC (major histocompatibility complex) Class I K(k)
CC molecule; an antibody-binding site of proteins A, G, I or Ig, and the
CC transmembrane domain of PDGFR (platelet-derived growth factor receptor)
CC or CD52. The method is used to select Mab with specificity for particular
CC antigens. Mab can be selected without separate culture of hybridomas, and
CC selection can be made against many antigens in a library, optionally on
CC the basis of strength of affinity for a particular antigen. Complex
CC mixtures of hybridomas can be used for selection, reducing the time and
CC cost involved in Mab selection. This sequence represents the bla protein
CC protein contained in the expression vector pSEX1G2 which contains the
CC bla protein, Neo-R and protein G described in the method of the invention
CC
XX
SQ Sequence 286 AA;

Query Match 100.0%; Score 975; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 7.4e-98;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGYIELDLSGKILESFRPERFPMWSTFKVLCGAVLSRID 60
DB 24 HPEITLVKVDADQAGARVGYIELDLSGKILESFRPERFPMWSTFKVLCGAVLSRID 83
QY 61 AGQEOIGRRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTTIGSP 120
DB 84 AGQEOIGRRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTTIGSP 143
QY 121 KELTSFLNMGDHYTRLDRWPEBELNEAIPNDRDITMPVAMATTYRKLLTGSLLTLASRQ 180
DB 144 KELTSFLNMGDHYTRLDRWPEBELNEAIPNDRDITMPVAMATTYRKLLTGSLLTLASRQ 203
QY 181 QLIDWMEADK 190
DB 204 QLIDWMEADK 213

RESULT 15

AAB50898
ID AAB50898 standard; protein; 286 AA.

AC AAB50898;

DT 20-MAR-2001 (first entry)

DE Protein encoded by bla resistance marker of integration vector pLO12306.

KM bla resistance marker; recombinant host cell; saccharification;
KM fermentation; polysaccharase; oligosaccharide degradation; cel2 gene;
KM glucanase; integration vector; pLO12306.

OS Unidentified.

XX WO200071729-A2.

XX 30-NOV-2000.

XX 26-MAY-2000; 2000MO-US014773.

XX 26-MAY-1999; 99US-0136376P.

XX (UYFL) UNIV FLORIDA RES FOUND.

PI Ingram LO, Zhou S;
XX
CC MPI: 2001-032043/04.
DR N-PSDB; AAC91455.

XX Recombinant host cells useful for producing polysaccharase for degrading
PT oligosaccharides, comprises a first heterologous polynucleotide encoding
PT polysaccharase under control of surrogate promoter.

PS Disclosure; Page 82-83; 87pp; English.

XX The present sequence is given in a specification relating to a
CC recombinant host cell suitable for simultaneous saccharification and
CC fermentation. The host cell contains at least one heterologous
CC polynucleotide encoding a polysaccharase under the transcriptional
CC control of a surrogate promoter capable of increasing expression of the
CC polysaccharase. The host cell also contains a second heterologous
CC polynucleotide encoding a secretory polypeptide to facilitate the
CC secretion of the expressed polysaccharase. The recombinant host cell is
CC useful for producing polysaccharase which is useful for enzymatically
CC degrading oligosaccharides such as lignocellulose, hemicellulose,
CC cellulose, pectin or their combinations, and fermenting the product to
CC ethanol, by simultaneous saccharification and fermenting processes. The
CC present sequence is encoded by an integration vector which was introduced
CC into cells to generate recombinant host cells. The vector contains a
CC surrogate promoter from *Zymomonas mobilis*, the cel2 gene from *Erwinia*
CC chrysanthemi, resistance markers bla and tet, and *Klebsiella oxytoca*
CC target sequence

SQ Sequence 286 AA;

Query Match 100.0%; Score 975; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 7.4e-98;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGYIELDLSGKILESFRPERFPMWSTFKVLCGAVLSRID 60
DB 24 HPEITLVKVDADQAGARVGYIELDLSGKILESFRPERFPMWSTFKVLCGAVLSRID 83
QY 61 AGQEOIGRRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTTIGSP 120
DB 84 AGQEOIGRRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTTIGSP 143
QY 121 KELTSFLNMGDHYTRLDRWPEBELNEAIPNDRDITMPVAMATTYRKLLTGSLLTLASRQ 180
DB 144 KELTSFLNMGDHYTRLDRWPEBELNEAIPNDRDITMPVAMATTYRKLLTGSLLTLASRQ 203
QY 181 QLIDWMEADK 190
DB 204 QLIDWMEADK 213

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Job time : 73.6679 secs

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OM protein - protein search, using sw model

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Total number of hits satisfying chosen parameters: 513545

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	975	100.0	286	1	US-07-721-775A-2
2	975	100.0	286	1	US-08-339-658-2
3	975	100.0	286	3	US-09-263-933-7
4	975	100.0	286	3	US-09-263-933-14
5	975	100.0	286	3	US-09-263-933-21
6	975	100.0	286	3	US-09-263-933-21
7	975	100.0	286	3	US-09-263-933-21
8	975	100.0	286	3	US-09-263-933-21
9	975	100.0	286	4	US-09-263-933-21
10	975	100.0	286	4	US-09-263-933-21
11	975	100.0	286	4	US-09-263-933-21
12	975	100.0	286	4	US-09-263-933-21
13	975	100.0	286	4	US-09-263-933-21
14	975	100.0	286	4	US-09-263-933-21
15	975	100.0	286	4	US-09-263-933-21
16	975	100.0	286	4	US-09-263-933-21
17	975	100.0	286	4	US-09-263-933-21
18	975	100.0	286	4	US-09-263-933-21
19	975	100.0	286	4	US-09-263-933-21
20	975	100.0	286	4	US-09-263-933-21
21	975	100.0	286	4	US-09-263-933-21
22	975	100.0	286	4	US-09-263-933-21
23	975	100.0	286	4	US-09-263-933-21
24	975	100.0	286	4	US-09-263-933-21
25	975	100.0	286	4	US-09-263-933-21
26	975	100.0	286	4	US-09-263-933-21
27	975	100.0	286	4	US-09-263-933-21

28	975	100.0	299	4	US-09-490-153-300	Sequence 300, App
29	975	100.0	299	4	US-09-490-324-285	Sequence 285, App
30	975	100.0	299	4	US-09-490-324-285	Sequence 298, App
31	975	100.0	299	4	US-09-490-324-285	Sequence 300, App
32	975	100.0	2307	3	US-09-263-933-2	Sequence 2, App1
33	975	100.0	2307	3	US-09-263-933-2	Sequence 9, App1
34	975	100.0	2307	3	US-09-263-933-2	Sequence 16, App1
35	975	100.0	2307	3	US-09-263-933-2	Sequence 2, App1
36	975	100.0	2307	4	US-09-919-901-16	Sequence 16, App1
37	975	100.0	2307	4	US-09-919-901-16	Sequence 2, App1
38	975	100.0	2307	4	US-10-191-966-2	Sequence 9, App1
39	975	100.0	2307	4	US-10-191-966-2	Sequence 16, App1
40	975	100.0	2307	4	US-10-191-966-2	Sequence 9, App1
41	974	99.9	286	4	US-09-555-510B-9	Sequence 9, App1
42	974	99.9	286	4	US-10-231-013-9	Sequence 9, App1
43	974	99.9	1293	4	US-09-170-495D-292	Sequence 292, App
44	974	99.9	1293	4	US-09-364-425B-57	Sequence 57, App1
45	970	99.5	263	1	US-08-407-544-2	Sequence 2, App1

ALIGNMENTS

RESULT 1
; Sequence 2, Application US/07721775A
; Patent No. 5180666
; GENERAL INFORMATION:
; APPLICANT: States, J. Christopher
; APPLICANT: Hines, Ronald N.
; APPLICANT: No. 5180666ak, Raymond F.
; TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
; TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Reising, Ethington, Barnard, Perry & Milton
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: U.S.A.
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07721,775A
; FILING DATE: 19910627
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-321WSU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (313) 689-3554
; TELEFAX: (313) 689-4071
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-721-775A-2

Query Match 100.0%; Score 975; DB 1; Length 286;
Best local Similarity 100.0%; Pred. No. 1e-107;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HPEITLVKVDADQAGRVGIELDINSKIIISRPFRPFPMSTFKYLICAVLSRID 60
DB 24 HPEITLVKVDADQAGRVGIELDINSKIIISRPFRPFPMSTFKYLICAVLSRID 83

QY 61 AGOEOLGRIRIHYSONDLVEYSPTVEKHLTDGMTVRELCSAAITMSDNTAANLLTTTIGP 120
DB 84 AGOEOLGRIRIHYSONDLVEYSPTVEKHLTDGMTVRELCSAAITMSDNTAANLLTTTIGP 143
QY 121 KETLAFILNMGDHYTRLDRWPELNEALPNDERDTTVPVAMATTLTKLTGELLTLASRQ 180
DB 144 KETLAFILNMGDHYTRLDRWPELNEALPNDERDTTVPVAMATTLTKLTGELLTLASRQ 203
QY 181 QUIDMWEADK 190
DB 204 QUIDMWEADK 213

RESULT 2

US-08-339-658-2
; Sequence 2, Application US/08339658
; Patent No. 5525482
; GENERAL INFORMATION:
; APPLICANT: States, J. Christopher
; APPLICANT: Hines, Ronald N.
; APPLICANT: No. 5525482ak, Raymond F.
; TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
; TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Reising, Ethington, Barnard, Perry & Milton
; STREET: P. O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: U.S.A.
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,658
; FILING DATE: 15-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,295
; FILING DATE: 09-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohl, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-321MSU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (313) 689-3554
; TELEFAX: (313) 689-4071
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-339-658-2

Query Match 100.0%; Score 975; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 1e-107;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEITLVKKADBDQAGAVGYIELDLSNGKILSFPRPERPPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKKADBDQAGAVGYIELDLSNGKILSFPRPERPPMSTFVLLCGAVLSRID 83
QY 61 AGOEOLGRIRIHYSONDLVEYSPTVEKHLTDGMTVRELCSAAITMSDNTAANLLTTTIGP 120
DB 84 AGOEOLGRIRIHYSONDLVEYSPTVEKHLTDGMTVRELCSAAITMSDNTAANLLTTTIGP 143
QY 121 KETLAFILNMGDHYTRLDRWPELNEALPNDERDTTVPVAMATTLTKLTGELLTLASRQ 180
DB 144 KETLAFILNMGDHYTRLDRWPELNEALPNDERDTTVPVAMATTLTKLTGELLTLASRQ 203

QY 181 QUIDMWEADK 190
DB 204 QUIDMWEADK 213

RESULT 3

US-09-263-933-7
; Sequence 7, Application US/09263933
; Patent No. 6280940
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/263,933
; CURRENT FILING DATE: 1999-03-08
; EARLIER APPLICATION NUMBER: 09/129,611
; EARLIER FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; US-09-263-933-7

Query Match 100.0%; Score 975; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 1e-107;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKKADBDQAGAVGYIELDLSNGKILSFPRPERPPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKKADBDQAGAVGYIELDLSNGKILSFPRPERPPMSTFVLLCGAVLSRID 83
QY 61 AGOEOLGRIRIHYSONDLVEYSPTVEKHLTDGMTVRELCSAAITMSDNTAANLLTTTIGP 120
DB 84 AGOEOLGRIRIHYSONDLVEYSPTVEKHLTDGMTVRELCSAAITMSDNTAANLLTTTIGP 143
QY 121 KETLAFILNMGDHYTRLDRWPELNEALPNDERDTTVPVAMATTLTKLTGELLTLASRQ 180
DB 144 KETLAFILNMGDHYTRLDRWPELNEALPNDERDTTVPVAMATTLTKLTGELLTLASRQ 203
QY 181 QUIDMWEADK 190
DB 204 QUIDMWEADK 213

RESULT 4

US-09-263-933-14
; Sequence 14, Application US/09263933
; Patent No. 6280940
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/263,933
; CURRENT FILING DATE: 1999-03-08
; EARLIER APPLICATION NUMBER: 09/129,611
; EARLIER FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; US-09-263-933-14

Query Match 100.0%; Score 975; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 1e-107;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKDAEDQAGVGYIELDINSKILSFPRPERFPMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVKDAEDQAGVGYIELDINSKILSFPRPERFPMSTFKVLLCGAVLSRID 83
QY 61 AGOBLGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGOBLGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFLLNMGDHYRLDRMBELNEAIPNDRDITTPVAAATTIRKLLTGELTLASRQ 180
DB 144 KELTAFLLNMGDHYRLDRMBELNEAIPNDRDITTPVAAATTIRKLLTGELTLASRQ 203
QY 181 QUIDMMEADK 190
DB 204 QUIDMMEADK 213

RESULT 5

US-09-263-933-21
Sequence 21, Application US/09263933
Patent No. 6280940

GENERAL INFORMATION:
APPLICANT: Potte, Karen E.
APPLICANT: Jackson, Roderica L.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
US-09-263-933-21

Query Match 100.0%; Score 975; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 1e-107;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKDAEDQAGVGYIELDINSKILSFPRPERFPMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVKDAEDQAGVGYIELDINSKILSFPRPERFPMSTFKVLLCGAVLSRID 83
QY 61 AGOBLGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGOBLGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFLLNMGDHYRLDRMBELNEAIPNDRDITTPVAAATTIRKLLTGELTLASRQ 180
DB 144 KELTAFLLNMGDHYRLDRMBELNEAIPNDRDITTPVAAATTIRKLLTGELTLASRQ 203
QY 181 QUIDMMEADK 190
DB 204 QUIDMMEADK 213

RESULT 6

US-09-025-769B-265
Sequence 265, Application US/09025769B
Patent No. 6300064

GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic

APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 265:

SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-265

Query Match 100.0%; Score 975; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 1e-107;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKDAEDQAGVGYIELDINSKILSFPRPERFPMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVKDAEDQAGVGYIELDINSKILSFPRPERFPMSTFKVLLCGAVLSRID 83
QY 61 AGOBLGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGOBLGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFLLNMGDHYRLDRMBELNEAIPNDRDITTPVAAATTIRKLLTGELTLASRQ 180
DB 144 KELTAFLLNMGDHYRLDRMBELNEAIPNDRDITTPVAAATTIRKLLTGELTLASRQ 203
QY 181 QUIDMMEADK 190
DB 204 QUIDMMEADK 213

RESULT 7

US-09-025-769B-362
Sequence 362, Application US/09025769B
Patent No. 6300064

GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B

PRIOR APPLICATION DATA:
FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000

TELEFAX: (212)596-9080

INFORMATION FOR SEQ ID NO: 362:

SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-025-769B-362

Query Match 100.0%; Score 975; DB 3; Length 286;

Best Local Similarity 100.0%; Pred. No. 1e-107;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADQDQAGVGYIEIDLSGKILSFRRPFRPPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKVKADQDQAGVGYIEIDLSGKILSFRRPFRPPMSTFVLLCGAVLSRID 83
QY 61 AGQOLGRRIHYSQNDLVEYSPVTEKHLTDGATVRELCSAITMSDNTAANLLTTIGSP 120
DB 84 AGQOLGRRIHYSQNDLVEYSPVTEKHLTDGATVRELCSAITMSDNTAANLLTTIGSP 143
QY 121 KeltaFLHMGDHYTRLDRWPEPEINEAIPNDRDITMPVAMATTLRKLLTGELLTLASRQ 180
DB 144 KeltaFLHMGDHYTRLDRWPEPEINEAIPNDRDITMPVAMATTLRKLLTGELLTLASRQ 203
QY 181 QLIDMMEADK 190
DB 204 QLIDMMEADK 213

RESULT 8

US-09-919-901-7
Sequence 7, Application US/09919901

Patent No. 6599738
GENERAL INFORMATION:

APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.

APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT

FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901

PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933

PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611

PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 7

LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-09-919-901-7

Query Match 100.0%; Score 975; DB 4; Length 286;

Best Local Similarity 100.0%; Pred. No. 1e-107;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADQDQAGVGYIEIDLSGKILSFRRPFRPPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKVKADQDQAGVGYIEIDLSGKILSFRRPFRPPMSTFVLLCGAVLSRID 83
QY 61 AGQOLGRRIHYSQNDLVEYSPVTEKHLTDGATVRELCSAITMSDNTAANLLTTIGSP 120
DB 84 AGQOLGRRIHYSQNDLVEYSPVTEKHLTDGATVRELCSAITMSDNTAANLLTTIGSP 143
QY 121 KeltaFLHMGDHYTRLDRWPEPEINEAIPNDRDITMPVAMATTLRKLLTGELLTLASRQ 180
DB 144 KeltaFLHMGDHYTRLDRWPEPEINEAIPNDRDITMPVAMATTLRKLLTGELLTLASRQ 203
QY 181 QLIDMMEADK 190
DB 204 QLIDMMEADK 213

RESULT 9

US-09-919-901-14

Sequence 14, Application US/09919901

Patent No. 6599738
GENERAL INFORMATION:

APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.

APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT

FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901

PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933

PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611

PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 14

LENGTH: 286

TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: :
US-09-919-901-14

Query Match 100.0%; Score 975; DB 4; Length 286;

Best Local Similarity 100.0%; Pred. No. 1e-107;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADQDQAGVGYIEIDLSGKILSFRRPFRPPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKVKADQDQAGVGYIEIDLSGKILSFRRPFRPPMSTFVLLCGAVLSRID 83
QY 61 AGQOLGRRIHYSQNDLVEYSPVTEKHLTDGATVRELCSAITMSDNTAANLLTTIGSP 120
DB 84 AGQOLGRRIHYSQNDLVEYSPVTEKHLTDGATVRELCSAITMSDNTAANLLTTIGSP 143
QY 121 KeltaFLHMGDHYTRLDRWPEPEINEAIPNDRDITMPVAMATTLRKLLTGELLTLASRQ 180
DB 144 KeltaFLHMGDHYTRLDRWPEPEINEAIPNDRDITMPVAMATTLRKLLTGELLTLASRQ 203
QY 181 QLIDMMEADK 190
DB 204 QLIDMMEADK 213

Db 204 QUIDMMEADK 213

RESULT 10

US-09-919-901-21

; Sequence 21, Application US/09919901

; Patent No. 6599738

; GENERAL INFORMATION:

; APPLICANT: Potts, Karen E.

; APPLICANT: Jackson, Roberta L.

; APPLICANT: Patrick, Amy K.

; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT

; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

; FILE REFERENCE: 0125-0005A

; CURRENT APPLICATION NUMBER: US/09/919,901

; CURRENT FILING DATE: 2001-08-02

; PRIOR APPLICATION NUMBER: 09/263,933

; PRIOR FILING DATE: 1999-02-08

; PRIOR APPLICATION NUMBER: 09/129,611

; PRIOR FILING DATE: 1998-08-05

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO: 21

; LENGTH: 286

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION:

US-09-919-901-21

Query Match 100.0%; Score 975; DB 4; Length 286;

Best Local Similarity 100.0%; Pred. No. 1e-107;

Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVAADQAGARVGYIELDNSGKILSFPRPFRPMSTFKVLLCGAVLSRID 60

Db 24 HPELVKVAADQAGARVGYIELDNSGKILSFPRPFRPMSTFKVLLCGAVLSRID 83

QY 61 AGQEQGLRRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANILLTTIGSP 120

Db 84 AGQEQGLRRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANILLTTIGSP 143

QY 121 KELTAFILNMGHVTRLDRWPELNEALPNDERDTTMPVAMATTLRKLLTGELLTLASRQ 180

Db 144 KELTAFILNMGHVTRLDRWPELNEALPNDERDTTMPVAMATTLRKLLTGELLTLASRQ 203

QY 181 QUIDMMEADK 190

Db 204 QUIDMMEADK 213

RESULT 11

US-09-490-070A-265

; Sequence 265, Application US/09490070A

; Patent No. 6696248

; GENERAL INFORMATION:

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

RESULT 12

US-09-490-070A-362

; Sequence 362, Application US/09490070A

; Patent No. 6696248

; GENERAL INFORMATION:

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,070A

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Colin G. Sandercock, Esq.

REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 37629-0005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 912-2000

TELEFAX: (202) 912-2020

INFORMATION FOR SEQ ID NO: 265:

SEQUENCE CHARACTERISTICS:

LENGTH: 286 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 265:

Query Match 100.0%; Score 975; DB 4; Length 286;

Best Local Similarity 100.0%; Pred. No. 1e-107;

Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVAADQAGARVGYIELDNSGKILSFPRPFRPMSTFKVLLCGAVLSRID 60

Db 24 HPELVKVAADQAGARVGYIELDNSGKILSFPRPFRPMSTFKVLLCGAVLSRID 83

QY 61 AGQEQGLRRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANILLTTIGSP 120

Db 84 AGQEQGLRRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANILLTTIGSP 143

QY 121 KELTAFILNMGHVTRLDRWPELNEALPNDERDTTMPVAMATTLRKLLTGELLTLASRQ 180

Db 144 KELTAFILNMGHVTRLDRWPELNEALPNDERDTTMPVAMATTLRKLLTGELLTLASRQ 203

QY 181 QUIDMMEADK 190

Db 204 QUIDMMEADK 213

RESULT 12

US-09-490-070A-362

; Sequence 362, Application US/09490070A

; Patent No. 6696248

; GENERAL INFORMATION:

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

; APPLICANT: Knappik, Achim

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESSES:

ADDRESSER: Colin G. Sandercock, Esq. c/o Heller Ehrman

ADDRESSER: White & McLaughlin

ADDRESSER: White & McLaughlin

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ADDRESSER: White & McLaughlin

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ADDRESSER: White & McLaughlin

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ADDRESSER: White & McLaughlin

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ADDRESSER: White & McLaughlin

STREET: 1666 K Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 362:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 362:
US-09-490-070A-362

Query Match 100.0%; Score 975; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 1e-107;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEILVKYKADBDQGARVGYIELDINSKILLESFRRPFRPMSTFVLLCGAVLSRID 60
DB 24 HPEILVKYKADBDQGARVGYIELDINSKILLESFRRPFRPMSTFVLLCGAVLSRID 83
QY 61 AGOGLGRRIHYSQNDLVEYSPTVEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120
DB 84 AGOGLGRRIHYSQNDLVEYSPTVEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 143
QY 121 KETLAFLLNMGDHYTRLDRWPELNEALPNDERDTMPEVAAATTLRKLLTGELLTLASRQ 180
DB 144 KETLAFLLNMGDHYTRLDRWPELNEALPNDERDTMPEVAAATTLRKLLTGELLTLASRQ 203
QY 181 QLIDMMEADK 190
DB 204 QLIDMMEADK 213

RESULT 13
US-09-490-153-265
Sequence 265, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Ilag, Vic
Pack, Peter
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-09-490-153-265

Query Match 100.0%; Score 975; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 1e-107;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEILVKYKADBDQGARVGYIELDINSKILLESFRRPFRPMSTFVLLCGAVLSRID 60
DB 24 HPEILVKYKADBDQGARVGYIELDINSKILLESFRRPFRPMSTFVLLCGAVLSRID 83
QY 61 AGOGLGRRIHYSQNDLVEYSPTVEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120
DB 84 AGOGLGRRIHYSQNDLVEYSPTVEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 143
QY 121 KETLAFLLNMGDHYTRLDRWPELNEALPNDERDTMPEVAAATTLRKLLTGELLTLASRQ 180
DB 144 KETLAFLLNMGDHYTRLDRWPELNEALPNDERDTMPEVAAATTLRKLLTGELLTLASRQ 203
QY 181 QLIDMMEADK 190
DB 204 QLIDMMEADK 213

RESULT 14
US-09-490-153-362
Sequence 362, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Ilag, Vic
Pack, Peter
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Reg.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 362:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 362:
US-09-490-153-362

Query Match 100.0%; Score 975; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 1e-107;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADDOIGARVGYIELDINSKILSPRPERFPMSTFKYLICGAVLSRID 60
DB 24 HPEITLVKVDADDOIGARVGYIELDINSKILSPRPERFPMSTFKYLICGAVLSRID 83
QY 61 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANLLTTIGSP 120
DB 84 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANLLTTIGSP 143
QY 121 KETLAFIHNMGDHTRLDRWEPELNEAIPNDRDITMPVAMATTIRKLLTGELTLASRQ 180
DB 144 KETLAFIHNMGDHTRLDRWEPELNEAIPNDRDITMPVAMATTIRKLLTGELTLASRQ 203
QY 181 QLIDWMEADK 190
DB 204 QLIDWMEADK 213

RESULT 15

US-10-191-966-7
Sequence 7, Application US/10191966
Patent No. 6790612
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-10-191-966-7

Query Match 100.0%; Score 975; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 1e-107;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADDOIGARVGYIELDINSKILSPRPERFPMSTFKYLICGAVLSRID 60
DB 24 HPEITLVKVDADDOIGARVGYIELDINSKILSPRPERFPMSTFKYLICGAVLSRID 83
QY 61 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANLLTTIGSP 120

DB 84 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANLLTTIGSP 143
QY 121 KETLAFIHNMGDHTRLDRWEPELNEAIPNDRDITMPVAMATTIRKLLTGELTLASRQ 180
DB 144 KETLAFIHNMGDHTRLDRWEPELNEAIPNDRDITMPVAMATTIRKLLTGELTLASRQ 203
QY 181 QLIDWMEADK 190
DB 204 QLIDWMEADK 213

Search completed: June 10, 2005, 11:01:16
Job time : 20.4801 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2005, 10:35:06 ; Search time 14.7307 Seconds
(without alignments)
1319.408 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_202

Perfect score: 1032

Sequence: 1 HPEITLVKVKADBDQAGARVG.....IDMWEADKVAGPLRSALPA 202

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*

1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1032	100.0	286	2	TS1301
2	1032	100.0	286	2	beta-lactamase (EC
3	1032	100.0	286	4	S47061
4	1027	99.5	286	1	beta-lactamase (EC
5	1027	99.5	286	4	PNACP
6	1019	98.7	286	2	beta-lactamase (EC
7	1014	98.3	286	2	S60312
8	1013	98.2	286	2	S60310
9	1013	98.2	286	2	S60311
10	1013	98.2	286	2	J01546
11	717	69.5	286	2	S16146
12	717	69.5	286	2	A60679
13	713	69.1	265	2	S00464
14	713	69.1	265	2	S02434
15	713	69.1	286	1	A44998
16	713	69.1	286	2	A60632
17	710	68.8	265	2	A60448
18	710	68.8	286	2	A37200
19	688.5	66.7	287	1	A44996
20	688	66.7	279	2	A24469
21	653	63.3	286	1	A44958
22	543	52.6	298	2	A41381
23	446.5	43.3	281	2	D95395
24	426.5	41.3	302	2	S61888
25	424	41.1	293	2	S04649
26	423.5	41.0	291	2	S42075
27	419.5	40.6	263	2	A54543
28	418.5	40.6	314	2	S06967
29	417.5	40.5	294	2	S16553

30	415.5	40.3	306	1	B45822	beta-lactamase (EC
31	410.5	39.8	386	2	G69674	beta-lactamase (EC
32	409.5	39.7	288	2	J01136	beta-lactamase (EC
33	408.5	39.6	306	2	S47330	penicillinase - Ba
34	408	39.5	305	2	A61156	beta-lactamase (EC
35	408	39.5	305	2	A57002	beta-lactamase (EC
36	408	39.5	305	2	A60680	beta-lactamase (EC
37	405.5	39.3	304	2	A49789	beta-lactamase (EC
38	405.5	39.3	304	2	A35001	beta-lactamase (EC
39	398.5	38.6	288	2	J50755	beta-lactamase (EC
40	397.5	38.5	311	2	JN0520	beta-lactamase (EC
41	395.5	38.3	291	2	JP0074	beta-lactamase (EC
42	393.5	38.1	263	2	S23929	beta-lactamase (EC
43	390	37.8	276	2	JH0268	beta-lactamase (EC
44	389.5	37.7	311	1	S02714	beta-lactamase (EC
45	388.5	37.6	305	1	C45822	beta-lactamase (EC

ALIGNMENTS

RESULT 1

TS1301
beta-lactamase (EC 3.5.2.6) - fission yeast (Schizosaccharomyces pombe)

C.Species: Schizosaccharomyces pombe

C.Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000

C.Accession: TS1301

R/WACH, A.; BRACHAT, A.; ALBERTSSEUT, C.; REBISCHUNG, C.; PHILIPPSEN, P.

Yeast 13, 1065-1075, 1997

A>Title: Heterologous His3 marker and GFP reporter modules for PCR-targeting in Saccharon

A.Reference number: 209587

A.Accession: TS1301

A>Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: DNA

A.Residues: 1-286 <WAC>

A.Cross-references: EMBL:AJ002683; PIDN:CAA05686.1

C.Genetics:

A.Gene: bla

C.Superfamily: beta-lactamase I

C.Keywords: hydrolase

Query Match 100.0%; Score 1032; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.2e-82;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	HPEITLVKVKADBDQAGARVGIIEDLNSGKILSFRRPFRPMSTFVLLCGAVLSRID	60
DB	24	HPEITLVKVKADBDQAGARVGIIEDLNSGKILSFRRPFRPMSTFVLLCGAVLSRID	83
QY	61	AGQEQIGRRHYSQNDIVESPVTEKHLTDGWTVEICSAITMSDNTAANLLTTIGSP	120
DB	84	AGQEQIGRRHYSQNDIVESPVTEKHLTDGWTVEICSAITMSDNTAANLLTTIGSP	143
QY	121	KEITAFILNMGDHYRLDRWEPELNEAIPNDRDITTMVMAATTKLITGELLTASRQ	180
DB	144	KEITAFILNMGDHYRLDRWEPELNEAIPNDRDITTMVMAATTKLITGELLTASRQ	203
QY	181	QIIDMWEADKVAGPLRSALPA 202	
DB	204	QIIDMWEADKVAGPLRSALPA 225	

RESULT 2

S47061
beta-lactamase (EC 3.5.2.6) - phage phi-X174

C.Species: phage phi-X174

C.Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C.Accession: S47061

R.Henrich, B.; Schmidtberger, B.

Submitted to the EMBL Data Library, July 1994

A.Description: A variant of phix174 gene E-based positive selection vectors with enhanced

A.Reference number: S47060

A.Accession: S47061

RESULT 5

140905
beta-lactamase (EC 3.5.2.6) - synthetic
C:Species: synthetic
A:Note: Cloning vector pCG1408 engineered and expressed in *Clavibacter xyli* subsp. *cynod*
C:Date: 15-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Oct-2000
C:Accession: 140905
R:Taylor, J.; Stearman, R.S.; Urcatani, B.B.
Plasmid 29, 241-244, 1993
A:Title: Development of a native plasmid as a cloning vector in *Clavibacter xyli* subsp.
A:Reference number: 140904; MUID:93361581; PMID:7689234
A:Accession: 140905
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-286 <RES>
A:Cross-references: EMBL:U21228; NID:9885956; PIND:AAA70411.1; PID:9885958
C:Keywords: hydrolase

Query Match 99.5%; Score 1027; DB 4; Length 286;
Best Local Similarity 99.0%; Pred. No. 3,2e-82;
Matches 200; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPEITLVKXADBDQAGAVGYIEIDLSGKILSFRRPFRPMSSTFKVLLCGAVLSRID 60
|||||
DB 24 HPEITLVKXADBDQAGAVGYIEIDLSGKILSFRRPFRPMSSTFKVLLCGAVLSRID 83
|||||
QY 61 AGOBLGRRIRHSQNDLVYSPVTEKHLTDGNTVRELCSAAITMSDNTAANILLTTIGCP 120
|||||
DB 84 AGOBLGRRIRHSQNDLVYSPVTEKHLTDGNTVRELCSAAITMSDNTAANILLTTIGCP 143
|||||
QY 121 KETAFLLNMGDHVTRLDRWPELNEALPNDERDPTMPVAAATTIRKLLTGELLTLASRQ 180
|||||
DB 144 KETAFLLNMGDHVTRLDRWPELNEALPNDERDPTMPVAAATTIRKLLTGELLTLASRQ 203
|||||
QY 181 QLIDMMEADKVAAGPLRSALPA 202
|||||
DB 204 QLIDMMEADKVAAGPLRSALPA 225
|||||

RESULT 6

S30113
beta-lactamase (EC 3.5.2.6) TEM-3 - *Klebsiella pneumoniae* plasmid pCFP04
C:Species: *Klebsiella pneumoniae*
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: S30113
R:Madilat, C.; Lourenco-Vital, J.; Goussard, S.; Courvalin, P.
Mol. Gen. Genet. 235, 113-121, 1992
A:Title: A new example of physical linkage between Tn1 and Tn21: the antibiotic multiple
A:Reference number: S30112; MUID:93062798; PMID:1331747
A:Accession: S30113
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <MAB>
A:Cross-references: UNIPROT:P00810; EMBL:X64523; NID:943797; PIND:CAA45828.1; PID:943798
C:Genetics:
A:Gene: bla(TEM-3)
A:Genome: plasmid
C:Superfamily: beta-lactamase I
C:Keywords: antibiotic resistance; hydrolase

Query Match 98.7%; Score 1019; DB 2; Length 286;
Best Local Similarity 98.0%; Pred. No. 1.6e-81;
Matches 198; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPEITLVKXADBDQAGAVGYIEIDLSGKILSFRRPFRPMSSTFKVLLCGAVLSRID 60
|||||
DB 24 HPEITLVKXADBDQAGAVGYIEIDLSGKILSFRRPFRPMSSTFKVLLCGAVLSRID 83
|||||
QY 61 AGOBLGRRIRHSQNDLVYSPVTEKHLTDGNTVRELCSAAITMSDNTAANILLTTIGCP 120
|||||
DB 84 AGOBLGRRIRHSQNDLVYSPVTEKHLTDGNTVRELCSAAITMSDNTAANILLTTIGCP 143
|||||
QY 121 KETAFLLNMGDHVTRLDRWPELNEALPNDERDPTMPVAAATTIRKLLTGELLTLASRQ 180
|||||

DB 144 KETAFLLNMGDHVTRLDRWPELNEALPNDERDPTMPVAAATTIRKLLTGELLTLASRQ 203
|||||
QY 181 QLIDMMEADKVAAGPLRSALPA 202
|||||
DB 204 QLIDMMEADKVAAGPLRSALPA 225
|||||

RESULT 7

S60312
extended spectrum beta-lactamase CAZ-7 - *Klebsiella pneumoniae*
C:Species: *Klebsiella pneumoniae*
C:Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 22-Jun-1999
C:Accession: S60312
R:Chanal, C.; Poupart, M.C.; Sirot, D.; Labie, R.; Sirot, J.; Cluzel, R.
Antimicrob. Agents Chemother. 36, 1817-1820, 1992
A:Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.
A:Reference number: S60310; MUID:93037315; PMID:1416873
A:Accession: S60312
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <CHA>
A:Cross-references: EMBL:X65254; NID:9296955; PIND:CAA46346.1; PID:9296956
C:Superfamily: beta-lactamase I

Query Match 98.3%; Score 1014; DB 2; Length 286;
Best Local Similarity 97.5%; Pred. No. 4.4e-81;
Matches 197; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITLVKXADBDQAGAVGYIEIDLSGKILSFRRPFRPMSSTFKVLLCGAVLSRID 60
|||||
DB 24 HPEITLVKXADBDQAGAVGYIEIDLSGKILSFRRPFRPMSSTFKVLLCGAVLSRID 83
|||||
QY 61 AGOBLGRRIRHSQNDLVYSPVTEKHLTDGNTVRELCSAAITMSDNTAANILLTTIGCP 120
|||||
DB 84 AGOBLGRRIRHSQNDLVYSPVTEKHLTDGNTVRELCSAAITMSDNTAANILLTTIGCP 143
|||||
QY 121 KETAFLLNMGDHVTRLDRWPELNEALPNDERDPTMPVAAATTIRKLLTGELLTLASRQ 180
|||||
DB 144 KETAFLLNMGDHVTRLDRWPELNEALPNDERDPTMPVAAATTIRKLLTGELLTLASRQ 203
|||||
QY 181 QLIDMMEADKVAAGPLRSALPA 202
|||||
DB 204 QLIDMMEADKVAAGPLRSALPA 225
|||||

RESULT 8

S60310
extended spectrum beta-lactamase CAZ-2 - *Klebsiella pneumoniae*
C:Species: *Klebsiella pneumoniae*
C:Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 22-Jun-1999
C:Accession: S60310
R:Chanal, C.; Poupart, M.C.; Sirot, D.; Labie, R.; Sirot, J.; Cluzel, R.
Antimicrob. Agents Chemother. 36, 1817-1820, 1992
A:Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.
A:Reference number: S60310; MUID:93037315; PMID:1416873
A:Accession: S60310
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <CHA>
A:Cross-references: EMBL:X65252; NID:9296951; PIND:CAA46344.1; PID:9296952
C:Superfamily: beta-lactamase I

Query Match 98.2%; Score 1013; DB 2; Length 286;
Best Local Similarity 97.5%; Pred. No. 5.4e-81;
Matches 197; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITLVKXADBDQAGAVGYIEIDLSGKILSFRRPFRPMSSTFKVLLCGAVLSRID 60
|||||
DB 24 HPEITLVKXADBDQAGAVGYIEIDLSGKILSFRRPFRPMSSTFKVLLCGAVLSRID 83
|||||
QY 61 AGOBLGRRIRHSQNDLVYSPVTEKHLTDGNTVRELCSAAITMSDNTAANILLTTIGCP 120
|||||

Db 84 AGOQLGRRIHYSQNDLVKSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 143
QY 121 KETLAFLLHNMGDHVTRLDRWPEPELNEAIPNDRDPTTVPAAATTLRKLLTGELLTLASRQ 180
Db 144 KETLAFLLHNMGDHVTRLDRWPEPELNEAIPNDRDPTTVPAAATTLRKLLTGELLTLASRQ 203
QY 181 QLIDWMEADKVAAGPLRSALPA 202
Db 204 QLIDWMEADKVAAGPLRSALPA 225

RESULT 9

S60311
beta-lactamase (EC 3.5.2.6) TEM-1 - Klebsiella pneumoniae transposon Tn1331
C/Species: Klebsiella pneumoniae
C/Date: 12-Apr-1996 #sequence revision 19-Apr-1996 #text_change 09-Jul-2004
C/Accession: S60311; F37392; F00498
R/Chanal, C.; Poupart, M.C.; Siroc, D.; Labia, R.; Siroc, J.; Cluzel, R.
AntiMicrob. Agents Chemother. 36, 1817-1820, 1992
A/Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.
A/Reference number: S60310; MUID:93037315; PMID:1416873
A/Accession: S60311
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-286 <CHA>
A/Cross-references: UNIPROT:Q99224; EMBL:X65253; NID:g296953; PIDN:CAA46345.1; PID:g2969
R/Toimaaky, M.E.
Plasmid 24, 218-226, 1990
A/Title: Sequencing and expression of aadA, bla, and tnpR from the multi-resistance trans
A/Reference number: A37392; MUID:91172904; PMID:1965948
A/Accession: F37392
A/Molecule type: DNA
A/Residues: 1-32 <TOL>
A/Cross-references: GB:M5547; NID:g155010; PIDN:AAA9408.1; PID:g155016
C/Genetics:
A:Gene: TEM-bla
C:Superfamily: beta-lactamase I
C/Keywords: antibiotic resistance; hydrolase
Query Match 98.2%; Score 1013; DB 2; Length 286;
Best Local Similarity 97.5%; Pred. No. 5.4e-81;
Matches 197; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 HPEFLVVKVKAEDQAGRVGTELDLNSGKLTSEFRPEPRPMMSTFKVLLCGAVLSRID 60
Db 24 HPEFLVVKVKAEDQAGRVGTELDLNSGKLTSEFRPEPRPMMSTFKVLLCGAVLSRID 83
QY 61 AGOQLGRRIHYSQNDLVKSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120
Db 84 AGOQLGRRIHYSQNDLVKSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 143
QY 121 KETLAFLLHNMGDHVTRLDRWPEPELNEAIPNDRDPTTVPAAATTLRKLLTGELLTLASRQ 180
Db 144 KETLAFLLHNMGDHVTRLDRWPEPELNEAIPNDRDPTTVPAAATTLRKLLTGELLTLASRQ 203
QY 181 QLIDWMEADKVAAGPLRSALPA 202
Db 204 QLIDWMEADKVAAGPLRSALPA 225

RESULT 10

U01546
Bla protein - Salmonella typhimurium plasmid NTP16
N/Alternate names: beta lactamase homolog
C/Species: Salmonella typhimurium
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: U01546
R/Cannon, P.M.; Scriver, P.
Plasmid 27, 220-230, 1992
A/Title: Complete nucleotide sequence and gene organization of plasmid NTP16.
A/Reference number: U01548; MUID:92383313; PMID:1325061
A/Accession: U01546
A/Status: translation not shown

A/Molecule type: DNA
A/Residues: 1-286 <CAN>
A/Cross-references: UNIPROT:Q812F9
C/Genetics:
A:Genome: plasmid
C:Superfamily: beta-lactamase I
Query Match 98.2%; Score 1013; DB 2; Length 286;
Best Local Similarity 98.0%; Pred. No. 5.4e-81;
Matches 198; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HPEFLVVKVKAEDQAGRVGTELDLNSGKLTSEFRPEPRPMMSTFKVLLCGAVLSRID 60
Db 24 HPEFLVVKVKAEDQAGRVGTELDLNSGKLTSEFRPEPRPMMSTFKVLLCGAVLSRID 83
QY 61 AGOQLGRRIHYSQNDLVKSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120
Db 84 AGOQLGRRIHYSQNDLVKSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 143
QY 121 KETLAFLLHNMGDHVTRLDRWPEPELNEAIPNDRDPTTVPAAATTLRKLLTGELLTLASRQ 180
Db 144 KETLAFLLHNMGDHVTRLDRWPEPELNEAIPNDRDPTTVPAAATTLRKLLTGELLTLASRQ 203
QY 181 QLIDWMEADKVAAGPLRSALPA 202
Db 204 QLIDWMEADKVAAGPLRSALPA 225

RESULT 11

S16146
beta-lactamase (EC 3.5.2.6) 2A precursor - Klebsiella pneumoniae plasmids
N/Alternate names: beta-lactamase SHV2A
C/Species: Klebsiella pneumoniae
C/Date: 21-Nov-1993 #sequence revision 10-Nov-1995 #text_change 15-Oct-1999
C/Accession: S16146; A35395; S18767
R/Podbielski, A.; Schoenling, J.; Melzer, B.; Warnatz, K.; Leusch, H.G.
J. Gen. Microbiol. 137, 569-578, 1991
A/Title: Molecular characterization of a new plasmid-encoded SHV-type beta-lactamase (SH
A/Reference number: S16146; MUID:91237320; PMID:2033379
A/Accession: S16146
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-286 <POD>
A/Cross-references: EMBL:X53817; NID:g43795; PIDN:CAA37813.1; PID:g43796
A/Experimental source: plasmid pZMP1
R/lee, K.Y.; Hopkins, J.D.; Syvanen, M.
J. Bacteriol. 172, 3229-3236, 1990
A/Title: Direct involvement of IS26 in an antibiotic resistance operon.
A/Reference number: A35395; MUID:90264317; PMID:2160941
A/Accession: A35395
A/Molecule type: DNA
A/Residues: 1-30, 'L', 32-286 <LEB>
A/Cross-references: GB:X62115; NID:g48988; PIDN:CAA44025.1; PID:g48990
A/Experimental source: plasmid BMH77
C/Genetics:
A:Gene: blaS2A
A:Genome: plasmid
C:Superfamily: beta-lactamase I
C/Keywords: antibiotic resistance; hydrolase
Query Match 69.5%; Score 717; DB 2; Length 286;
Best Local Similarity 67.7%; Pred. No. 3.9e-55;
Matches 136; Conservative 29; Mismatches 36; Indels 0; Gaps 0;

QY 2 PETLVVKVKAEDQAGRVGTELDLNSGKLTSEFRPEPRPMMSTFKVLLCGAVLSRID 61
Db 23 PETLVVKVKAEDQAGRVGTELDLNSGKLTSEFRPEPRPMMSTFKVLLCGAVLSRID 82
QY 62 AGOQLGRRIHYSQNDLVKSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 121
Db 83 AGOQLGRRIHYSQNDLVKSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 142
QY 122 ELTAFLLHNMGDHVTRLDRWPEPELNEAIPNDRDPTTVPAAATTLRKLLTGELLTLASRQ 181

Db 143 G|T|A|T|R|Q|I|G|D|N|V|R|L|D|W|E|T|E|L|N|E|A|L|P|G|D|A|R|D|T|T|P|A|S|M|A|T|L|R|K|L|T|S|Q|R|S|A|R|S|Q|R|Q 202
Qy 182 L|I|D|W|E|A|D|K|V|A|G|P|L|R|S|A|L|P|A 202
Db 203 L|I|Q|W|V|D|R|V|A|G|P|L|R|S|V|L|P|A 223

RESULT 12

A60679
beta-lactamase (EC 3.5.2.6) SHV-2 precursor - *Salmonella typhimurium* plasmid pHT1
C:Species: *Salmonella typhimurium*
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Aug-2004
C:Accession: A60679
R:Garbary-Chenon, A.; Godard, V.; Labia, R.; Nicot, J.C.
Anticarb. Agents Chemother. 34, 1444-1446, 1990
A:Title: Nucleotide sequence of SHV-2 beta-lactamase gene.
A:Reference number: A60679; MUID:90351141; PMID:2201259
A:Accession: A60679
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-286 <BAR>
A:Cross-references: GB:L47119; NID:9972890; PIDN:AAA75015.1; PID:9972891
C:Genetics:
A:Genome: plasmid
C:Superfamily: Beta-lactamase I
C:Keywords: antibiotic resistance; hydrolase
F:1-21/Domain: signal sequence #status predicted <SIG>

Query Match 69.5%; Score 717; DB 2; Length 286;
Best Local Similarity 67.7%; Pred. No. 3.9e-55;
Matches 136; Conservative 29; Mismatches 36; Indels 0; Gaps 0;

Qy 2 P|E|T|V|K|V|D|A|D|Q|G|A|R|G|Y|I|E|L|D|N|S|G|I|E|S|F|P|E|R|F|P|M|S|T|F|K|V|L|G|C|A|V|L|R|D|A 61
Db 23 P|Q|P|E|Q|I|Q|S|S|Q|S|G|R|V|G|M|E|M|D|L|A|S|G|R|T|L|T|A|R|A|D|R|F|P|M|S|T|F|K|V|L|G|C|A|V|L|R|D|A 82
Qy 62 G|Q|E|Q|R|R|I|H|Y|S|O|N|D|V|E|S|P|V|T|E|K|H|L|D|G|M|T|V|R|E|L|C|S|A|I|T|S|D|N|T|A|N|L|L|T|T|G|G|P|K 121
Db 83 G|D|E|Q|R|R|I|H|Y|Q|D|L|V|D|S|P|V|S|E|K|H|L|D|G|M|T|V|R|E|L|C|A|A|I|T|S|D|N|S|A|N|L|L|T|A|V|G|G|P|A 142
Qy 122 E|L|T|A|F|L|H|M|G|H|V|R|L|D|W|E|P|E|L|N|E|A|I|P|N|D|R|D|T|T|P|V|A|A|T|T|K|L|T|G|E|L|L|T|A|S|R|Q 181
Db 143 G|T|A|T|R|Q|I|G|D|N|V|R|L|D|W|E|T|E|L|N|E|A|L|P|G|D|A|R|D|T|T|P|A|S|M|A|T|L|R|K|L|T|S|Q|R|S|A|R|S|Q|R|Q 202
Qy 182 L|I|D|W|E|A|D|K|V|A|G|P|L|R|S|A|L|P|A 202
Db 203 L|I|Q|W|V|D|R|V|A|G|P|L|R|S|V|L|P|A 223

RESULT 13

S00464
beta-lactamase (EC 3.5.2.6) class A - *Escherichia coli* plasmid p453
N:Alternate names: beta-lactamase P1T-2; beta-lactamase SHV-1
C:Species: *Escherichia coli*
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1993
C:Accession: S00464
R:Barthelemy, M.; Peduzzi, J.; Labia, R.
Biochem. J. 251, 73-79, 1988
A:Title: Complete amino acid sequence of p453-plasmid-mediated P1T-2 beta-lactamase (SHV)
A:Reference number: S00464; MUID:88268817; PMID:3260490
A:Accession: S00464
A:Molecule type: protein
A:Residues: 1-265 <BAR>
C:Genetics:
A:Genome: plasmid
C:Superfamily: beta-lactamase I
C:Keywords: antibiotic resistance; hydrolase

Query Match 69.1%; Score 713; DB 2; Length 265;
Best Local Similarity 67.7%; Pred. No. 7.9e-55;
Matches 136; Conservative 29; Mismatches 36; Indels 0; Gaps 0;

Qy 2 P|E|T|V|K|V|D|A|D|Q|G|A|R|G|Y|I|E|L|D|N|S|G|I|E|S|F|P|E|R|F|P|M|S|T|F|K|V|L|G|C|A|V|L|R|D|A 61
Db 2 P|Q|P|E|Q|I|Q|S|S|Q|S|G|R|V|G|M|E|M|D|L|A|S|G|R|T|L|T|A|R|A|D|R|F|P|M|S|T|F|K|V|L|G|C|A|V|L|R|D|A 61

Qy 62 G|Q|E|Q|R|R|I|H|Y|S|O|N|D|V|E|S|P|V|T|E|K|H|L|D|G|M|T|V|R|E|L|C|S|A|I|T|S|D|N|T|A|N|L|L|T|T|G|G|P|K 121
Db 62 G|D|E|Q|R|R|I|H|Y|Q|D|L|V|D|S|P|V|S|E|K|H|L|D|G|M|T|V|R|E|L|C|A|A|I|T|S|D|N|S|A|N|L|L|T|A|V|G|G|P|A 121

Qy 122 E|L|T|A|F|L|H|M|G|H|V|R|L|D|W|E|P|E|L|N|E|A|I|P|N|D|R|D|T|T|P|V|A|A|T|T|K|L|T|G|E|L|L|T|A|S|R|Q 181
Db 122 G|T|A|T|R|Q|I|G|D|N|V|R|L|D|W|E|T|E|L|N|E|A|L|P|G|D|A|R|D|T|T|P|A|S|M|A|T|L|R|K|L|T|S|Q|R|S|A|R|S|Q|R|Q 181

Qy 182 L|I|D|W|E|A|D|K|V|A|G|P|L|R|S|A|L|P|A 202
Db 182 L|I|Q|W|V|D|R|V|A|G|P|L|R|S|V|L|P|A 202

RESULT 14

S02434
beta-lactamase (EC 3.5.2.6) SHV-2 - *Escherichia coli*
C:Species: *Escherichia coli*
C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993
C:Accession: S02434
R:Barthelemy, M.; Peduzzi, J.; Yaghlane, H.B.; Labia, R.
FEBS Lett. 231, 217-220, 1988
A:Title: Single amino acid substitution between SHV-1 beta-lactamase and cefotaxime-hydr
A:Reference number: S02434; MUID:88196385; PMID:3129309
A:Accession: S02434
A:Molecule type: protein
A:Residues: 1-265 <BAR>
C:Superfamily: beta-lactamase I
C:Keywords: antibiotic resistance; hydrolase

Query Match 69.1%; Score 713; DB 2; Length 265;
Best Local Similarity 67.7%; Pred. No. 7.9e-55;
Matches 136; Conservative 29; Mismatches 36; Indels 0; Gaps 0;

Qy 2 P|E|T|V|K|V|D|A|D|Q|G|A|R|G|Y|I|E|L|D|N|S|G|I|E|S|F|P|E|R|F|P|M|S|T|F|K|V|L|G|C|A|V|L|R|D|A 61
Db 2 P|Q|P|E|Q|I|Q|S|S|Q|S|G|R|V|G|M|E|M|D|L|A|S|G|R|T|L|T|A|R|A|D|R|F|P|M|S|T|F|K|V|L|G|C|A|V|L|R|D|A 61

Qy 62 G|Q|E|Q|R|R|I|H|Y|S|O|N|D|V|E|S|P|V|T|E|K|H|L|D|G|M|T|V|R|E|L|C|S|A|I|T|S|D|N|T|A|N|L|L|T|T|G|G|P|K 121
Db 62 G|D|E|Q|R|R|I|H|Y|Q|D|L|V|D|S|P|V|S|E|K|H|L|D|G|M|T|V|R|E|L|C|A|A|I|T|S|D|N|S|A|N|L|L|T|A|V|G|G|P|A 121

Qy 122 E|L|T|A|F|L|H|M|G|H|V|R|L|D|W|E|P|E|L|N|E|A|I|P|N|D|R|D|T|T|P|V|A|A|T|T|K|L|T|G|E|L|L|T|A|S|R|Q 181
Db 122 G|T|A|T|R|Q|I|G|D|N|V|R|L|D|W|E|T|E|L|N|E|A|L|P|G|D|A|R|D|T|T|P|A|S|M|A|T|L|R|K|L|T|S|Q|R|S|A|R|S|Q|R|Q 181

Qy 182 L|I|D|W|E|A|D|K|V|A|G|P|L|R|S|A|L|P|A 202
Db 182 L|I|Q|W|V|D|R|V|A|G|P|L|R|S|V|L|P|A 202

RESULT 15

A44998
beta-lactamase (EC 3.5.2.6) SHV-2 - *Klebsiella ozaena* plasmid pBP60
C:Species: *Klebsiella ozaena*
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004
C:Accession: A44998; S12703
R:Hulet, A.; Couture, F.; Levesque, R.C.
Anticarb. Agents Chemother. 34, 1725-1732, 1990
A:Title: Nucleotide sequence and phylogeny of SHV-2 beta-lactamase.
A:Reference number: A44998; MUID:91136192; PMID:2285285
A:Accession: A44998
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-286 <HUI>
A:Cross-references: UNIPROT:P14558; GB:M95179; NID:9150488; PIDN:AAA25526.1; PID:9150489
R:Podolski, A.; Melzer, B.
Nucleic Acids Res. 18, 4916, 1990
A:Title: Nucleotide sequence of the gene encoding the SHV-2 beta-lactamase (bla(SHV-2))
A:Reference number: S12703; MUID:90370479; PMID:2395654

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:35:06 ; Search time 13.8556 Seconds

(without alignments)
1319,408 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_190

Perfect score: 975

Sequence: 1 HPELTIVKVKDADQIGARVGV.....GELTLTASRQQLIDWMEADK 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

PIR 79: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	975	100.0	286	2 TS1301	beta-lactamase (EC
2	975	100.0	286	2 S47061	beta-lactamase (EC
3	975	100.0	286	4 S41975	beta-lactamase (EC
4	970	99.5	286	1 PNECP	beta-lactamase (EC
5	970	99.5	286	4 I40905	beta-lactamase (EC
6	962	98.7	286	2 S30113	beta-lactamase (EC
7	957	98.2	286	2 S60312	extended spectrum
8	956	98.1	286	2 S60310	extended spectrum
9	956	98.1	286	2 S60311	beta-lactamase (EC
10	956	98.1	286	2 J01546	Bla protein - Salm
11	666	68.3	286	2 S16146	beta-lactamase (EC
12	666	68.3	286	2 A60679	beta-lactamase (EC
13	662	67.9	286	2 S00464	beta-lactamase (EC
14	662	67.9	286	2 S02434	beta-lactamase (EC
15	662	67.9	286	1 A44958	beta-lactamase (EC
16	662	67.9	286	1 A60632	beta-lactamase (EC
17	659	67.6	286	2 A60448	beta-lactamase (EC
18	659	67.6	286	2 A37200	beta-lactamase (EC
19	644	66.1	279	2 A24469	beta-lactamase (EC
20	637.5	65.4	287	1 A44966	beta-lactamase (EC
21	611	62.7	286	1 A44958	beta-lactamase (EC
22	523	53.6	298	2 A41381	beta-lactamase (EC
23	431.5	44.3	281	2 D95995	probable Beta lact
24	410.5	42.1	314	2 S06967	beta-lactamase (EC
25	407.5	41.8	294	2 S16553	beta-lactamase (EC
26	406	41.6	293	2 S04649	beta-lactamase (EC
27	401.5	41.2	263	2 A54543	beta-lactamase (EC
28	401.5	41.2	302	2 S36188	beta-lactamase (EC
29	400.5	41.1	306	1 B45822	beta-lactamase (EC

30	398.5	40.9	291	2 S42075	beta-lactamase (EC
31	395.5	40.6	306	2 G69674	beta-lactamase (EC
32	390.5	40.1	311	2 JN0520	beta-lactamase (EC
33	389.5	39.9	306	2 S47330	penicillinase - Ba
34	381	39.1	305	2 A61156	beta-lactamase (EC
35	381	39.1	305	2 A57002	beta-lactamase (EC
36	381	39.1	305	2 A60680	beta-lactamase (EC
37	380.5	39.0	291	2 JF0074	beta-lactamase (EC
38	378.5	38.8	263	2 S23929	beta-lactamase (EC
39	373.5	38.3	305	1 C45822	beta-lactamase (EC
40	372	38.2	310	2 JI0091	beta-lactamase (EC
41	371.5	38.1	288	2 JQ1136	beta-lactamase (EC
42	371.5	38.1	311	1 S02714	beta-lactamase (EC
43	367.5	37.7	304	2 A49789	beta-lactamase (EC
44	367.5	37.7	304	2 A35001	beta-lactamase (EC
45	366.5	37.6	307	1 PNB5L	beta-lactamase (EC

ALIGNMENTS

RESULT 1

TS1301 beta-lactamase (EC 3.5.2.6) - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000

C:Accession: TS1301

R:WACH, A.; BRACHAT, A.; ALBERTSSEGUI, C.; REBISCHUNG, C.; PHILIPSEN, P.

Yeast 13, 1065-1075, 1997

A:Title: Heterologous His3 marker and GFP reporter modules for PCR-targeting in Saccharon

A:Reference number: Z09587

A:Accession: TS1301

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-286 <MAC>

A:Cross-references: EMBL:AJ002683; PIDN:CAA05686.1

C:Genetics:

A:Gene: bla

C:Superfamily: beta-lactamase I

C:Keywords: hydrolase

Query Match 100.0%; Score 975; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.8e-80;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELTIVKVKDADQIGARVGYIELDNGSKILIESRPERFRPMSTFKYLIGAVLSRID 60

DB 24 HPELTIVKVKDADQIGARVGYIELDNGSKILIESRPERFRPMSTFKYLIGAVLSRID 83

QY 61 AGQEQIGRIHYSQNDIVESFVTEKHLTDGNTVELCSAATMDSNFTANLLTTIGSP 120

DB 84 AGQEQIGRIHYSQNDIVESFVTEKHLTDGNTVELCSAATMDSNFTANLLTTIGSP 143

QY 121 KELTAFILNMGDVTIRLDRWEPDELNEAIPNDRDITPMVAMATTLRKLLTGELTLASRQ 180

DB 144 KELTAFILNMGDVTIRLDRWEPDELNEAIPNDRDITPMVAMATTLRKLLTGELTLASRQ 203

QY 181 QLIIDWMEADK 190

DB 204 QLIIDWMEADK 213

RESULT 2

S47061 beta-lactamase (EC 3.5.2.6) - phage phi-X174

C:Species: phage phi-X174

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S47061

R:Hentrich, B.; Schmidberger, B.

Submitted to the EMBL Data Library, July 1994

A:Description: A variant of phix174 gene B-based positive selection vectors with enhancer

A:Reference number: S47060

A:Accession: S47061

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-286 <HEN>
A:Cross-references: UNIPROT:Q38058; EMBL:Z35638; NID:G520996; PIDN:CAA84692.1; PID:G5209
C:Superfamily: beta-lactamase I
C:Keywords: hydrolase

Query Match 100.0%; Score 975; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.8e-80;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADADQAGAVGYIELDINSKILSFRRPFRPMSSTFKVLLCGAVLSRID 60
DB HPELVKVKADADQAGAVGYIELDINSKILSFRRPFRPMSSTFKVLLCGAVLSRID 83
QY 61 AGOBLGRIRIHSQNDLVEYSPVTEKHLTDGMTVELCSAATMSDNTAANLLTTIGCP 120
DB AGOBLGRIRIHSQNDLVEYSPVTEKHLTDGMTVELCSAATMSDNTAANLLTTIGCP 143
QY 121 KELTAFILNMGDHYTRLDRWPELNEALPNDERTTTPVAAATTKLLTGELLTLASRQ 180
DB KELTAFILNMGDHYTRLDRWPELNEALPNDERTTTPVAAATTKLLTGELLTLASRQ 203
QY 181 QLIDWMEADK 190
DB 204 QLIDWMEADK 213

RESULT 3
S41975
beta-lactamase (EC 3.5.2.6) precursor - synthetic
C:Species: synthetic
C:Date: 25-Dec-1994 #sequence_revision 22-Aug-1996 #text_change 20-Oct-2000
C:Accession: S41975
R:Kasster, K.H.; Montcoliv, L.; Kern, H.; Thulke, M.; Schutz, G.
Gene 148; 67-70; 1994
A:Title: Universal beta-galactosidase cloning vectors for promoter analysis and gene tar
A:Reference number: A57991; MUID:95011660; PMID:7926839
A:Accession: S41975
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-286 <KAS>
A:Cross-references: EMBL:X76682; NID:G453622; PIDN:CAA54104.1; PID:G453623
A:Note: submitted to the EMBL Data Library, December 1993
C:Keywords: hydrolase

Query Match 100.0%; Score 975; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.8e-80;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADADQAGAVGYIELDINSKILSFRRPFRPMSSTFKVLLCGAVLSRID 60
DB HPELVKVKADADQAGAVGYIELDINSKILSFRRPFRPMSSTFKVLLCGAVLSRID 83
QY 61 AGOBLGRIRIHSQNDLVEYSPVTEKHLTDGMTVELCSAATMSDNTAANLLTTIGCP 120
DB AGOBLGRIRIHSQNDLVEYSPVTEKHLTDGMTVELCSAATMSDNTAANLLTTIGCP 143
QY 121 KELTAFILNMGDHYTRLDRWPELNEALPNDERTTTPVAAATTKLLTGELLTLASRQ 180
DB KELTAFILNMGDHYTRLDRWPELNEALPNDERTTTPVAAATTKLLTGELLTLASRQ 203
QY 181 QLIDWMEADK 190
DB 204 QLIDWMEADK 213

RESULT 4
PNECP
beta-lactamase (EC 3.5.2.6) precursor - Escherichia coli plasmid
N:Alternate names: beta-lactamase TEM-6 (for Dlat-6 DNA); penicillinase
C:Species: Escherichia coli
C:Date: 30-Nov-1980 #sequence_revision 01-Sep-1981 #text_change 16-Aug-2004

C:Accession: A93821; A93820; A35387; S24415; A01005
R:Succliffe, J.G.
Proc. Natl. Acad. Sci. U.S.A. 75, 3737-3741, 1978
A:Title: Nucleotide sequence of the ampicillin resistance gene of Escherichia coli plasmid
A:Reference number: A93821; MUID:75012484; PMID:358200
A:Accession: A93821

A:Molecule type: DNA
A:Residues: 1-286 <STU>
A:Cross-references: UNIPROT:P00810; GB:V00613; GB:J01832; NID:G43710; PIDN:CAA23886.1; P1
A:Experimental source: plasmid pBR322

R:Amber, R.P.; Scott, G.K.
Proc. Natl. Acad. Sci. U.S.A. 75, 3732-3736, 1978
A:Title: Partial amino acid sequence of penicillinase coded by Escherichia coli plasmid f
A:Reference number: A93820; MUID:75012483; PMID:358199
A:Accession: A93820

A:Molecule type: protein
A:Residues: 24-36, 'K', 38-286 <AMB>
A:Experimental source: plasmid R6K
R:Kornacki, J.A.; Burlage, R.S.; Figurski, D.H.
J. Bacteriol. 172, 3040-3050, 1990

A:Title: The kil-kor regulon of broad-host-range plasmid RK2: nucleotide sequence, polype
A:Reference number: A35387; MUID:90264294; PMID:2160936
A:Accession: A35387

A:Molecule type: DNA
A:Residues: 182-286 <ROR>
A:Cross-references: GB:M32794; NID:G152521; PIDN:AAA26408.1; PID:G152522
A:Experimental source: PK2

R:Cousens, S.; Sougkoff, W.; Mabilat, C.; Bauernfeind, A.; Courvalin, P.
U. Gen. Microbiol. 137, 2681-2687, 1991

A:Title: An ISI-like element is responsible for high-level synthesis of extended-spectrum
A:Reference number: S24415; MUID:92166702; PMID:1665171
A:Accession: S24415

A:Status: translation not shown
A:Molecule type: DNA

A:Residues: 1-101, 'K', 103-161, 'H', 163-286 <GOU>
A:Cross-references: EMBL:X57972; NID:G41816; PIDN:CAA41038.1; PID:G41817
A:Experimental source: ISI-like blaT-6 DNA
R:Succliffe, J.G.

Cold Spring Harb. Symp. Quant. Biol. 43, 77-90, 1979
A:Title: Complete nucleotide sequence of the Escherichia coli plasmid pBR322.

A:Reference number: A80923; MUID:80002802; PMID:383387

A:Contents: annotation

C:Comment: Like most penicillinases from gram-negative bacteria, this enzyme, coded by a
C:Genetics:

A:Genome: plasmid

C:Superfamily: Beta-lactamase I

C:Keywords: antibiotic resistance; hydrolase; membrane protein

F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-286/Product: beta-lactamase #status experimental <MAT>
F:68/Active site: Ser #status predicted

F:75-121/Diulfide bonds: #status predicted

Query Match 99.5%; Score 970; DB 1; Length 286;
Best Local Similarity 98.9%; Pred. No. 1.6e-79;
Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPELVKVKADADQAGAVGYIELDINSKILSFRRPFRPMSSTFKVLLCGAVLSRID 60
DB HPELVKVKADADQAGAVGYIELDINSKILSFRRPFRPMSSTFKVLLCGAVLSRID 83
QY 61 AGOBLGRIRIHSQNDLVEYSPVTEKHLTDGMTVELCSAATMSDNTAANLLTTIGCP 120
DB AGOBLGRIRIHSQNDLVEYSPVTEKHLTDGMTVELCSAATMSDNTAANLLTTIGCP 143
QY 121 KELTAFILNMGDHYTRLDRWPELNEALPNDERTTTPVAAATTKLLTGELLTLASRQ 180
DB KELTAFILNMGDHYTRLDRWPELNEALPNDERTTTPVAAATTKLLTGELLTLASRQ 203
QY 181 QLIDWMEADK 190
DB 204 QLIDWMEADK 213

RESULT 5

140905 beta-lactamase (EC 3.5.2.6) - synthetic

C:Species: synthetic

A:Note: Cloning vector pCG1408 engineered and expressed in *Clavibacter xyli* subsp. *cynod*

C:Date: 15-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Oct-2000

C:Accession: I40905

R:Taylor, J.; Stearman, R.S.; Urcanti, B.B.

Plasmid 29, 241-244, 1993

A:Title: Development of a native plasmid as a cloning vector in *Clavibacter xyli* subsp.

A:Reference number: I40904; MUID:93361581; PMID:7689234

A:Accession: I40905

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-286 <RES>

A:Cross-references: EMBL:U21228; NID:9885956; PIND:AAA70411.1; PID:9885958

C:Keywords: hydrolase

Query Match 99.5%; Score 970; DB 4; Length 286;

Best Local Similarity 98.9%; Pred. No. 1.6e-79;

Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HPEITLVKXDAEDQAGAVGYIELDLSGKILSFPRPERPMMSTFKVLLCGAVLSRD 60
|||||
Db 24 HPEITLVKXDAEDQAGAVGYIELDLSGKILSFPRPERPMMSTFKVLLCGAVLSRD 83

Qy 61 AGOEOLGRRIHYSQNDLVYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 120
|||||
Db 84 AGOEOLGRRIHYSQNDLVYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 143

Qy 121 KELTAFLLNMGDHTVRLDRWPELNEALPNDERDTTMAPAATTIRKLLTGLTLASRQ 180
|||||
Db 144 KELTAFLLNMGDHTVRLDRWPELNEALPNDERDTTMAPAATTIRKLLTGLTLASRQ 203

Qy 181 QLIDMMEADK 190
|||||
Db 204 QLIDMMEADK 213

RESULT 6

S30113 beta-lactamase (EC 3.5.2.6) TEM-3 - *Klebsiella pneumoniae* plasmid pCFE04C:Species: *Klebsiella pneumoniae*

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C:Accession: S30113

R:Mabilat, C.; Lourencao-Vital, J.; Gousard, S.; Courvalin, P.

Mol. Gen. Genet. 235, 113-121, 1992

A:Title: A new example of physical linkage between TnI and Tn21: the antibiotic multiple

A:Reference number: S30112; MUID:93062798; PMID:1331747

A:Accession: S30113

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-286 <MA>

A:Cross-references: UNIPROT:P00810; EMBL:X64523; NID:943797; PIND:CAA45828.1; PID:943798

C:Genetics:

A:Gene: bla(TEM-3)

A:Genome: plasmid

A:Superfamily: beta-lactamase I

C:Keywords: antibiotic resistance; hydrolase

Query Match 98.7%; Score 962; DB 2; Length 286;

Best Local Similarity 97.9%; Pred. No. 8.6e-79;

Matches 186; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HPEITLVKXDAEDQAGAVGYIELDLSGKILSFPRPERPMMSTFKVLLCGAVLSRD 60
|||||
Db 24 HPEITLVKXDAEDQAGAVGYIELDLSGKILSFPRPERPMMSTFKVLLCGAVLSRD 83

Qy 61 AGOEOLGRRIHYSQNDLVYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 120
|||||
Db 84 AGOEOLGRRIHYSQNDLVYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 143

Qy 121 KELTAFLLNMGDHTVRLDRWPELNEALPNDERDTTMAPAATTIRKLLTGLTLASRQ 180
|||||

Db 144 KELTAFLLNMGDHTVRLDRWPELNEALPNDERDTTMAPAATTIRKLLTGLTLASRQ 203
|||||

Qy 181 QLIDMMEADK 190
|||||

Db 204 QLIDMMEADK 213
|||||

RESULT 7

S60312 extended spectrum beta-lactamase CAZ-7 - *Klebsiella pneumoniae*C:Species: *Klebsiella pneumoniae*

C:Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 22-Jun-1999

C:Accession: S60312

R:Chanal, C.; Poupart, M.C.; Strot, D.; Labia, R.; Strot, J.; Cluzel, R.

Antimicrob. Agents Chemother. 36, 1817-1820, 1992

A:Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.

A:Reference number: S60310; MUID:93037315; PMID:1416873

A:Accession: S60312

A:Status: preliminary; translation not shown

A:Molecule type: DNA

A:Residues: 1-286 <CHA>

A:Cross-references: EMBL:X65254; NID:9296955; PIND:CAA46346.1; PID:9296956

C:Superfamily: beta-lactamase I

Query Match 98.2%; Score 957; DB 2; Length 286;

Best Local Similarity 97.4%; Pred. No. 2.4e-78;

Matches 185; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HPEITLVKXDAEDQAGAVGYIELDLSGKILSFPRPERPMMSTFKVLLCGAVLSRD 60
|||||
Db 24 HPEITLVKXDAEDQAGAVGYIELDLSGKILSFPRPERPMMSTFKVLLCGAVLSRD 83

Qy 61 AGOEOLGRRIHYSQNDLVYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 120
|||||
Db 84 AGOEOLGRRIHYSQNDLVYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 143

Qy 121 KELTAFLLNMGDHTVRLDRWPELNEALPNDERDTTMAPAATTIRKLLTGLTLASRQ 180
|||||
Db 144 KELTAFLLNMGDHTVRLDRWPELNEALPNDERDTTMAPAATTIRKLLTGLTLASRQ 203

Qy 181 QLIDMMEADK 190
|||||
Db 204 QLIDMMEADK 213
|||||

RESULT 8

S60310 extended spectrum beta-lactamase CAZ-2 - *Klebsiella pneumoniae*C:Species: *Klebsiella pneumoniae*

C:Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 22-Jun-1999

C:Accession: S60310

R:Chanal, C.; Poupart, M.C.; Strot, D.; Labia, R.; Strot, J.; Cluzel, R.

Antimicrob. Agents Chemother. 36, 1817-1820, 1992

A:Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.

A:Reference number: S60310; MUID:93037315; PMID:1416873

A:Accession: S60310

A:Status: preliminary; translation not shown

A:Molecule type: DNA

A:Residues: 1-286 <CHA>

A:Cross-references: EMBL:X65252; NID:9296951; PIND:CAA46344.1; PID:9296952

C:Superfamily: beta-lactamase I

Query Match 98.1%; Score 956; DB 2; Length 286;

Best Local Similarity 97.4%; Pred. No. 3e-78;

Matches 185; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HPEITLVKXDAEDQAGAVGYIELDLSGKILSFPRPERPMMSTFKVLLCGAVLSRD 60
|||||
Db 24 HPEITLVKXDAEDQAGAVGYIELDLSGKILSFPRPERPMMSTFKVLLCGAVLSRD 83

Qy 61 AGOEOLGRRIHYSQNDLVYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 120
|||||

Db 84 AGOBLGRRIHYSQNDLVKSPVTEKHLTDGWTVELCSAAITMSDNTAAILTTIGSP 143
QY 121 KETLAFILNMGDHVTRLDRWPEPELNEALPNDERDITMPVAAATTLRKLLTGELLTLASRQ 180
Db 144 KETLAFILNMGDHVTRLDRWPEPELNEALPNDERDITMPVAAATTLRKLLTGELLTLASRQ 203
QY 181 QLIDWMEADK 190
Db 204 QLIDWMEADK 213

RESULT 9

S60311
beta-lactamase (EC 3.5.2.6) TEM-1 - Klebsiella pneumoniae transposon Tn1331
C:Species: Klebsiella pneumoniae
C:Date: 12-Apr-1996 #sequence revision 19-Apr-1996 #text_change 09-Jul-2004
C:Accession: S60311, F37392, F00498
R:Chanai, C.; Poupart, M.C.; Siroc, D.; Labia, R.; Siroc, J.; Cluzel, R.
Antimicrob. Agents Chemother. 36, 1817-1820, 1992
A:Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.
A:Reference number: S60310; MUID:93037315; PMID:1416873
A:Accession: S60311
A:Status: preliminary; translation not shown
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <CHA>
A:Cross-references: UNIPROT:Q99224; EMBL:X65253; NID:g296953; PIDN:CAA46345.1; PID:g2969
R:Totmaeky, M.B.
Plasmid 24, 218-226, 1990
A:Title: Sequencing and expression of aadA, bla, and tnpR from the multiresistance trans
A:Reference number: A57392; MUID:91172904; PMID:1963948
A:Accession: F37392
A:Molecule type: DNA
A:Residues: 1-32 <TOL>
A:Cross-references: GB:M55547; NID:g155010; PIDN:AAA98408.1; PID:g155016
C:Genetics:
A:Gene: TEM-bla
C:Superfamily: beta-lactamase I
C:Keywords: antibiotic resistance; hydrolase

Query Match 98.1%; Score 956; DB 2; Length 286;
Best Local Similarity 97.4%; Pred. No. 3e-78; 2; Indels 0; Gaps 0;
Matches 185; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITLVKKAEDQCGARVGYIELDINSKILLESFRRPFRPMMSTFVLLCGAVLSRID 60
Db 24 HPEITLVKKAEDQCGARVGYIELDINSKILLESFRRPFRPMMSTFVLLCGAVLSRID 83
QY 61 AGOBLGRRIHYSQNDLVKSPVTEKHLTDGWTVELCSAAITMSDNTAAILTTIGSP 120
Db 84 AGOBLGRRIHYSQNDLVKSPVTEKHLTDGWTVELCSAAITMSDNTAAILTTIGSP 143
QY 121 KETLAFILNMGDHVTRLDRWPEPELNEALPNDERDITMPVAAATTLRKLLTGELLTLASRQ 180
Db 144 KETLAFILNMGDHVTRLDRWPEPELNEALPNDERDITMPVAAATTLRKLLTGELLTLASRQ 203
QY 181 QLIDWMEADK 190
Db 204 QLIDWMEADK 213

RESULT 10

QY1546
Bla protease - Salmonella typhimurium plasmid NTP16
N:Alternate names: beta lactamase homolog
C:Species: Salmonella typhimurium
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: J01546
R:Canon, P.M.; Strike, P.
Plasmid 27, 220-230, 1992
A:Title: Complete nucleotide sequence and gene organization of plasmid NTP16.
A:Reference number: J01538; MUID:92383313; PMID:1325061
A:Accession: J01546
A:Status: translation not shown

A:Molecule type: DNA
A:Residues: 1-286 <CAN>
A:Cross-references: UNIPROT:Q8L2F9
C:Genetics:
A:Genome: plasmid
C:Superfamily: beta-lactamase I

Query Match 98.1%; Score 956; DB 2; Length 286;
Best Local Similarity 97.9%; Pred. No. 3e-78;
Matches 186; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HPEITLVKKAEDQCGARVGYIELDINSKILLESFRRPFRPMMSTFVLLCGAVLSRID 60
Db 24 HPEITLVKKAEDQCGARVGYIELDINSKILLESFRRPFRPMMSTFVLLCGAVLSRID 83
QY 61 AGOBLGRRIHYSQNDLVKSPVTEKHLTDGWTVELCSAAITMSDNTAAILTTIGSP 120
Db 84 AGOBLGRRIHYSQNDLVKSPVTEKHLTDGWTVELCSAAITMSDNTAAILTTIGSP 143
QY 121 KETLAFILNMGDHVTRLDRWPEPELNEALPNDERDITMPVAAATTLRKLLTGELLTLASRQ 180
Db 144 KETLAFILNMGDHVTRLDRWPEPELNEALPNDERDITMPVAAATTLRKLLTGELLTLASRQ 203
QY 181 QLIDWMEADK 190
Db 204 QLIDWMEADK 213

RESULT 11

S16146
beta-lactamase (EC 3.5.2.6) 2A precursor - Klebsiella pneumoniae plasmids
N:Alternate names: beta-lactamase SHV2A
C:Species: Klebsiella pneumoniae
C:Date: 21-Nov-1993 #sequence revision 10-Nov-1995 #text_change 15-Oct-1999
C:Accession: S16146, A35395, S18767
R:Podolski, A.; Schoenling, J.; Welzer, B.; Warnatz, K.; Leusch, H.G.
J. Gen. Microbiol. 137, 569-578, 1991
A:Title: Molecular characterization of a new plasmid-encoded SHV-type beta-lactamase (SH
A:Reference number: S16146; MUID:91237320; PMID:2033379
A:Accession: S16146
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <POD>
A:Cross-references: EMBL:X53817; NID:g43795; PIDN:CAA37813.1; PID:g43796
A:Experimental source: Plasmid pZMP1
R:Lee, K.Y.; Hopkins, J.D.; Syvanen, M.
J. Bacteriol. 172, 3229-3236, 1990
A:Title: Direct involvement of IS26 in an antibiotic resistance operon.
A:Reference number: A35395; MUID:90264317; PMID:2160941
A:Molecule type: DNA
A:Residues: 1-30, 'L', 32-286 <LEE>
A:Cross-references: GB:X52115; NID:g48988; PIDN:CAA44025.1; PID:g48990
A:Experimental source: Plasmid BW77
C:Genetics:
A:Gene: blaS2A
A:Genome: plasmid
C:Superfamily: beta-lactamase I
C:Keywords: antibiotic resistance; hydrolase

Query Match 68.3%; Score 666; DB 2; Length 286;
Best Local Similarity 66.7%; Pred. No. 3.1e-52;
Matches 126; Conservative 28; Mismatches 35; Indels 0; Gaps 0;

QY 2 PETLVKVDADQCGARVGYIELDINSKILLESFRRPFRPMMSTFVLLCGAVLSRID 61
Db 23 PETLVKVDADQCGARVGYIELDINSKILLESFRRPFRPMMSTFVLLCGAVLSRID 82
QY 62 GOBLGRRIHYSQNDLVKSPVTEKHLTDGWTVELCSAAITMSDNTAAILTTIGSP 121
Db 83 GOBLGRRIHYSQNDLVKSPVTEKHLTDGWTVELCSAAITMSDNTAAILTTIGSP 142
QY 122 ELTAFILNMGDHVTRLDRWPEPELNEALPNDERDITMPVAAATTLRKLLTGELLTLASRQ 181

Query Match	67.9%	Score 662	DB 2	Length 265;
Best Local Similarity	66.7%	Pred. NO. 6.4e-52;		
Matches 126; Conservative	28;	Mismatches 35;	Indels 0;	Gaps 0

A;Cross-references: UNIPROT:P14558; GB:M95179; NID:gl50488; PIDD:AAA25526.1; PID:gl50489
R;Podbielski, A.; Melzer, B.
Nucleic Acids Res. 18, 4916, 1990
A;Title: Nucleotide sequence of the gene encoding the SHV-2 beta-lactamase (bla(SHV-2)) (C
A;Reference number: 512703; MUID:90370479; PMID:2395654

A/Accession: S12703
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1286 <POD>
A/Cross-references: EMBL:X53433; NID:g43789; PIDN:CAA37524.1; PID:g43790
C/Genetics:
A/Genome: plasmid
C/Superfamily: Beta-lactamase I
C/Keywords: antibiotic resistance; hydrolase

Query Match 67.9%; Score 662; DB 1; Length 286;
Best local Similarity 66.7%; Pred. No. 7.1e-52;
Matches 126; Conservative 28; Mismatches 35; Indels 0; Gaps 0;

```
QY 2 PETLVKVDADDOICARVGYTELDLNSGKILESFRPERFPMSTPKYLGCATLSRIDA 61
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 23 PQLBQIKLSESQLSGRVGMLEMDLASGRITLTAMRADERFPWSTFKVVLGAVIARVDA 82
   |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 62 GOEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAITMSDNTANLLTTIGSPK 121
   |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 83 GDEQLERKIHYRQODLVDPSPVSEKHLADGMTVGELCAAITMSDNSAANLLLATVGSPA 142
   |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 122 ELTAFLNMGDPVTRLDREPEPLNEAIPNDEBDTTPVAMATTLRKLLTGLLTASRQ 181
   |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 143 GLTAFLRQIGDVTTRLDREPEPLNEALPGDARDTTTPASMAATLRKLLTSQRLSARSQR 202
   |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 182 LIDWMEADK 190
   ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 203 LLQMWVDDK 211
   ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
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Search completed: June 10, 2005, 10:58:47
Job time : 13.8556 secs

XX (PANO-) PANORAMA RES INC.
PA

XX Balint RF, Her J;
PI

XX WPI; 2001-451857/48.
DR

XX N-PSDB; AAD10411.
DR

XX Interaction-dependent enzyme association systems for detecting
PT interactions between two or three polypeptides, especially in human
PT therapeutics, diagnostics or prognostics, comprise circularly permuted
PT proteins.

XX Claim 38; Fig 2; 104pp; English.
PS

XX The invention relates to new interaction-dependent enzyme association
CC (IDEA) systems that comprise a fusion sequence that encodes for a
CC circularly permuted, interaction-activated proteins that reassemble to
CC form functionally reconstituted marker proteins which produce a
CC detectable signal upon the association of two oligopeptides, or upon
CC simultaneous association of two oligopeptides with a third oligopeptide.
CC The marker protein is preferably a type A beta-lactamase, especially TEM-
CC 1 beta-lactamase of Escherichia coli. The oligopeptide is a member of a
CC proteome library selected from single chain antibody Fv fragment library,
CC an antibody light chain variable region library and a peptide library
CC displayed within thioredoxin. The idea systems are useful for detecting
CC and identifying interactions between intracellular as well as
CC extracellular proteins, particularly between two or three polypeptides.
CC The systems are also useful in selecting with a single marker protein the
CC incorporation of multiple genetic traits in a host cell. In particular,
CC the systems are useful in many applications in human therapeutics,
CC diagnostics and prognostics, as well as in high-throughput screenings
CC systems for the discovery and validation of pharmaceutical targets and
CC drugs. Prior systems (e.g. E. coli Dimer Detection System, yeast two-
CC hybrid system or selective infective phage system) require multiple steps
CC between interaction and phenotype, which cause severe loss of efficiency
CC due to high false positive and false negative rates. The present system
CC is capable of simultaneous detection of multiple interactions between
CC extra-cellular as well as intracellular proteins in a high throughput
CC format. The circularly permuted marker proteins comprising interaction-
CC dependent enzymes find use in cell-based sensors for activation or
CC inhibition of metabolic or signal transduction pathways, in high-
CC throughput mapping of pair-wise protein-protein interactions within and
CC between the proteomes of cells, tissues and pathogenic organisms, and in
CC cell-based screens for high-throughput selection of inhibitors of any
CC protein-protein interaction. The present sequence is Escherichia coli
CC mature TEM-1 beta-lactamase enzyme from plasmid pBR322. TEM-1 beta-
CC lactamase is a product of ampicillin resistance gene. The enzyme has two
CC domains, alpha-omega and mu
CC

XX Sequence 263 AA;
SQ

Query Match 100.0%; Score 1032; DB 4; Length 263;
Best Local Similarity 100.0%; Pred. No. 1.5e-103;

Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADQEDGAVGYIEIDNSGKILSFREPERPPMSTFKVLLCGAVLSRID 60
DB 1 HPELVKVKADQEDGAVGYIEIDNSGKILSFREPERPPMSTFKVLLCGAVLSRID 60
QY 61 AGQQLGRRIHYSONDIVESPVTEKHLTDGMTVRELCSSAATMSDNTAANLLTTTGGP 120
DB 61 AGQQLGRRIHYSONDIVESPVTEKHLTDGMTVRELCSSAATMSDNTAANLLTTTGGP 120
QY 121 KETLAFPLHNMGDHVTRLDRWPEPEINEALPNDERDTWVAVATTLRKLLTGELLTLASRQ 180
DB 121 KETLAFPLHNMGDHVTRLDRWPEPEINEALPNDERDTWVAVATTLRKLLTGELLTLASRQ 180
QY 181 QLIDMEADKVAQPLRLSALPA 202
DB 181 QLIDMEADKVAQPLRLSALPA 202
QY 181 QLIDMEADKVAQPLRLSALPA 202
DB 181 QLIDMEADKVAQPLRLSALPA 202

RESULT 2
AAB36692

ID AAB36692 standard; protein; 263 AA.
XX

XX AAB36692;
AC

XX 15-MAR-2001 (first entry)
DT

XX Escherichia coli mature TEM-1 beta-lactamase protein sequence.
DE

XX Interaction-activated protein, beta-lactamase; protein interaction.
KW

XX Escherichia coli.
OS

XX WO200071702-A1.
PN

XX 30-NOV-2000.
PD

XX 16-MAR-2000; 2000WO-US007108.
PF

XX 25-MAY-1999; 99US-0135926P.
PR

XX 13-JAN-2000; 2000US-0175968P.
PR

XX (PANO-) PANORAMA RES INC.
PA

XX Balint RF, Her J;
PI

XX WPI; 2001-032034/04.
DR

XX N-PSDB; AAC90773.
DR

XX Novel fragment complementation system to identify interactions between
PT polypeptides comprises fragment pairs having first and second members
PT that reassemble into a marker protein which has a directly detectable
PT signal.

XX Disclosure; Fig 2; 94pp; English.
PS

XX The present invention describes a fragment complementation system (I)
CC which comprises a first oligopeptide (OP1) containing an N-terminal
CC fragment with a C-terminal break point and a second oligopeptide (OP2)
CC comprising a C-terminal with a N-terminal breakpoint, in which the C and
CC N terminal fragments are both derived from a marker protein (MP) and
CC reassemble to form a functionally reconstituted MP. Methods from the
CC present invention are used for monitoring the occurrence of protein-
CC protein interactions in a sample, identifying oligopeptide interactions
CC between two different proteomes, identifying epitopes that bind to an
CC immunoglobulin (Ig) variable region, for identifying interactions between
CC an extracellular domain of a transmembrane protein and a polypeptide, for
CC high-throughput identification of compounds that inhibit phosphorylation-
CC regulated signal transducers, forming a enzyme complementation system for
CC selecting simultaneous incorporation of multiple genetic elements into a
CC host cell and for activating a beta-lactam derivative of an antitumor
CC compound in a host who is in need of it. The present sequence represents
CC the Escherichia coli mature TEM-1 beta-lactamase, which is used in the
CC exemplification of the present invention
CC

SQ Sequence 263 AA;
SQ

Query Match 100.0%; Score 1032; DB 4; Length 263;
Best Local Similarity 100.0%; Pred. No. 1.5e-103;

Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADQEDGAVGYIEIDNSGKILSFREPERPPMSTFKVLLCGAVLSRID 60
DB 1 HPELVKVKADQEDGAVGYIEIDNSGKILSFREPERPPMSTFKVLLCGAVLSRID 60
QY 61 AGQQLGRRIHYSONDIVESPVTEKHLTDGMTVRELCSSAATMSDNTAANLLTTTGGP 120
DB 61 AGQQLGRRIHYSONDIVESPVTEKHLTDGMTVRELCSSAATMSDNTAANLLTTTGGP 120
QY 121 KETLAFPLHNMGDHVTRLDRWPEPEINEALPNDERDTWVAVATTLRKLLTGELLTLASRQ 180
DB 121 KETLAFPLHNMGDHVTRLDRWPEPEINEALPNDERDTWVAVATTLRKLLTGELLTLASRQ 180
QY 181 QLIDMEADKVAQPLRLSALPA 202
DB 181 QLIDMEADKVAQPLRLSALPA 202

Oy 181 OLIDMEADKVAGPLRSALPA 202
 Db 181 OLIDMEADKVAGPLRSALPA 202

RESULT 3
 ID ADJ67709 standard; protein; 263 AA.
 AC ADJ67709;
 DT 20-MAY-2004 (first entry)
 DE Escherichia coli TBM-1 beta-lactamase.

KM fragment complementation system; marker protein;
 KM multiple genetic element incorporation; antibiotic resistance;
 KM beta-lactam derivative activation; anti-tumour compound;
 KM functional reassembly; protein-protein interaction; proteome interaction;
 KM immunoglobulin variable region; immune cell protein; CD40;
 KM phosphorylation-regulated cell signal transducer; TBM-1 Beta-lactamase;
 enzyme.

OS Escherichia coli.
 XX
 XX US2004038317-A1.
 PD 26-FEB-2004.
 PF 22-SEP-2003; 2003US-00668778.
 PR 15-MAR-1999; 99US-0124339P.
 PR 25-MAY-1999; 99US-0135926P.
 PR 13-JAN-2000; 2000US-0175968P.
 PR 15-MAR-2000; 2000US-00526106.

XX (KALO-) KALOBROS INC.
 PA
 P1 Balint RF, Her J;
 DR WPI; 2004-203222/19.
 DR N-PSDB; ADJ67708.

PT Fragment complementation system for detecting immunoglobulin epitope, has
 PT first oligopeptide containing N-terminal fragment with C-terminal break-
 PT point, second oligopeptide containing C-terminal fragment with N-terminal
 PT break-point.
 XX
 PS Disclosure; SEQ ID NO 2; 47pp; English.

XX The invention describes a fragment complementation system (I) comprising
 CC a first oligopeptide having an N-terminal fragment with a C-terminal
 CC break-point, and a second oligopeptide having a C-terminal fragment with
 CC a N-terminal break-point, where the N-terminal fragment and the C-
 CC terminal fragment each are derived from a marker protein and reassemble
 CC to form a functionally reconstituted marker protein. (I) is useful for
 CC selecting simultaneous incorporation of multiple genetic elements into a
 CC host cell, and activating a beta-lactam derivative of an anti-tumour
 CC compound in a host. The method described is useful for identifying a
 CC second oligopeptide to which a first oligopeptide binds, involving co-
 CC expressing the first and second oligopeptides. Binding of the first
 CC oligopeptide to the second oligopeptide results in the functional
 CC reassembly of the marker protein. The method is also useful for
 CC monitoring the occurrence of protein-protein interactions in a sample;
 CC identifying oligopeptide interactions between two different proteomes;
 CC and identifying epitopes that bind to an immunoglobulin variable region.
 CC (I) or an expression cassette (II), encoding a selectable N or C-terminal
 CC peptide, is useful for identifying interactions between an extra cellular
 CC domain of a transmembrane protein and a polypeptide, where the
 CC transmembrane protein is an immune cell protein, preferably CD40. (I) or
 CC (II) is useful for high-throughput identification of compound that
 CC inhibit phosphorylation-regulated cell signal transducers. (I)

CC efficiently detects multiple interaction between extracellular and
 CC intracellular protein with high throughput format. This is the amino acid
 CC sequence of antibiotic resistance enzyme TBM-1 beta-lactamase that can be
 CC used as a selectable gene in the fragment complementation system of the
 CC invention.

SQ Sequence 263 AA;
 Query Match 100.0%; Score 1032; DB 8; Length 263;
 Best Local Similarity 100.0%; Pred. No. 1.5e-103;
 Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HPEITLVKVDADQAGARVGYIELDNGSKILIESFRPERPMSSTFKVLLCGAVLSRID 60
 Db 1 HPEITLVKVDADQAGARVGYIELDNGSKILIESFRPERPMSSTFKVLLCGAVLSRID 60

Oy 61 AGQEQIGRIHYSQNDLVYSPTVEKHLTDGMTVEILCSAATIMSNDTANILLTTIGCP 120
 Db 61 AGQEQIGRIHYSQNDLVYSPTVEKHLTDGMTVEILCSAATIMSNDTANILLTTIGCP 120

Oy 121 KELTAFILNMGDHYTRLDREPELNEALPNDERDTTVPVAMATTIRKLLTGSELLTLASRQ 180
 Db 121 KELTAFILNMGDHYTRLDREPELNEALPNDERDTTVPVAMATTIRKLLTGSELLTLASRQ 180

Oy 181 OLIDMEADKVAGPLRSALPA 202
 Db 181 OLIDMEADKVAGPLRSALPA 202

RESULT 4
 ID AAW16634 standard; protein; 264 AA.
 XX AAW16634;
 AC AAW16634;
 DT 09-AUG-1997 (first entry)
 DE Beta-lactamase (including signal peptide).

XX Gene directed enzyme prodng therapy; GDEPT;
 KM virus directed enzyme prodng therapy; VDEPT; beta-lactamase; cancer;
 KM HIV; inflammation.
 XX
 OS Escherichia coli.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..23
 FT /label= sig_peptide

XX WO9719180-A2.
 PN
 XX
 PD 29-MAY-1997.
 XX
 PF 19-NOV-1996; 96WO-GB002845.
 XX
 PR 20-NOV-1995; 95GB-00023703.
 XX
 PA (GLAX) GLAXO GROUP LTD.
 PI
 XX Dev I, Moore JT, Ohmstede C;
 DR WPI; 1997-298117/27.
 DR N-PSDB; AAT66736.

PT Molecular chimaera for gene or virus directed enzyme prodng therapy -
 PT useful for treatment of cancer, viral infection or inflammation.
 XX
 PS Example; Page 28; 38pp; English.

XX Escherichia coli beta-lactamase (AAW16634), including the signal peptide,
 CC is the expression product of a molecular chimaera, designated pcMV-BL
 CC (AAT66737), in which the beta-lactamase gene is under control of the CMV
 CC intermediate/early promoter. Vectors consisting of a transcriptional

CC regulatory DNA sequence linked to a beta-lactamase gene can be used for
 CC enzyme producing therapy. Expression of the beta-lactamase in a targeted
 CC cell allows conversion of a produg into an agent toxic to the cell for
 CC treatment of cancer. viral. (e.g. HIV) infection or inflammation.
 CC Secretion of the enzyme has the advantage of increasing neighbouring cell
 CC kill

XX Sequence 264 AA;

Query Match 100.0%; Score 1032; DB 2; Length 264;

Best Local Similarity 100.0%; Pred. No. 1.5e-103; Indels 0; Gaps 0;

Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKDADBDQGVGYIEIDLSGKILSFPRPERPMMSTFVLLCGAVLSRID 60

Db 2 HPELVKVKDADBDQGVGYIEIDLSGKILSFPRPERPMMSTFVLLCGAVLSRID 61

QY 61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGMYRELCSAAITMSDNTAAILLTTIGCP 120

Db 62 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGMYRELCSAAITMSDNTAAILLTTIGCP 121

QY 121 KELTSFLNMGDHYTRLDRMEPELNEAIPNDEBDTTPVMAATTLRKLLTGELTLASRQ 180

Db 122 KELTSFLNMGDHYTRLDRMEPELNEAIPNDEBDTTPVMAATTLRKLLTGELTLASRQ 181

QY 181 QLIDMMEADKVAGPLRSALPA 202

Db 182 QLIDMMEADKVAGPLRSALPA 203

RESULT 5

AAW18680 ID AAW18680 standard; protein; 264 AA.

XX AAW18680;

XX 13-AUG-1997 (first entry)

XX Intracellularly-expressed beta-lactamase.

XX Producing therapy; gene directed enzyme producing therapy; GDBPT;

XX Virus directed enzyme producing therapy; VDEPT; lung cancer;

XX beta-lactamase; PCMV-delIBL.

XX Escherichia coli.

XX W09719183-A2.

XX 29-MAY-1997.

XX 19-NOV-1996; 96MO-GB002846.

XX 20-NOV-1995; 95GB-00023703.

XX (GLAXO) GLAXO GROUP LTD.

XX Dev I, Moore JT, Sethna PB;

XX WPI; 1997-298118/27.

XX N-PSDB; AAT70311.

XX DNA construct for gene-directed enzyme producing therapy of lung cancer -

XX comprises lung- or neuroendocrine-specific promoter controlling

XX expression of produg-converting enzyme.

XX Example 811; Page 32-34; 53pp; English.

XX The intracellular form (AAW18680) of TEM beta-lactamase is expressed by

XX PCMV-delIBL (AAT70311) in which a PCR-amplified beta-lactamase coding

XX sequence, minus the signal sequence, is placed under control of the

XX intermediate/early promoter of cytomegalovirus. Intracellular beta-

XX lactamase constructs, placed under control of promoter/enhancer elements

XX of lung-associated protein or neuroendocrine marker protein genes, can be

CC used in novel chimaeric molecules for use in producing therapy of lung

CC cancer

XX Sequence 264 AA;

Query Match 100.0%; Score 1032; DB 2; Length 264;

Best Local Similarity 100.0%; Pred. No. 1.5e-103; Indels 0; Gaps 0;

Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKDADBDQGVGYIEIDLSGKILSFPRPERPMMSTFVLLCGAVLSRID 60

Db 2 HPELVKVKDADBDQGVGYIEIDLSGKILSFPRPERPMMSTFVLLCGAVLSRID 61

QY 61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGMYRELCSAAITMSDNTAAILLTTIGCP 120

Db 62 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGMYRELCSAAITMSDNTAAILLTTIGCP 121

QY 121 KELTSFLNMGDHYTRLDRMEPELNEAIPNDEBDTTPVMAATTLRKLLTGELTLASRQ 180

Db 122 KELTSFLNMGDHYTRLDRMEPELNEAIPNDEBDTTPVMAATTLRKLLTGELTLASRQ 181

QY 181 QLIDMMEADKVAGPLRSALPA 202

Db 182 QLIDMMEADKVAGPLRSALPA 203

RESULT 6

AAW31575 ID AAW31575 standard; protein; 286 AA.

XX AAW31575;

XX 10-MAR-2003 (revised)

XX 04-JUN-1993 (first entry)

XX Ampicillin resistance protein.

XX CYP1A1; PRNH127; PRNH155; xeroderma pigmentosum group A; XPA;

XX xenobiotics; circular; chimeric cytochrome P4501A1.

XX Homo sapiens.

XX US5180666-A.

XX 19-JAN-1993.

XX 27-JUN-1991; 91US-00721775.

XX 27-JUN-1991; 91US-00721775.

XX (UYWA-) UNIV WAYNE STATE.

XX States JC, Hines RM, Novak RF;

XX WPI; 1993-052845/06.

XX N-PSDB; AAQ36498.

XX In vitro method for testing mutagenicity of a chemical - by metabolising

XX chemical cell line consisting of transformed fibroblasts having

XX detectable cytochrome P450 mixed function oxidase activity and detecting

XX gene damage.

XX Disclosure; Col 21-24; 24pp; English.

XX The expression constructs PRNH127 and PRNH155 contain identical sequences

XX but were constructed using different strategies (see AAQ36498). The

XX constructs comprise exons 2-7 of human CYP1A1 gene under the control of

XX the inducible mouse metallothionein (MT-1) promoter. The constructs also

XX contain an open reading frame in the opposite orientation to the

XX cytochrome P450 exons. This ORF encodes ampicillin resistance. The

XX constructs are suitable for transformation of human fibroblasts derived

XX from the xeroderma pigmentosum group A. Cultures of the transformed

XX fibroblasts can be used to test substances for mutagenicity. The presence

CC of the inducible cytochrome P450 gene allows metabolism of the substance
CC to mutagenic metabolites. (Updated on 10-MAR-2003 to add missing OS
field.)

XX Sequence 286 AA;

Query Match 100.0%; Score 1032; DB 2; Length 286;

Best Local Similarity 100.0%; Pred. No. 1.7e-103; Mismatches 0; Indels 0; Gaps 0;

Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKXVDADQAGARVGYIELDLSGKILSPREPERFPMSTFKVLLCGAVLSRID 60

DB 24 HPEITLVKXVDADQAGARVGYIELDLSGKILSPREPERFPMSTFKVLLCGAVLSRID 83

QY 61 AGQEQIGRRIRHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMDSNTANILLTTIGSP 120

DB 84 AGQEQIGRRIRHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMDSNTANILLTTIGSP 143

QY 121 KELTAFILNMGDHTRLDRWEPBELNEAIPNDRDITTPVAMATTIRKLLTGELITLASRQ 180

DB 144 KELTAFILNMGDHTRLDRWEPBELNEAIPNDRDITTPVAMATTIRKLLTGELITLASRQ 203

QY 181 QLIIDWEADKVAAGPILRSALPA 202

DB 204 QLIIDWEADKVAAGPILRSALPA 225

RESULT 7

AAR97619 AAR97619 standard; protein; 286 AA.

XX AAR97619;

DT 20-AUG-1996 (first entry)

DE Secretory beta-lactamase.

KW Gene therapy; gene directed enzyme prodng therapy; GDEPT;

KM virus directed enzyme prodng therapy; VDEPT; prodng activation;

KW cytotoxic; cytostatic; cancer; tumour; retrovirus; vector;

KW beta-lactamase; cephalosporin.

OS Synthetic.

XX MO6616179-A1.

PD 30-MAY-1996.

PF 20-NOV-1995; 95WO-GB002716.

PR 18-NOV-1994; 94GB-00023367.

PA (WBL) WBLCOMB FOUND LTD.

PI Dev IK, Moore JT, Ohmstede C;

DR WPI; 1996-268615/27.

DR N-PSDB; AAT29220.

XX Molecular chimera for use in enzyme gene therapy - is activated in a

XX target cell to express a secretible enzyme which cleaves a prodng

XX outside the cell into a cytotoxic or cytostatic agent.

XX Example 3; Page 57-58; 73pp; English.

XX A secretory beta-lactamase (AAR97619) is expressed from DNA construct

XX PCMV-BL (AAT29220), in which the beta-lactamase coding sequence is under

XX the control of the intermediate/early cytomegalovirus promoter. Beta-

XX lactamase delivery to mammalian cells confers sensitivity to

XX cephalosporin prodngs. Liposomal DNA/5-fluorouracil prodng combinations

XX resulted in 8.c. tumour regression in mice bearing A549 tumours. Survival

XX of mice bearing human large cell lung H460 intrathoracic (i.t.) tumours

XX was increased upon i.t. injection of the secretory beta-lactamase DNA

CC construct

XX Sequence 286 AA;

Query Match 100.0%; Score 1032; DB 2; Length 286;

Best Local Similarity 100.0%; Pred. No. 1.7e-103; Mismatches 0; Indels 0; Gaps 0;

Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKXVDADQAGARVGYIELDLSGKILSPREPERFPMSTFKVLLCGAVLSRID 60

DB 24 HPEITLVKXVDADQAGARVGYIELDLSGKILSPREPERFPMSTFKVLLCGAVLSRID 83

QY 61 AGQEQIGRRIRHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMDSNTANILLTTIGSP 120

DB 84 AGQEQIGRRIRHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMDSNTANILLTTIGSP 143

QY 121 KELTAFILNMGDHTRLDRWEPBELNEAIPNDRDITTPVAMATTIRKLLTGELITLASRQ 180

DB 144 KELTAFILNMGDHTRLDRWEPBELNEAIPNDRDITTPVAMATTIRKLLTGELITLASRQ 203

QY 181 QLIIDWEADKVAAGPILRSALPA 202

DB 204 QLIIDWEADKVAAGPILRSALPA 225

RESULT 8

AAR96423 AAR96423 standard; protein; 286 AA.

XX AAR96423;

DT 25-MAR-2003 (revised)

DT 25-NOV-1996 (first entry)

DE Cytochrome P450 (CYP1A1 construct).

KW cytochrome; P450; metallothionein; mouse; human; cytotoxicity; assay;

KW metabolism.

OS Homo sapiens.

XX US5525482-A.

PD 11-JUN-1996.

PF 15-NOV-1994; 94US-00339658.

PR 27-JUN-1991; 91US-00721775.

PR 09-DEC-1992; 92US-00990295.

PA (UYMA-) UNIV WAYNE STATE.

PI Hines RN, Novak RF, States JC;

DR WPI; 1996-286397/29.

DR N-PSDB; AAT30354.

XX Testing chemicals for cytotoxicity to human by detecting gene damage -

XX PT using recombinant fibroblasts transformed with cytochrome P450 gene under

XX control of inducible promoter.

XX Disclosure; Col 17-24; 26pp; English.

XX The present sequence is encoded by a chimeric mouse metallothionein-

XX cytochrome P4501A1 (CYP1A1) expression construct. Two clones, pRNH127 and

XX pRNH15, were isolated by different methods and which both had the same

XX sequence. The CYP1A1 construct is used in assays to test for cytotoxicity

XX of humans to a chemical. The method comprises exposing human fibroblast

XX cells normally not including any cytochrome P450 activity to potentially

XX toxic chemicals. The cells having been transformed to express cytochrome

XX P450, under the control of a controllable promoter through the CYP1A1

XX gene, upon exposure to the chemical in vitro. The chemical is metabolised

XX intracellularly into a cytochrome metabolite by oxidation within the

CC fibroblasts through the intracellular cytochrome P450 mixed function
 CC oxidase enzymes expressed by the cells. Gene damage in the test cells is
 CC detected as an indication of cytotoxicity of the chemical. (Updated on 25
 CC -MAR-2003 to correct PF field.)

XX Sequence 286 AA;

Query Match 100.0%; Score 1032; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 1.7e-103;
 Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKXKADBDQGAHVGYIELDLSNGKILSFPRPERPPMSTFKVLLCGAVLSRID 60
 |||||
 DB 24 HPEITLVKXKADBDQGAHVGYIELDLSNGKILSFPRPERPPMSTFKVLLCGAVLSRID 83
 QY 61 AGOGLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAIIWSDNTAANLLTTIGSP 120
 |||||
 DB 84 AGOGLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAIIWSDNTAANLLTTIGSP 143
 QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDTTTPVMAATTLRKLLTGELLTIASRQ 180
 |||||
 DB 144 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDTTTPVMAATTLRKLLTGELLTIASRQ 203
 QY 181 QLIDMMEADKVAGPLRSALPA 202
 |||||
 DB 204 QLIDMMEADKVAGPLRSALPA 225

RESULT 9
 AAW16635

ID AAW16635 standard; protein; 286 AA.

XX AAW16635;

DT 09-AUG-1997 (first entry)

DE Beta-lactamase (no signal peptide).

XX Gene directed enzyme prodng therapy; GDEPT;
 KW virus directed enzyme prodng therapy; VDEPT; beta-lactamase; cancer;
 KW HIV; inflammation.

XX Escherichia coli.

XX WO9719180-A2.

XX PD 29-MAY-1997.

XX PF 19-NOV-1996; 96WO-GB002845.

XX PR 20-NOV-1995; 95GB-00023703.

XX PA (GLAX) GLAXO GROUP LTD.

XX FI Dev I, Moore JT, Ohmsted C;

XX WIPI; 1997-298117/27.

XX DR N-PSDB; AAT66737.

PT Molecular chimera for gene or virus directed enzyme prodng therapy -
 useful for treatment of cancer, viral infection or inflammation.

PS Example; Page 26; 38pp; English.

XX Escherichia coli beta-lactamase (AAW16635), lacking the signal peptide,
 CC is the expression product of a molecular chimera, designated pCMV-delBL
 CC (AAT66738), in which the beta-lactamase gene is under control of the CMV
 CC intermediate/early promoter. Vectors consisting of a transcriptional
 CC regulatory DNA sequence linked to a beta-lactamase gene can be used for
 CC enzyme prodng therapy. Intracellular expression of the beta-lactamase in
 CC a targeted cell allows conversion of a prodng into an agent toxic to
 CC the cell for treatment of cancer, viral (e.g. HIV) infection or
 CC inflammation

XX Sequence 286 AA;

Query Match 100.0%; Score 1032; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 1.7e-103;
 Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKXKADBDQGAHVGYIELDLSNGKILSFPRPERPPMSTFKVLLCGAVLSRID 60
 |||||
 DB 24 HPEITLVKXKADBDQGAHVGYIELDLSNGKILSFPRPERPPMSTFKVLLCGAVLSRID 83
 QY 61 AGOGLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAIIWSDNTAANLLTTIGSP 120
 |||||
 DB 84 AGOGLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAIIWSDNTAANLLTTIGSP 143
 QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDTTTPVMAATTLRKLLTGELLTIASRQ 180
 |||||
 DB 144 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDTTTPVMAATTLRKLLTGELLTIASRQ 203
 QY 181 QLIDMMEADKVAGPLRSALPA 202
 |||||
 DB 204 QLIDMMEADKVAGPLRSALPA 225

RESULT 10

ID AAW18679 standard; protein; 286 AA.

XX AAW18679;

DT 13-AUG-1997 (first entry)

DE Secretory beta-lactamase.

XX Prodng therapy; gene directed enzyme prodng therapy; GDEPT;
 KW virus directed enzyme prodng therapy; VDEPT; lung cancer;
 KW beta-lactamase; pCMV-BL.

XX Escherichia coli.

XX Key location/Qualifiers

FT Peptide 1..23

FT Protein /label= Sig_peptide

FT /label= Mat_protein

XX WO9719183-A2.

XX PD 29-MAY-1997.

XX PF 19-NOV-1996; 96WO-GB002846.

XX PR 20-NOV-1995; 95GB-00023703.

XX PA (GLAX) GLAXO GROUP LTD.

XX PI Dev I, Moore JT, Sethna PB;

XX WIPI; 1997-298118/27.

XX DR N-PSDB; AAT70309.

PT DNA construct for gene-directed enzyme prodng therapy of lung cancer -
 comprises lung- or neuroendocrine-specific promoter controlling
 PT expression of prodng-converting enzyme.

PS Example 8ii; Page 26-27; 53pp; English.

XX The secreted form (AAW18679) of TEM beta-lactamase is expressed by pCMV-
 CC BL (AAT70309) in which a PCR-amplified beta-lactamase coding sequence is
 CC placed under control of the intermediate/early promoter of
 CC cytomegalovirus. Secretory beta-lactamase constructs, placed under
 CC control of promoter/enhancer elements of lung- associated protein or
 CC neuroendocrine marker protein genes, can be used in novel chimeric

CC molecules for use in prodrg therapy of lung cancer
XX Sequence 286 AA;
SQ
Query Match 100.0%; Score 1032; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.7e-103;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEITLVKVDADQAGVGYIELDNSGKILIESRPERPFPMSTFKVLLCGAVLSRD 60
DB 24 HPEITLVKVDADQAGVGYIELDNSGKILIESRPERPFPMSTFKVLLCGAVLSRD 83
QY 61 AGOEOLGRRIRHSQNDLVEYSPVTEKHLTDGVTVELCSAATMSDNTANLLTTIGSP 120
DB 84 AGOEOLGRRIRHSQNDLVEYSPVTEKHLTDGVTVELCSAATMSDNTANLLTTIGSP 143
QY 121 KELTAFILNMGDHYTRLDRWBEPELNEAIPNDRDITTPVAMATTIRKLLTGELTLASRQ 180
DB 144 KELTAFILNMGDHYTRLDRWBEPELNEAIPNDRDITTPVAMATTIRKLLTGELTLASRQ 203
QY 181 OLIDWMEADKVAAGPILRSALPA 202
DB 204 OLIDWMEADKVAAGPILRSALPA 225
RESULT 11
ID AAY08529 standard; protein; 286 AA.
XX AAY08529;
AC AAY08529;
XX
DT 03-AUG-1999 (first entry)
XX
DE Vector pASK75 beta-1a protein.
XX
XX Firefly; luciferase; tetracycline; transcriptional control; Tetr; Teta;
KW tetracycline repressor; tetracycline promoter; luminescence; luxCDABE;
KW insect; Tn10; medicine; dosage; cheese production; antibiotic; foodstuff;
KW allergy.
XX
XX Synthetic.
XX OS
XX MO9925866-A1.
PN
XX 27-MAY-1999.
PD
XX
XX 11-NOV-1998; 98WO-FI000873.
PF
XX 14-NOV-1997; 97FI-00004235.
PR
XX
XX (KORP/) KOREBELA M.
PA (KARP/) KARP M.
PA (KURI/) KURITTU J.
PI Korpela M, Karp M, Kurittu J;
XX
XX WPI: 1999-338015/28.
DR N-PSDB; AAV72418.
DR
XX
XX Assaying for tetracycline using recombinant prokaryotic cells.
PT
XX
XX Discloure; Page 47-48; 67pp; English.
PS
XX
XX This invention describes a novel tetracycline assay that uses recombinant
CC prokaryotic cells comprising a luciferase gene under the transcriptional
CC control of a tetracycline repressor and tetracycline promoter and
CC involves the detection of luminescence emitted from the cells. The assay
CC can be used to distinguish tetracycline from other microbial agents. The
CC invention also describes a novel plasmid comprising either the luxCDABE
CC genes, a tetracycline repressor (Tetr) and a tetracycline promoter (Teta)
CC from Tn10, or the insect luciferase gene, a tetracycline repressor (Tetr)
CC and a tetracycline promoter (Teta) from Tn10. The tetracycline assay
CC method can be used for the determination of tetracycline in a sample,

CC e.g. to study the dosage and penetration of the medicine. The method can
CC also be used to test cheese production, as cheese making bacteria are not
CC able to work in the presence of tetracycline. The method can also be used
CC to determine the presence or concentration of antibiotics in foodstuffs,
CC e.g. for allergic people. The present assay method does not rely on the
CC growth of microbes as do conventional tests, and so is much more rapid.
CC The present assay is also more sensitive, as even a small amount of
CC luminescence can be detected
XX
XX Sequence 286 AA;
SQ
Query Match 100.0%; Score 1032; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.7e-103;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEITLVKVDADQAGVGYIELDNSGKILIESRPERPFPMSTFKVLLCGAVLSRD 60
DB 24 HPEITLVKVDADQAGVGYIELDNSGKILIESRPERPFPMSTFKVLLCGAVLSRD 83
QY 61 AGOEOLGRRIRHSQNDLVEYSPVTEKHLTDGVTVELCSAATMSDNTANLLTTIGSP 120
DB 84 AGOEOLGRRIRHSQNDLVEYSPVTEKHLTDGVTVELCSAATMSDNTANLLTTIGSP 143
QY 121 KELTAFILNMGDHYTRLDRWBEPELNEAIPNDRDITTPVAMATTIRKLLTGELTLASRQ 180
DB 144 KELTAFILNMGDHYTRLDRWBEPELNEAIPNDRDITTPVAMATTIRKLLTGELTLASRQ 203
QY 181 OLIDWMEADKVAAGPILRSALPA 202
DB 204 OLIDWMEADKVAAGPILRSALPA 225
RESULT 12
ID AAB10442 standard; protein; 286 AA.
XX AAB10442
AC AAB10442;
XX
DT 01-DEC-2000 (first entry)
XX
XX Expression vector pSEX15G2 bla protein.
XX
XX
XX Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
KW B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.
KW
XX
XX Synthetic.
XX OS
XX DE19900635-A1.
PN
XX 13-JUL-2000.
PD
XX
XX 11-JAN-1999; 99DE-01000635.
PF
XX 11-JAN-1999; 99DE-01000635.
PR
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA
XX Breilting F, Poustka A, Moldenhauer G;
XX
XX WPI: 2000-499832/45.
DR N-PSDB; AAV71430.
DR
XX
XX Selecting monoclonal antibodies, by expressing them on the surface of
PT hybridomas attached to antibody-binding protein, then reaction with
PT antibody library.
XX
PS
XX Claim 16; Fig 3; 22pp; German.
XX
XX This invention describes a novel method for the selection of monoclonal
CC antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma
CC cells to produce antibody-producing hybridomas such that the antibodies
CC are presented at the surface of the hybridomas by an antibody-binding
CC protein (I); and (ii) binding the antibody to antigens (Ag). The

CC invention also describes antibody-binding proteins (I) that comprise a
CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa
CC chain or a murine MHC (major histocompatibility complex) Class I k(k)
CC molecule; an antibody-binding site of proteins A, G, L or Ig, and the
CC transmembrane domain of PDGFR (platelet-derived growth factor receptor)
CC or CD53. The method is used to select Mab with specificity for particular
CC antigens. Mab can be selected without separate culture of hybridomas, and
CC selection can be made against many antigens in a library, optionally on
CC the basis of strength of affinity for a particular antigen. Complex
CC mixtures of hybridomas can be used for selection, reducing the time and
CC cost involved in Mab selection. This sequence represents the bla protein
CC protein contained in the expression vector pSEX114 which contains the
CC bla protein, Neo-R and protein G described in the method of the invention
CC
SQ Sequence 286 AA;

Query Match 100.0%; Score 1032; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.7e-103; Indels 0; Gaps 0;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPETLVKVKADQKADQAGVGYIELDLSGKILSFPRPERFPMWSTFKVLLCGAVLSRID 60
DB 24 HPETLVKVKADQKADQAGVGYIELDLSGKILSFPRPERFPMWSTFKVLLCGAVLSRID 83
QY 61 AGQSGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATWSDNTAAVLLTTIGSP 120
DB 84 AGQSGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATWSDNTAAVLLTTIGSP 143
QY 121 KEITAFILNMGDHTRLDREWEPELNEAIPNDERDTVMVAMATTIRKLLTGELITLASRQ 180
DB 144 KEITAFILNMGDHTRLDREWEPELNEAIPNDERDTVMVAMATTIRKLLTGELITLASRQ 203
QY 181 QLIDWMEADKVAAGPLRSALPA 202
DB 204 QLIDWMEADKVAAGPLRSALPA 225

RESULT 13
AAB10438
ID AAB10438 standard; protein; 286 AA.

XX AAB10438;

DT 01-DEC-2000 (first entry)

DE Expression vector pSEX114 bla protein.

XX Expression vector; antibody binding protein; monoclonal antibody; Neo-R;

KM B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.

XX Synthetic.

PN DE19900635-A1.

PD 13-JUL-2000.

PF 11-JAN-1999; 99DE-01000635.

PR 11-JAN-1999; 99DE-01000635.

PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

PI Breitling F, Poustka A, Moldenhauer G;

DR MPI; 2000-499832/45.

DR N-PSDB; AAA71428.

XX Selecting monoclonal antibodies, by expressing them on the surface of
PT hybridomas attached to antibody-binding protein, then reaction with
XX antibody library.

XX Claim 16; Fig 1; 22pp; German.

CC This invention describes a novel method for the selection of monoclonal
CC antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma
CC cells to produce antibody-producing hybridomas such that the antibodies
CC are presented at the surface of the hybridomas by an antibody-binding
CC protein (I); and (ii) binding the antibody to antigens (Ag). The
CC invention also describes antibody-binding proteins (I) that comprise a
CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa
CC chain or a murine MHC (major histocompatibility complex) Class I k(k)
CC molecule; an antibody-binding site of proteins A, G, L or Ig, and the
CC transmembrane domain of PDGFR (platelet-derived growth factor receptor)
CC or CD53. The method is used to select Mab with specificity for particular
CC antigens. Mab can be selected without separate culture of hybridomas, and
CC selection can be made against many antigens in a library, optionally on
CC the basis of strength of affinity for a particular antigen. Complex
CC mixtures of hybridomas can be used for selection, reducing the time and
CC cost involved in Mab selection. This sequence represents the Neo-R
CC protein contained in the expression vector pSEX114 which contains the
CC bla protein, Neo-R and protein G described in the method of the invention
CC
SQ Sequence 286 AA;

Query Match 100.0%; Score 1032; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.7e-103; Indels 0; Gaps 0;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPETLVKVKADQKADQAGVGYIELDLSGKILSFPRPERFPMWSTFKVLLCGAVLSRID 60
DB 24 HPETLVKVKADQKADQAGVGYIELDLSGKILSFPRPERFPMWSTFKVLLCGAVLSRID 83
QY 61 AGQSGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATWSDNTAAVLLTTIGSP 120
DB 84 AGQSGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATWSDNTAAVLLTTIGSP 143
QY 121 KEITAFILNMGDHTRLDREWEPELNEAIPNDERDTVMVAMATTIRKLLTGELITLASRQ 180
DB 144 KEITAFILNMGDHTRLDREWEPELNEAIPNDERDTVMVAMATTIRKLLTGELITLASRQ 203
QY 181 QLIDWMEADKVAAGPLRSALPA 202
DB 204 QLIDWMEADKVAAGPLRSALPA 225

RESULT 14
AAB10440
ID AAB10440 standard; protein; 286 AA.

XX AAB10440;

DT 01-DEC-2000 (first entry)

DE Expression vector pSEX114 bla protein.

XX Expression vector; antibody binding protein; monoclonal antibody; Neo-R;

KM B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.

XX Synthetic.

PN DE19900635-A1.

PD 13-JUL-2000.

PF 11-JAN-1999; 99DE-01000635.

PR 11-JAN-1999; 99DE-01000635.

PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

PI Breitling F, Poustka A, Moldenhauer G;

DR MPI; 2000-499832/45.

DR N-PSDB; AAA71429.

XX Selecting monoclonal antibodies, by expressing them on the surface of

PT hybridomas attached to antibody-binding protein, then reaction with
PT antibody library.

Claim 16; Fig 2; 22pp; German.

CC This invention describes a novel method for the selection of monoclonal
CC antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma
CC cells to produce antibody-producing hybridomas such that the antibodies
CC are presented at the surface of the hybridomas by an antibody-binding
CC protein (I); and (ii) binding the antibody to antigens (Ag). The
CC invention also describes antibody-binding proteins (I) that comprise a
CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa
CC chain or a murine MHC (major histocompatibility complex) Class I k(k)
CC molecule; an antibody-binding site of proteins A, G, L or Ig, and the
CC transmembrane domain of PDGFR (platelet-derived growth factor receptor)
CC or CD52. The method is used to select Mab with specificity for particular
CC antigens. Mab can be selected without separate culture of hybridomas, and
CC selection can be made against many antigens in a library, optionally on
CC the basis of strength of affinity for a particular antigen. Complex
CC mixtures of hybridomas can be used for selection, reducing the time and
CC cost involved in Mab selection. This sequence represents the bla protein
CC protein contained in the expression vector pSEXlig2 which contains the
CC bla protein. Neo-R and protein G described in the method of the invention
XX
XX Sequence 286 AA;

SQ Sequence 286 AA;

Query Match	100.0%;	Score 1032;	DB 3;	Length 286;
Best Local Similarity	100.0%;	Pred. No. 1.7e-103;		
Matches 202; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

[illegible]

RESULT 15

ID AAB50898 standard; protein; 286 AA.

AC AAB50898;

DT 20-MAR-2001 (first entry)

DE Protein encoded by bla resistance marker of integration vector pLO12306.

bla resistance marker; recombinant host cell; saccharification; fermentation; polysaccharase; oligosaccharide degradation; cell gene glucanase; integration vector; pLO12306.

OS Unidentified

PN WO200071729-A2.

PD 30-NOV-2000.

PF 26-MAY-2000; 2000WO-US014773.

PR 26-MAY-1999; 99US-0136376P.

PA (UYFL) UNIV FLORIDA RES FOUND.

PI	Ingram LO, Zhou S;
XX	
DR	WPI; 2001-032043/04
DR	N-PSDB; AAC91455.
DR	

PT Recombinant host cells useful for producing polysaccharase for degrading
PT oligosaccharides, comprises a first heterologous polynucleotide encoding
PT polysaccharase under control of surrogate promoter.

PS Disclosure; Page 82-83; 87pp; English.

The present sequence is given in a specification relating to a recombinant host cell suitable for simultaneous saccharification and fermentation. The host cell contains at least one heterologous polynucleotide encoding a polysaccharase under the transcriptional control of a surrogate promoter capable of increasing expression of the polysaccharase. The host cell also contains a second heterologous polynucleotide encoding a secretory polypeptide to facilitate the secretion of the expressed polysaccharase. The recombinant host cell is useful for producing polysaccharase which is useful for enzymatically degrading oligosaccharides such as lignocellulose, hemicellulose, cellulose, pectin or their combinations, and fermenting the product to ethanol, by simultaneous saccharification and fermentation processes. The present sequence is encoded by an integration vector which was introduced into cells to generate recombinant host cells. The vector contains a surrogate promoter from *Zymomonas mobilis*, the *celZ* gene from *Erythrina chrysanthemi*, resistance markers *bla* and *tet*, and *Klebsiella oxytoca* target sequence

SQ Sequence 286 AA;

Query Match	100.0%;	Score 1032;	DB 4;	Length 286;
Best Local Similarity	100.0%;	Pred. No. 1	7e-103;	
Matches 202;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Qy	1	HEPTLVKVDABEQGARVGYIELDNGSKILIESRPEREPPMSTFVLLCGAVLRID	60
Db	24	HEPTLVKVDABEQGARVGYIELDNGSKILIESRPEREPPMSTFVLLCGAVLRID	83
Qy	61	AGGEOUGRRIRHYSONDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTTIGP	120
Db	84	AGGEOUGRRIRHYSONDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTTIGP	143
Qy	121	KEITATILHNMGGHYTRLDRMEPELNEAIPNDRERTPMVAAATTLRKLITGELLTLASRQ	180
Db	144	KEITATILHNMGGHYTRLDRMEPELNEAIPNDRERTPMVAAATTLRKLITGELLTLASRQ	203
Qy	181	QLIDMEADKVAAGPLLRSALPA	202
Db	204	QLIDMEADKVAAGPLLRSALPA	225

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2005, 10:36:31 ; Search time 20.7105 Seconds
(without alignments)
728.091 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_202

Perfect score: 1032
Sequence: 1 HPEITLVKVKADMDQAGARVG.....IDWMEADKVGAPILRSALPA 202

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/1aa/PCUS_COMB.pep:*

6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1032	100.0	286	1	US-07-721-775A-2
2	1032	100.0	286	1	US-08-339-658-2
3	1032	100.0	286	3	US-09-263-933-7
4	1032	100.0	286	3	US-09-263-933-14
5	1032	100.0	286	3	US-09-263-933-21
6	1032	100.0	286	3	US-09-025-769B-265
7	1032	100.0	286	3	US-09-025-769B-362
8	1032	100.0	286	4	US-09-919-901-7
9	1032	100.0	286	4	US-09-919-901-14
10	1032	100.0	286	4	US-09-919-901-21
11	1032	100.0	286	4	US-09-490-070A-265
12	1032	100.0	286	4	US-09-490-070A-362
13	1032	100.0	286	4	US-09-490-153-265
14	1032	100.0	286	4	US-09-490-153-362
15	1032	100.0	286	4	US-10-191-966-7
16	1032	100.0	286	4	US-10-191-966-14
17	1032	100.0	286	4	US-10-191-966-21
18	1032	100.0	286	4	US-09-490-324-265
19	1032	100.0	286	4	US-09-490-324-362
20	1032	100.0	286	4	US-09-025-769B-285
21	1032	100.0	286	4	US-09-025-769B-298
22	1032	100.0	286	3	US-09-025-769B-300
23	1032	100.0	286	4	US-09-490-070A-285
24	1032	100.0	286	4	US-09-490-070A-298
25	1032	100.0	286	4	US-09-490-070A-300
26	1032	100.0	286	4	US-09-490-153-285
27	1032	100.0	286	4	US-09-490-153-298

28	1032	100.0	286	4	US-09-490-153-300	Sequence 300, App
29	1032	100.0	286	4	US-09-490-324-285	Sequence 285, App
30	1032	100.0	286	4	US-09-490-324-298	Sequence 298, App
31	1032	100.0	286	4	US-09-490-324-300	Sequence 300, App
32	1032	100.0	286	3	US-09-263-933-2	Sequence 2, Appl1
33	1032	100.0	286	3	US-09-263-933-9	Sequence 9, Appl1
34	1032	100.0	286	3	US-09-263-933-16	Sequence 16, Appl1
35	1032	100.0	286	4	US-09-919-901-2	Sequence 2, Appl1
36	1032	100.0	286	4	US-09-919-901-9	Sequence 9, Appl1
37	1032	100.0	286	4	US-09-919-901-16	Sequence 16, Appl1
38	1032	100.0	286	4	US-10-191-966-2	Sequence 2, Appl1
39	1032	100.0	286	4	US-10-191-966-9	Sequence 9, Appl1
40	1032	100.0	286	4	US-10-191-966-16	Sequence 16, Appl1
41	1031	99.9	286	4	US-09-555-510B-9	Sequence 9, Appl1
42	1031	99.9	286	4	US-10-231-013-9	Sequence 9, Appl1
43	1031	99.9	1293	4	US-09-170-486D-292	Sequence 292, App
44	1031	99.9	1293	4	US-09-364-425B-57	Sequence 57, Appl1
45	1027	99.5	263	1	US-08-407-544-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1

US-07-721-775A-2

Sequence 2, Application US/07721775A

Patent No. 5180666

GENERAL INFORMATION:

APPLICANT: States, J. Christopher

APPLICANT: Hines, Ronald N.

APPLICANT: No. 5180666ak, Raymond F.

TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING

TITLE OR INVENTION: MUTAGENICITY OF A CHEMICAL

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESSES:

ADDRESSER: Reising, Echtington, Barnard, Perry & Milton

STREET: P. O. Box 4390

CITY: Troy

STATE: Michigan

COUNTRY: U.S.A.

ZIP: 48099

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07721, 775A

FILING DATE: 19910627

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Kohn, Kenneth I.

REGISTRATION NUMBER: 30,955

REFERENCE/DOCKET NUMBER: P-321WSU

TELECOMMUNICATION INFORMATION:

TELEPHONE: (313) 689-3554

TELEFAX: (313) 689-4071

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 286 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-721-775A-2

Query Match

Best Local Similarity 100.0%; Score 1032; DB 1; Length 286;

Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADMDQAGARVGIIELDINSKILIESRPERPPMNSTFYVLGAVLSRID 60

DB 24 HPEITLVKVKADMDQAGARVGIIELDINSKILIESRPERPPMNSTFYVLGAVLSRID 83

QY 61 AGOQOLGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGP 120
DB 84 AGOQOLGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGP 143
QY 121 KETLAFILNMGDHVTRLDRWPEPELNEALPNDERDTTVPVAAATLTKLLTGBLLTLASRQ 180
DB 144 KETLAFILNMGDHVTRLDRWPEPELNEALPNDERDTTVPVAAATLTKLLTGBLLTLASRQ 203
QY 181 QLIDMEADKVAAGPLRLSALPA 202
DB 204 QLIDMEADKVAAGPLRLSALPA 225

RESULT 2
US-08-339-658-2
Sequence 2, Application US/08339658
Patent No. 5525482
GENERAL INFORMATION:
APPLICANT: States, J. Christopher
APPLICANT: Hines, Ronald N.
APPLICANT: No. 5525482ak, Raymond F.
TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reising, Ethington, Barnard, Perry & Milton
STREET: P.O. Box 4390
CITY: Troy
STATE: Michigan
COUNTRY: U.S.A.
ZIP: 48099
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,658
FILING DATE: 15-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,295
FILING DATE: 09-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: P-321WSU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 689-3554
TELEFAX: (313) 689-4071
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-339-658-2

Query Match 100.0%; Score 1032; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.6e-113;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEITLVKKAEDDQAGARVGYIELDLSNGKILSFPRPERPMMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKKAEDDQAGARVGYIELDLSNGKILSFPRPERPMMSTFVLLCGAVLSRID 83
QY 61 AGOQOLGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGP 120
DB 84 AGOQOLGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGP 143
QY 121 KETLAFILNMGDHVTRLDRWPEPELNEALPNDERDTTVPVAAATLTKLLTGBLLTLASRQ 180
DB 144 KETLAFILNMGDHVTRLDRWPEPELNEALPNDERDTTVPVAAATLTKLLTGBLLTLASRQ 203

QY 181 QLIDMEADKVAAGPLRLSALPA 202
DB 204 QLIDMEADKVAAGPLRLSALPA 225

RESULT 3
US-09-263-933-7
Sequence 7, Application US/09263933
Patent No. 6280940
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
US-09-263-933-7

Query Match 100.0%; Score 1032; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.6e-113;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEITLVKKAEDDQAGARVGYIELDLSNGKILSFPRPERPMMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKKAEDDQAGARVGYIELDLSNGKILSFPRPERPMMSTFVLLCGAVLSRID 83
QY 61 AGOQOLGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGP 120
DB 84 AGOQOLGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGP 143
QY 121 KETLAFILNMGDHVTRLDRWPEPELNEALPNDERDTTVPVAAATLTKLLTGBLLTLASRQ 180
DB 144 KETLAFILNMGDHVTRLDRWPEPELNEALPNDERDTTVPVAAATLTKLLTGBLLTLASRQ 203
QY 181 QLIDMEADKVAAGPLRLSALPA 202
DB 204 QLIDMEADKVAAGPLRLSALPA 225

RESULT 4
US-09-263-933-14
Sequence 14, Application US/09263933
Patent No. 6280940
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
US-09-263-933-14

Query Match 100.0%; Score 1032; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.6e-113;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADADQAGARVGYIELDINSKILSFRRPFRPMSSTFKVLLCGAVLSRID 60
DB HPELVKVKADADQAGARVGYIELDINSKILSFRRPFRPMSSTFKVLLCGAVLSRID 83
QY 61 AGQEQGRIRIHVSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 120
DB AGQEQGRIRIHVSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KETLTFILNMGDHYRLDRMBEPLNEALPNDERDITTPVAAATTIRKLLTGELLTLASRQ 180
DB KETLTFILNMGDHYRLDRMBEPLNEALPNDERDITTPVAAATTIRKLLTGELLTLASRQ 203
QY 181 QIIDMMEADKVAAGPILRSALPA 202
DB QIIDMMEADKVAAGPILRSALPA 225

RESULT 5

US-09-263-933-21
; Sequence 21, Application US/09263933
; Patent No. 6280940

GENERAL INFORMATION:

APPLICANT: Potte, Karen E.
APPLICANT: Jackson, Roderica L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
US-09-263-933-21

Query Match 100.0%; Score 1032; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.6e-113;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADADQAGARVGYIELDINSKILSFRRPFRPMSSTFKVLLCGAVLSRID 60
DB HPELVKVKADADQAGARVGYIELDINSKILSFRRPFRPMSSTFKVLLCGAVLSRID 83
QY 61 AGQEQGRIRIHVSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 120
DB AGQEQGRIRIHVSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KETLTFILNMGDHYRLDRMBEPLNEALPNDERDITTPVAAATTIRKLLTGELLTLASRQ 180
DB KETLTFILNMGDHYRLDRMBEPLNEALPNDERDITTPVAAATTIRKLLTGELLTLASRQ 203
QY 181 QIIDMMEADKVAAGPILRSALPA 202
DB QIIDMMEADKVAAGPILRSALPA 225

RESULT 6

US-09-025-769B-265
; Sequence 265, Application US/09025769B
; Patent No. 6300064

GENERAL INFORMATION:

APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic

APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 265:

SEQUENCE CHARACTERISTICS:

LENGTH: 286 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-025-769B-265

Query Match 100.0%; Score 1032; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.6e-113;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADADQAGARVGYIELDINSKILSFRRPFRPMSSTFKVLLCGAVLSRID 60
DB HPELVKVKADADQAGARVGYIELDINSKILSFRRPFRPMSSTFKVLLCGAVLSRID 83
QY 61 AGQEQGRIRIHVSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 120
DB AGQEQGRIRIHVSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KETLTFILNMGDHYRLDRMBEPLNEALPNDERDITTPVAAATTIRKLLTGELLTLASRQ 180
DB KETLTFILNMGDHYRLDRMBEPLNEALPNDERDITTPVAAATTIRKLLTGELLTLASRQ 203
QY 181 QIIDMMEADKVAAGPILRSALPA 202
DB QIIDMMEADKVAAGPILRSALPA 225

RESULT 7

US-09-025-769B-362
; Sequence 362, Application US/09025769B
; Patent No. 6300064

GENERAL INFORMATION:

APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 362:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-362

Query Match 100.0%; Score 1032; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.6e-113; Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKKVKAEDDQAGRVGTYIEDLNSGKILBSFRPERPPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKKVKAEDDQAGRVGTYIEDLNSGKILBSFRPERPPMSTFVLLCGAVLSRID 83
QY 61 AGGOLGRRHYSONDLYEVSPTVEKHLTDGMYRELCSAITSNDTNAULLTTIGCP 120
DB 84 AGGOLGRRHYSONDLYEVSPTVEKHLTDGMYRELCSAITSNDTNAULLTTIGCP 143
QY 121 KETAFILNMGDHYTRLDRWEPELNEAIPNDRDTMPVMAATTLRKLLTGELLTLASRQ 180
DB 144 KETAFILNMGDHYTRLDRWEPELNEAIPNDRDTMPVMAATTLRKLLTGELLTLASRQ 203
QY 181 QIIDWMEADKVAGPLRLSALPA 202
DB 204 QIIDWMEADKVAGPLRLSALPA 225

RESULT 8
US-09-919-901-7
Sequence 7, Application US/09919901
Patent No. 6599738
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7

LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION:
US-09-919-901-7

Query Match 100.0%; Score 1032; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.6e-113; Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKKVKAEDDQAGRVGTYIEDLNSGKILBSFRPERPPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKKVKAEDDQAGRVGTYIEDLNSGKILBSFRPERPPMSTFVLLCGAVLSRID 83
QY 61 AGGOLGRRHYSONDLYEVSPTVEKHLTDGMYRELCSAITSNDTNAULLTTIGCP 120
DB 84 AGGOLGRRHYSONDLYEVSPTVEKHLTDGMYRELCSAITSNDTNAULLTTIGCP 143
QY 121 KETAFILNMGDHYTRLDRWEPELNEAIPNDRDTMPVMAATTLRKLLTGELLTLASRQ 180
DB 144 KETAFILNMGDHYTRLDRWEPELNEAIPNDRDTMPVMAATTLRKLLTGELLTLASRQ 203
QY 181 QIIDWMEADKVAGPLRLSALPA 202
DB 204 QIIDWMEADKVAGPLRLSALPA 225

RESULT 9
US-09-919-901-14
Sequence 14, Application US/09919901
Patent No. 6599738
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION:
US-09-919-901-14

Query Match 100.0%; Score 1032; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.6e-113; Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKKVKAEDDQAGRVGTYIEDLNSGKILBSFRPERPPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKKVKAEDDQAGRVGTYIEDLNSGKILBSFRPERPPMSTFVLLCGAVLSRID 83
QY 61 AGGOLGRRHYSONDLYEVSPTVEKHLTDGMYRELCSAITSNDTNAULLTTIGCP 120
DB 84 AGGOLGRRHYSONDLYEVSPTVEKHLTDGMYRELCSAITSNDTNAULLTTIGCP 143
QY 121 KETAFILNMGDHYTRLDRWEPELNEAIPNDRDTMPVMAATTLRKLLTGELLTLASRQ 180
DB 144 KETAFILNMGDHYTRLDRWEPELNEAIPNDRDTMPVMAATTLRKLLTGELLTLASRQ 203
QY 181 QIIDWMEADKVAGPLRLSALPA 202

Db 204 QUIDMEADKVAAGPLLRSLPA 225

RESULT 10

US-09-919-901-21

Sequence 21, Application US/09919901

Patent No. 6599738

GENERAL INFORMATION:

APPLICANT: Potte, Karen E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patrick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT

TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

FILE REFERENCE: 0125-0005A

CURRENT FILING DATE: 2001-08-02

PRIOR FILING DATE: 1999-02-08

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patent Ver. 2.0

SEQ ID NO 21

LENGTH: 286

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION:

US-09-919-901-21

Query Match 100.0%; Score 1032; DB 4; Length 286;

Best Local Similarity 100.0%; Pred. No. 1.6e-113;

Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADADQAGVGYIELDINSKILSFRRPFRPMSTFKVLLCGAVLSRID 60

Db 24 HPELVKVKADADQAGVGYIELDINSKILSFRRPFRPMSTFKVLLCGAVLSRID 83

QY 61 AGQELGRIRHYSQNDLYEYSPVTEKHLTDGVTVELCSAAITMSDNTAANLLTTIGP 120

Db 84 AGQELGRIRHYSQNDLYEYSPVTEKHLTDGVTVELCSAAITMSDNTAANLLTTIGP 143

QY 121 KETLFLNMGDHVRILDRWPELNEALPNDERDTTMAPVAMATTIRKLLTGSLTLASRQ 180

Db 144 KETLFLNMGDHVRILDRWPELNEALPNDERDTTMAPVAMATTIRKLLTGSLTLASRQ 203

QY 181 QUIDMEADKVAAGPLLRSLPA 202

Db 204 QUIDMEADKVAAGPLLRSLPA 225

RESULT 11

US-09-490-070A-265

Sequence 265, Application US/09490070A

Patent No. 6696248

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

APPLICANT: Pack, Peter

APPLICANT: Ilag, Vic

APPLICANT: Ge, Liming

APPLICANT: Moroney, Simon

APPLICANT: Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESSES:

ADDRESS: Colin G. Sandercock, Esq. c/o Heller Ehrman

White & McLaughlin

STREET: 1666 K Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,070A

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Colin G. Sandercock, Esq.

REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 37629-0005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 912-2000

TELEFAX: (202) 912-2020

INFORMATION FOR SEQ ID NO: 265:

SEQUENCE CHARACTERISTICS:

LENGTH: 286 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 265:

US-09-490-070A-265

Query Match 100.0%; Score 1032; DB 4; Length 286;

Best Local Similarity 100.0%; Pred. No. 1.6e-113;

Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADADQAGVGYIELDINSKILSFRRPFRPMSTFKVLLCGAVLSRID 60

Db 24 HPELVKVKADADQAGVGYIELDINSKILSFRRPFRPMSTFKVLLCGAVLSRID 83

QY 61 AGQELGRIRHYSQNDLYEYSPVTEKHLTDGVTVELCSAAITMSDNTAANLLTTIGP 120

Db 84 AGQELGRIRHYSQNDLYEYSPVTEKHLTDGVTVELCSAAITMSDNTAANLLTTIGP 143

QY 121 KETLFLNMGDHVRILDRWPELNEALPNDERDTTMAPVAMATTIRKLLTGSLTLASRQ 180

Db 144 KETLFLNMGDHVRILDRWPELNEALPNDERDTTMAPVAMATTIRKLLTGSLTLASRQ 203

QY 181 QUIDMEADKVAAGPLLRSLPA 202

Db 204 QUIDMEADKVAAGPLLRSLPA 225

RESULT 12

US-09-490-070A-362

Sequence 362, Application US/09490070A

Patent No. 6696248

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

APPLICANT: Pack, Peter

APPLICANT: Ilag, Vic

APPLICANT: Ge, Liming

APPLICANT: Moroney, Simon

APPLICANT: Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESSES:

ADDRESS: Colin G. Sandercock, Esq. c/o Heller Ehrman

White & McLaughlin

STREET: 1666 K Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 362:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 362:
US-09-490-070A-362

Query Match 100.0%; Score 1032; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.6e-113; Indels 0; Gaps 0;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	HPETLVKKAEDQLGARVGYIELDINSKILLESFRRPRERPMSTFKVLLCGAVLSRID	60
DB	24	HPETLVKKAEDQLGARVGYIELDINSKILLESFRRPRERPMSTFKVLLCGAVLSRID	83
QY	61	AGQOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP	120
DB	84	AGQOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP	143
QY	121	KELTAPFLHMGDHYTRLDRWPELNEALPNDERDTMPVAMATTLRKLLTGLLTLASRQ	180
DB	144	KELTAPFLHMGDHYTRLDRWPELNEALPNDERDTMPVAMATTLRKLLTGLLTLASRQ	203
QY	181	QLIDMMEADKVAGPLRSALPA	202
DB	204	QLIDMMEADKVAGPLRSALPA	225

RESULT 13
US-09-490-153-265
Sequence 265, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-09-490-153-265

Query Match 100.0%; Score 1032; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.6e-113; Indels 0; Gaps 0;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	HPETLVKKAEDQLGARVGYIELDINSKILLESFRRPRERPMSTFKVLLCGAVLSRID	60
DB	24	HPETLVKKAEDQLGARVGYIELDINSKILLESFRRPRERPMSTFKVLLCGAVLSRID	83
QY	61	AGQOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP	120
DB	84	AGQOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP	143
QY	121	KELTAPFLHMGDHYTRLDRWPELNEALPNDERDTMPVAMATTLRKLLTGLLTLASRQ	180
DB	144	KELTAPFLHMGDHYTRLDRWPELNEALPNDERDTMPVAMATTLRKLLTGLLTLASRQ	203
QY	181	QLIDMMEADKVAGPLRSALPA	202
DB	204	QLIDMMEADKVAGPLRSALPA	225

RESULT 14
US-09-490-153-362
Sequence 362, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 362:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 362:
US-09-430-153-362

Query Match 100.0%; Score 1032; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.6e-113;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKTKDAEDQIGARVGYIELDLSGKILSFPRPERFPMSTFKYLICGAVLSRID 60
DB 24 HPEITLVKTKDAEDQIGARVGYIELDLSGKILSFPRPERFPMSTFKYLICGAVLSRID 83
QY 61 AGQEQIGRIRIHSQNDLVEYSPVTEKHLTDGWTARELCSAITMSDNTAANLLTTIGSP 120
DB 84 AGQEQIGRIRIHSQNDLVEYSPVTEKHLTDGWTARELCSAITMSDNTAANLLTTIGSP 143
QY 121 KETAFILNMGDHYTRLDRWEPBELNEAIPNDERDTTMAPVAMATTLRKLLTGELLTLASRQ 180
DB 144 KETAFILNMGDHYTRLDRWEPBELNEAIPNDERDTTMAPVAMATTLRKLLTGELLTLASRQ 203
QY 181 QLIDMMEADKVAGPILRSALPA 202
DB 204 QLIDMMEADKVAGPILRSALPA 225

RESULT 15

US-10-191-966-7
Sequence 7, Application US/10191966
Patent No. 6790612
GENERAL INFORMATION:
APPLICANT: Potte, Karen B.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
PRIOR FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-10-191-966-7

Query Match 100.0%; Score 1032; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.6e-113;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKTKDAEDQIGARVGYIELDLSGKILSFPRPERFPMSTFKYLICGAVLSRID 60
DB 24 HPEITLVKTKDAEDQIGARVGYIELDLSGKILSFPRPERFPMSTFKYLICGAVLSRID 83
QY 61 AGQEQIGRIRIHSQNDLVEYSPVTEKHLTDGWTARELCSAITMSDNTAANLLTTIGSP 120

DB 84 AGQEQIGRIRIHSQNDLVEYSPVTEKHLTDGWTARELCSAITMSDNTAANLLTTIGSP 143
QY 121 KETAFILNMGDHYTRLDRWEPBELNEAIPNDERDTTMAPVAMATTLRKLLTGELLTLASRQ 180
DB 144 KETAFILNMGDHYTRLDRWEPBELNEAIPNDERDTTMAPVAMATTLRKLLTGELLTLASRQ 203
QY 181 QLIDMMEADKVAGPILRSALPA 202
DB 204 QLIDMMEADKVAGPILRSALPA 225

Search completed: June 10, 2005, 11:01:17
Job time : 21.7105 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:23:36 ; Search time 67.6736 Seconds
(without alignments)
1528.512 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_202
Perfect score: 1032
Sequence: 1 HPELVKVKYKADQAGARVG.....IDMWEADKVAAGPLRSALPA 202

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03: *
1: uniprot_sprot: *
2: uniprot_trernbl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1032	100.0	229	2	Q6WY5 Klebsiella
2	1032	100.0	231	2	Q6WY4 Hafnia alve
3	1032	100.0	241	2	Q6WY8 Klebsiella
4	1032	100.0	242	2	Q6WY3 Escherichia
5	1032	100.0	285	2	Q6KB67 hordeum vul
6	1032	100.0	286	2	Q38058 bacterioph
7	1032	100.0	286	2	Q00626 staphylococ
8	1032	100.0	286	2	Q79C16 methylobact
9	1032	100.0	286	2	Q79DR3 Escherichia
10	1027	99.5	225	2	Q38212 bacterioph
11	1027	99.5	232	2	Q6PRU7 Escherichia
12	1027	99.5	255	2	Q84H50 Escherichia
13	1027	99.5	261	2	Q84H49 Escherichia
14	1027	99.5	264	2	Q6PRU6 acinetobact
15	1027	99.5	281	2	Q6QIV0 serratia ma
16	1027	99.5	282	2	Q6QIV1 serratia ma
17	1027	99.5	286	1	BLAT_ECOLI
18	1027	99.5	286	1	BLAT_SALTI
19	1027	99.5	286	2	Q53043 Klebsiella
20	1027	99.5	286	2	Q8KSD3 Klebsiella
21	1027	99.5	286	2	Q8VP43 Klebsiella
22	1027	99.5	286	2	Q93328 Escherichia
23	1027	99.5	286	2	Q934D7 Escherichia
24	1027	99.5	286	2	Q93A77 Escherichia
25	1027	99.5	286	2	Q93G13 Klebsiella
26	1027	99.5	286	2	Q6A253 haemophilus
27	1027	99.5	286	2	Q6LBN9 pseudomonas
28	1027	99.5	286	2	Q6LVC6 neisseria g
29	1027	99.5	286	2	Q6TMI1 streptococ
30	1027	99.5	286	2	Q6UVM7 acinetobact
31	1027	99.5	286	2	Q6W7J4 Escherichia

32	1027	99.5	286	2	Q6W9J1 enterobacte
33	1027	99.5	286	2	Q6W9X2 zymomonas m
34	1027	99.5	286	2	Q6WZD4 acinetobact
35	1027	99.5	286	2	Q7B3X5 citrobacter
36	1027	99.5	286	2	Q7B899 Klebsiella
37	1027	99.5	286	2	Q7BP57 shigella fl
38	1027	99.5	286	2	Q7BR75 neisseria m
39	1027	99.5	286	2	Q7DFV3 salmonella
40	1027	99.5	286	2	Q7DHD3 serratia ma
41	1027	99.5	286	2	Q844X1 Klebsiella
42	1027	99.5	286	2	Q8GA85 Escherichia
43	1027	99.5	286	2	Q9EYX1 Escherichia
44	1027	99.5	286	2	Q9K582 Klebsiella
45	1027	99.5	286	2	Q9R770 Escherichia

ALIGNMENTS

RESULT 1	ALIGNMENTS
Q6WY5	Q6WY5
ID Q6WY5	PRELIMINARY; PRT; 229 AA.
AC Q6WY5;	
DT 05-JUL-2004 (TREMBLrel. 27, Created)	
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)	
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)	
DE Beta-lactamase (Fragment).	
GN Name=BlatEM;	
OS Klebsiella oxytoca.	
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	
OC Enterobacteriaceae; Klebsiella.	
OX NCBI_Taxid=571;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=MISC126;	
RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;	
RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.	
DR HSBP; P00807; IKGE.	
DR HSBP; P00807; IKGE.	
DR InterPro; IPR000871; Beta_lactamase_A.	
DR PRINTS; PR00118; BLACTAMASEA.	
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.	
FT NON_TER	
FT NON_TER	
SQ SEQUENCE 229 AA; 25067 MW; C85582C2617F4467 CRC64;	
Query Match 100.0%; Score 1032; DB 2; Length 229;	
Best Local Similarity 100.0%; Pred. No. 1.3e-77;	
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1 HPELVKVKYKADQAGARVGITELDINSKLTLESPREPRPMMSTFVLLCGAVLSRID 60	
DB 2 HPELVKVKYKADQAGARVGITELDINSKLTLESPREPRPMMSTFVLLCGAVLSRID 61	
QY 61 AGOBLGRIRHSQNDIVESPVTEKHLTDGVTRELSAATIMSNDTAAVLLTTIGSP 120	
DB 62 AGOBLGRIRHSQNDIVESPVTEKHLTDGVTRELSAATIMSNDTAAVLLTTIGSP 121	
QY 121 KELTAFILNMGDHYTRLDWSEBELNEALPNDERDTTVPVAAATTLTKLLTGLTLTASRQ 180	
DB 122 KELTAFILNMGDHYTRLDWSEBELNEALPNDERDTTVPVAAATTLTKLLTGLTLTASRQ 181	
QY 181 QIIMMEADKVAAGPLRSALPA 202	
DB 182 QIIMMEADKVAAGPLRSALPA 203	
RESULT 2	
Q6WY4	Q6WY4
ID Q6WY4	PRELIMINARY; PRT; 232 AA.
AC Q6WY4;	
DT 05-JUL-2004 (TREMBLrel. 27, Created)	
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)	

DT 05-JUL-2004 (TREMBLrel. 27, last annotation update)
DE Beta-Lactamase (Fragment).
GN Name=blatEM;
OS Hafnia alvei.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Hafnia.
OX NCBI_TaxID=569;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=MISC198;
RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
RL Submitted (APR-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY265886; AAP93844.1; --
DR HSSP; P00807; IKGE.
DR InterPro; IPR000871; Beta_lactamase_A.
DR PRINTS; PR00118; BLACTAMASE.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1
FT NON_TER 232
SQ SEQUENCE 232 AA; 25380 MW; 3D5DFD85582C261 CRC64;

Query Match 100.0%; Score 1032; DB 2; Length 232;

Best Local Similarity 100.0%; Pred. No. 1.3e-77;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGAVGYIEIDLSGKILSFRRPERPPMSTFVLLCGAVLSRID 60
DB 2 HPEITLVKVKADBDQAGAVGYIEIDLSGKILSFRRPERPPMSTFVLLCGAVLSRID 61
QY 61 AGQEQIGRRIRHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120
DB 62 AGQEQIGRRIRHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 121
QY 121 KELTAFILNMGDHTRLDWRPELNEALPNDERDTMPVAAATLRKLLTGELITLASRQ 180
DB 122 KELTAFILNMGDHTRLDWRPELNEALPNDERDTMPVAAATLRKLLTGELITLASRQ 181
QY 181 QIIDMMEADKVAAGPLRSALPA 202
DB 182 QIIDMMEADKVAAGPLRSALPA 203

RESULT 3

Q6MWY8 PRELIMINARY; PRT; 241 AA.

AC Q6MWY8;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, last annotation update)
DE Beta-Lactamase (Fragment).
GN Name=blatEM;
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=MISC112;
RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
RL Submitted (APR-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY265882; AAP93840.1; --
DR HSSP; P00807; IKGE.
DR InterPro; IPR00146; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASE.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1
FT NON_TER 241
SQ SEQUENCE 241 AA; 26407 MW; 38DF2AFDF0C5807D CRC64;

Query Match 100.0%; Score 1032; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.4e-77;

Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGAVGYIEIDLSGKILSFRRPERPPMSTFVLLCGAVLSRID 60
DB 7 HPEITLVKVKADBDQAGAVGYIEIDLSGKILSFRRPERPPMSTFVLLCGAVLSRID 66
QY 61 AGQEQIGRRIRHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120
DB 67 AGQEQIGRRIRHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 126
QY 121 KELTAFILNMGDHTRLDWRPELNEALPNDERDTMPVAAATLRKLLTGELITLASRQ 180
DB 127 KELTAFILNMGDHTRLDWRPELNEALPNDERDTMPVAAATLRKLLTGELITLASRQ 186
QY 181 QIIDMMEADKVAAGPLRSALPA 202
DB 187 QIIDMMEADKVAAGPLRSALPA 208

RESULT 4

Q6MWY3 PRELIMINARY; PRT; 242 AA.

AC Q6MWY3;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, last annotation update)
DE Beta-Lactamase (Fragment).
GN Name=blatEM;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=TA005;
RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
RL Submitted (APR-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY265887; AAP93845.1; --
DR HSSP; P00807; IKGE.
DR InterPro; IPR00146; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASE.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1
FT NON_TER 242
SQ SEQUENCE 242 AA; 26554 MW; 38C3DFA8A5A3807D CRC64;

Query Match 100.0%; Score 1032; DB 2; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.4e-77;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGAVGYIEIDLSGKILSFRRPERPPMSTFVLLCGAVLSRID 60
DB 8 HPEITLVKVKADBDQAGAVGYIEIDLSGKILSFRRPERPPMSTFVLLCGAVLSRID 67
QY 61 AGQEQIGRRIRHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120
DB 68 AGQEQIGRRIRHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 127
QY 121 KELTAFILNMGDHTRLDWRPELNEALPNDERDTMPVAAATLRKLLTGELITLASRQ 180
DB 128 KELTAFILNMGDHTRLDWRPELNEALPNDERDTMPVAAATLRKLLTGELITLASRQ 187
QY 181 QIIDMMEADKVAAGPLRSALPA 202
DB 188 QIIDMMEADKVAAGPLRSALPA 209

RESULT 5

Q6KB67 PRELIMINARY; PRT; 285 AA.

ID Q6KB67;
AC Q6KB67;

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DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
NCBI_TaxID=4513;
RX
RP SEQUENCE FROM N.A.
RC TISSUE=First leaf;
RA Jansen C., Korell M., Beckey C., Biedenkopf D., Kogel K.H.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ717739; CAG30723.1; -.
DR HSSP; P0807; IALQ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASE.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW Hypothetical protein.
FT NON TER 285
SQ SEQUENCE 285 AA; 31371 MW; A2F22753375FA930 CRC64;

Query Match 100.0%; Score 1032; DB 2; Length 285;
Best Local Similarity 100.0%; Pred. No. 1.7e-77;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKQADQDQGVYIEIDLSGKILSEFRPERPPMSTFVLLCGAVLSRID 60
DB HPEITLVKQADQDQGVYIEIDLSGKILSEFRPERPPMSTFVLLCGAVLSRID 83
QY 61 AGQQLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAIIWSDNTAAILLTTIGCP 120
DB AGQQLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAIIWSDNTAAILLTTIGCP 143
QY 84 AGQQLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAIIWSDNTAAILLTTIGCP 143
DB 121 KEITAFILNMGDHYTRLDRWEPELNEALPNDERDPTMVAAATTLRKLLTGELLTLASRQ 180
DB 144 KEITAFILNMGDHYTRLDRWEPELNEALPNDERDPTMVAAATTLRKLLTGELLTLASRQ 203
QY 181 QIIDWMEADKVAGPLLRGALPA 202
DB 204 QIIDWMEADKVAGPLLRGALPA 225

RESULT 6
ID Q38058 PRELIMINARY; PRT; 286 AA.
AC Q38058;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Beta lactamase.
GN Name=bla;
OS Bacteriophaga phi-X174.
OC Viruses; ssDNA viruses; Microviridae; Microvirus.
NCBI_TaxID=10847;
RX
RP SEQUENCE FROM N.A.
RC MEDLINE=95172401; PubMed=7867948; DOI=10.1016/0378-1119(94)00839-X;
RA Henrich B., Schmidtberger B.;
RL "A variant of phiX174 gene E-based positive selection vectors with
enhanced lytic potential.";
RL Gene 154:51-54 (1995).
DB EMBL; Z35638; CAA84692.1; -.
DB PIR; S47061; S47061.
DR HSSP; Q9R435; IHTZ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASE.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
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SQ SEQUENCE 286 AA; 31557 MW; 5BB2F22753375FA9 CRC64;

Query Match 100.0%; Score 1032; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.7e-77;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKQADQDQGVYIEIDLSGKILSEFRPERPPMSTFVLLCGAVLSRID 60
DB HPEITLVKQADQDQGVYIEIDLSGKILSEFRPERPPMSTFVLLCGAVLSRID 83
QY 24 HPEITLVKQADQDQGVYIEIDLSGKILSEFRPERPPMSTFVLLCGAVLSRID 83
DB 61 AGQQLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAIIWSDNTAAILLTTIGCP 120
DB 84 AGQQLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAIIWSDNTAAILLTTIGCP 143
QY 121 KEITAFILNMGDHYTRLDRWEPELNEALPNDERDPTMVAAATTLRKLLTGELLTLASRQ 180
DB 144 KEITAFILNMGDHYTRLDRWEPELNEALPNDERDPTMVAAATTLRKLLTGELLTLASRQ 203
QY 181 QIIDWMEADKVAGPLLRGALPA 202
DB 204 QIIDWMEADKVAGPLLRGALPA 225

RESULT 7
ID 000626 PRELIMINARY; PRT; 286 AA.
AC 000626; 008022; 008102; 009393; 009396; 009397; 009398; 009399;
AC 009400; 009401; 009402; 009403; 009404; 009405; 009406; 009407;
AC 009408; 009481; 009482; 009483; 009490; 057339;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Beta-lactamase.
OS Staphylococcus aureus.
CG Plasmid J3356/POX7/3, and Plasmid J3356/POX7/1.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
RX
RP SEQUENCE FROM N.A.
RC PLASMID=J3356/POX7/3, and J3356/POX7/1;
RX MEDLINE=96422755; PubMed=8825372; DOI=10.1006/plae.1995.0005;
RA Needham C., Noble W.C., Dyke K.G.;
RL "The staphylococcal insertion sequence IS25 is active.";
RL Plasmid 34:198-205 (1995).
DB EMBL; U36912; AAB3957.1; -.
DB EMBL; U36911; AAB3956.1; -.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASE.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW Plasmid.
SQ SEQUENCE 286 AA; 31557 MW; 5BB2F22753375FA9 CRC64;

Query Match 100.0%; Score 1032; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.7e-77;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKQADQDQGVYIEIDLSGKILSEFRPERPPMSTFVLLCGAVLSRID 60
DB HPEITLVKQADQDQGVYIEIDLSGKILSEFRPERPPMSTFVLLCGAVLSRID 83
QY 24 HPEITLVKQADQDQGVYIEIDLSGKILSEFRPERPPMSTFVLLCGAVLSRID 83
DB 61 AGQQLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAIIWSDNTAAILLTTIGCP 120
DB 84 AGQQLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAIIWSDNTAAILLTTIGCP 143
QY 121 KEITAFILNMGDHYTRLDRWEPELNEALPNDERDPTMVAAATTLRKLLTGELLTLASRQ 180
DB 144 KEITAFILNMGDHYTRLDRWEPELNEALPNDERDPTMVAAATTLRKLLTGELLTLASRQ 203
QY 181 QIIDWMEADKVAGPLLRGALPA 202
DB 204 QIIDWMEADKVAGPLLRGALPA 225
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RESULT 8

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079CL6 PRELIMINARY; PRT: 286 AA.
ID Q79CL6
AC Q79CL6;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Beta-lactamase.
GN Name-bla;
OS Methylobacillus flagellatum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Methylotritales;
OC Methylotritaceae; Methylobacillus.
OX NCBI_TaxID=405;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97074643; PubMed=8917070; DOI=10.1016/0378-1119(96)00114-X;
RA Serebrijski I.G., Vassil V.M., Tsygankov Y.D.;
RT "Two new members of the BioB superfamily: cloning, sequencing and
expression of bioB genes of Methylobacillus flagellatum and
RT Corynebacterium glutamicum.";
RL Gene 175:15-22 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Serebrijski I., Vassil V., Tsygankov Y.;
RL Submitted (JUL-1995) to the EMBL/Genbank/DBJ databases.
DR EMBL; U31280; AAC4581.1; -.
DR HSSP; P00807; IALO.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR00871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;

Query Match 100.0%; Score 1032; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 1,7e-77;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKKVDAEDDQGVGVGIEIDLSGKILSFRRPERRPMMSTFVLLCGAVLSRID 60
DB 24 HPELVKKVDAEDDQGVGVGIEIDLSGKILSFRRPERRPMMSTFVLLCGAVLSRID 83
QY 61 AGQQLGRRIHYSONDLVEYSPTVEKHLTDGMTVRELCSAITSNDTAAVLLTTTGGP 120
DB 84 AGQQLGRRIHYSONDLVEYSPTVEKHLTDGMTVRELCSAITSNDTAAVLLTTTGGP 143
QY 121 KETLAFILNMGDHVTRLDRWEPELNEAIPNDRDRTMPVAAVTLTKLLTGELLTLASRQ 180
DB 144 KETLAFILNMGDHVTRLDRWEPELNEAIPNDRDRTMPVAAVTLTKLLTGELLTLASRQ 203
QY 181 QLIWMMEADKVAGPLRSALPA 202
DB 204 QLIWMMEADKVAGPLRSALPA 225

RESULT 9
079DR3 PRELIMINARY; PRT: 286 AA.
ID Q79DR3
AC Q79DR3;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Mutant extended-spectrum beta-lactamase precursor (EC 3.5.2.6).
GN Name-bla; Synonyms=blatm-116;
OS Escherichia coli.
OC Plasmid pRP4;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=K-12;
RA Maneewannakul K., Maneewannakul S., Ippen-Jhler K.;
RL Submitted (AUG-1991) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12; PLASMID=pRP4;
RA Rondot S., Anthony K., Dubel S., Ida N., Beyreuther K., Frost L.,
RA Little M., Breitling F.;
RL Submitted (APR-1997) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC PLASMID=pRP4;
RX MEDLINE=96189310; PubMed=9514792; DOI=10.1006/abio.1997.2558;
RA Schlieper D., Von Wilcken-Bergmann B., Schmidt M., Sobek H.,
RA Mueller-Hill B.;
RT "A positive selection vector for cloning of long polymerase chain
RT reaction fragments based on a lethal mutant of the csp gene
RT Escherichia coli.";
RL Anal. Biochem. 257:203-209 (1998).
RN [4]
RP SEQUENCE FROM N.A.
RX PubMed=15243036;
RA Jeong S.H., Bae I.K., Lee J.H., Sohn S.G., Kang G.H., Jeon G.J.,
RA Kim Y.H., Jeong B.C., Lee S.H.;
RT "Molecular Characterization of Extended-Spectrum Beta-Lactamases
RT Produced by Clinical Isolates of Klebsiella pneumoniae and Escherichia
RT coli from a Korean Nationwide Survey.";
RL J. Clin. Microbiol. 42:2902-2906 (2004).
DR EMBL; M74750; AAA24057.1; -.
DR EMBL; Y12694; CAA73226.1; -.
DR EMBL; AJ001614; CAA04868.1; -.
DR EMBL; AY425988; AAQ95605.1; -.
DR HSSP; P00807; IALO.
DR GO; GO:0008800; F:beta-lactamase activity; IEA.
DR GO; GO:0016787; F:hydrolyase activity; IEA.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR00871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW Hydrolyase; plasmid; signal.
FT SIGNAL 23
SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;

Query Match 100.0%; Score 1032; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 1,7e-77;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKKVDAEDDQGVGVGIEIDLSGKILSFRRPERRPMMSTFVLLCGAVLSRID 60
DB 24 HPELVKKVDAEDDQGVGVGIEIDLSGKILSFRRPERRPMMSTFVLLCGAVLSRID 83
QY 61 AGQQLGRRIHYSONDLVEYSPTVEKHLTDGMTVRELCSAITSNDTAAVLLTTTGGP 120
DB 84 AGQQLGRRIHYSONDLVEYSPTVEKHLTDGMTVRELCSAITSNDTAAVLLTTTGGP 143
QY 121 KETLAFILNMGDHVTRLDRWEPELNEAIPNDRDRTMPVAAVTLTKLLTGELLTLASRQ 180
DB 144 KETLAFILNMGDHVTRLDRWEPELNEAIPNDRDRTMPVAAVTLTKLLTGELLTLASRQ 203
QY 181 QLIWMMEADKVAGPLRSALPA 202
DB 204 QLIWMMEADKVAGPLRSALPA 225

RESULT 10
Q38212 PRELIMINARY; PRT: 225 AA.
ID Q38212
AC Q38212;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Bacteriophage f1-R208 amplicillinase gene mutation. (Fragment).

```

OS Bacteriophage f1.
 OC Viruses; ssDNA viruses; Inoviridae; Inovirus.
 NC NCB1_TaxID=10863;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86278026; PubMed=3525535;
 RA Topal M.D., Badie J.S., Conrad M.;
 RT "O-6-methylguanine mutation and repair is nonuniform: Selection for
 RL DNA most interactive with O-6-methylguanine."; J. Biol. Chem. 261:9879-9885 (1986).
 DR EMBL; M14017; AAA32208.1; -.
 DR HSSP; Q9R435; 1HTZ.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASRA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 FT NON_TER
 SQ SEQUENCE 225 AA; 25022 MW; 009BF841D618BA09 CRC64;

Query Match 99.5%; Score 1027; DB 2; Length 225;
 Best Local Similarity 99.0%; Pred. No. 3.3e-77;
 Matches 200; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPELVKVKADBDQAGVGYIELDLSGKILSFRRPFRPFPMSSTFKVLLCGAVLSRID 60
 DB 24 HPELVKVKADBDQAGVGYIELDLSGKILSFRRPFRPFPMSSTFKVLLCGAVLSRID 83
 QY 61 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTANILLTTIGSP 120
 DB 84 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTANILLTTIGSP 143
 QY 121 KETLAFILNMGDHYTRLDRMEPELNEAIPNDRDRTMPVMAATTLRKLLTGELLTLASRQ 180
 DB 144 KETLAFILNMGDHYTRLDRMEPELNEAIPNDRDRTMPVMAATTLRKLLTGELLTLASRQ 203
 QY 181 QLIDMMEADKVAAGPLRSALPA 202
 DB 204 QLIDMMEADKVAAGPLRSALPA 225

RESULT 11
 ID 06PRU7 PRELIMINARY; PRT; 232 AA.
 AC 06PRU7;
 DT 05-JUN-2004 (TREMBlrel. 27, Created)
 DT 05-JUN-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUN-2004 (TREMBlrel. 27, Last annotation update)
 DE Inhibitor-resistant TEM beta-lactamase (Fragment).
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 NC NCB1_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=U3;
 RL Submitted (MAR-2004) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY553761; AAS86427.1; -.
 DR HSSP; P00807; 1ALQ.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASRA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 FT NON_TER
 SQ SEQUENCE 232 AA; 25558 MW; 5791CD285EE70BB0 CRC64;

Query Match 99.5%; Score 1027; DB 2; Length 232;
 Best Local Similarity 99.0%; Pred. No. 3.4e-77;
 Matches 200; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPELVKVKADBDQAGVGYIELDLSGKILSFRRPFRPFPMSSTFKVLLCGAVLSRID 60
 DB 15 HPELVKVKADBDQAGVGYIELDLSGKILSFRRPFRPFPMSSTFKVLLCGAVLSRID 74
 QY 61 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTANILLTTIGSP 120
 DB 75 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTANILLTTIGSP 134
 QY 121 KETLAFILNMGDHYTRLDRMEPELNEAIPNDRDRTMPVMAATTLRKLLTGELLTLASRQ 180
 DB 135 KETLAFILNMGDHYTRLDRMEPELNEAIPNDRDRTMPVMAATTLRKLLTGELLTLASRQ 194
 QY 181 QLIDMMEADKVAAGPLRSALPA 202
 DB 195 QLIDMMEADKVAAGPLRSALPA 216

RESULT 12
 ID 084H50 PRELIMINARY; PRT; 255 AA.
 AC 084H50;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE TEM-117 beta-lactamase (Fragment).
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 NC NCB1_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Box A.T.A., Pauw A., Leverstein-vanhal M.A.;
 RL Submitted (JUN-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY130282; AAN05026.1; -.
 DR HSSP; Q9R435; 1HTZ.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASRA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 FT NON_TER
 SQ SEQUENCE 255 AA; 27906 MW; DCBB28B65978C3A6 CRC64;

Query Match 99.5%; Score 1027; DB 2; Length 255;
 Best Local Similarity 99.0%; Pred. No. 3.8e-77;
 Matches 200; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPELVKVKADBDQAGVGYIELDLSGKILSFRRPFRPFPMSSTFKVLLCGAVLSRID 60
 DB 12 HPELVKVKADBDQAGVGYIELDLSGKILSFRRPFRPFPMSSTFKVLLCGAVLSRID 71
 QY 61 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTANILLTTIGSP 120
 DB 72 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTANILLTTIGSP 131
 QY 121 KETLAFILNMGDHYTRLDRMEPELNEAIPNDRDRTMPVMAATTLRKLLTGELLTLASRQ 180
 DB 132 KETLAFILNMGDHYTRLDRMEPELNEAIPNDRDRTMPVMAATTLRKLLTGELLTLASRQ 191
 QY 181 QLIDMMEADKVAAGPLRSALPA 202
 DB 192 QLIDMMEADKVAAGPLRSALPA 213

RESULT 13
 ID 084H49 PRELIMINARY; PRT; 261 AA.
 AC 084H49;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE TEM-110 beta-lactamase (Fragment).

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OS Klebsiella oxytoca.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
ON NCBI_TaxID=571;
RP SEQUENCE FROM N.A.
RA Box A.T.A., Paauw A., Leverstein-vanhal M.A., Verhoef J., Fluit A.C.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY130283; AAN05027.1; -.
DR HSSP; O9R435; 1HTZ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1 1
SQ SEQUENCE 261 AA; 28738 MW; 4F748F773A08CBB CRC64;

Query Match 99.5%; Score 1027; DB 2; Length 261;
Best Local Similarity 99.0%; Pred. No. 3.9e-77;
Matches 200; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPELVKVKADQDQAGRVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRD 60
DB 12 HPELVKVKADQDQAGRVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRD 71
QY 61 AGGOLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP 120
DB 72 AGGOLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP 131
QY 121 KETLAFPHNMGDHYTRLDRWEPELNEAIPNDRDTMPVAMATTLRKLLTGELLTLASRQ 180
DB 132 KETLAFPHNMGDHYTRLDRWEPELNEAIPNDRDTMPVAMATTLRKLLTGELLTLASRQ 191
QY 181 QLIDMEADKVAAGPLRSALPA 202
DB 192 QLIDMEADKVAAGPLRSALPA 213

RESULT 14
Q6PRU6 PRELIMINARY; PRT; 264 AA.
AC Q6PRU6;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DS TEM Beta-lactamase (Fragment).
OS Acinetobacter sp. U11.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=269266;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=U11;
RC Ghannadi S., Hosseini-Mazinan S.M.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY583762; AAS6428.1; -.
DR HSSP; P00807; 1ALQ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1 1
SQ SEQUENCE 264 AA; 28986 MW; A4F071CF7489352C CRC64;

Query Match 99.5%; Score 1027; DB 2; Length 264;
Best Local Similarity 99.0%; Pred. No. 4e-77;
Matches 200; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPELVKVKADQDQAGRVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRD 60

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DB 12 HPELVKVKADQDQAGRVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRD 71
QY 61 AGGOLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP 120
DB 72 AGGOLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP 131
QY 121 KETLAFPHNMGDHYTRLDRWEPELNEAIPNDRDTMPVAMATTLRKLLTGELLTLASRQ 180
DB 132 KETLAFPHNMGDHYTRLDRWEPELNEAIPNDRDTMPVAMATTLRKLLTGELLTLASRQ 191
QY 181 QLIDMEADKVAAGPLRSALPA 202
DB 192 QLIDMEADKVAAGPLRSALPA 213

RESULT 15
Q6QIV0 PRELIMINARY; PRT; 281 AA.
AC Q6QIV0;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DS TEM-1 beta-lactamase (Fragment).
GN Name=blatEM-1;
OS Serratia marcescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=ES-42, ES-46, ES-71, and ES-11;
RA Yatsuyanagi J., Saito S., Harata S., Suzuki N., Amano K.-I.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY538700; AAS46846.1; -.
DR EMBL; AY538701; AAS46847.1; -.
DR EMBL; AY538702; AAS46848.1; -.
DR EMBL; AY538698; AAS46844.1; -.
DR HSSP; P00807; 1ALQ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 281 281
SQ SEQUENCE 281 AA; 30837 MW; C8934B9C696057BF CRC64;

Query Match 99.5%; Score 1027; DB 2; Length 281;
Best Local Similarity 99.0%; Pred. No. 4.3e-77;
Matches 200; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPELVKVKADQDQAGRVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRD 60
DB 24 HPELVKVKADQDQAGRVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRD 83
QY 61 AGGOLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGGOLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KETLAFPHNMGDHYTRLDRWEPELNEAIPNDRDTMPVAMATTLRKLLTGELLTLASRQ 180
DB 144 KETLAFPHNMGDHYTRLDRWEPELNEAIPNDRDTMPVAMATTLRKLLTGELLTLASRQ 203
QY 181 QLIDMEADKVAAGPLRSALPA 202
DB 204 QLIDMEADKVAAGPLRSALPA 225

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Search completed: June 10, 2005, 10:57:03
 Job time : 68.6736 secs

QY 181 QUIDMMEADKVAGPILRSALPAGWFIADKSGAGERSRGIITAAIGPDG 228
 DB 181 QUIDMMEADKVAGPILRSALPAGWFIADKSGAGERSRGIITAAIGPDG 228

RESULT 3
 ADJ67709
 ID ADJ67709 standard; protein; 263 AA.
 AC ADJ67709;
 XX 20-MAY-2004 (first entry)
 DE Escherichia coli TEM-1 beta-lactamase.
 XX
 KM fragment complementation system; marker protein;
 KM multiple genetic element incorporation; antibiotic resistance;
 KM beta-lactam derivative activation; anti-tumour compound;
 KM functional reassembly; protein-protein interaction; proteome interaction;
 KM immunoglobulin variable region; immune cell protein; CD40;
 KM phosphorylation-regulated cell signal transducer; TEM-1 beta-lactamase;
 KM enzyme.
 XX Escherichia coli.
 OS
 XX US2004038317-A1.
 PV
 XX 26-FEB-2004.
 PD
 XX 22-SEP-2003; 2003US-00668778.
 PF
 XX 15-MAR-1999; 99US-0124339P.
 PR 25-MAY-1999; 99US-0135926P.
 PR 13-JAN-2000; 2000US-0175968P.
 PR 15-MAR-2000; 2000US-00526106.
 XX
 PA (KALO-) KALOBIOIS INC.
 PI Balint RF, Her J;
 DR WPI; 2004-203222/19.
 DR N-PSDB; ADJ67708.
 XX
 PT Fragment complementation system for detecting immunoglobulin epitope, has
 PT first oligopeptide containing N-terminal fragment with C-terminal break-
 PT point, second oligopeptide containing C-terminal fragment with N-terminal
 PT break-point.
 XX
 PS Disclosure; SEQ ID NO 2; 47bp; English.

CC efficiently detects multiple interaction between extracellular and
 CC intracellular protein with high throughput format. This is the amino acid
 CC sequence of antibiotic resistance enzyme TEM-1 beta-lactamase that can be
 CC used as a selectable gene in the fragment complementation system of the
 CC invention.
 XX
 XX SQ Sequence 263 AA;
 Query Match 100.0%; Score 1170; DB 8; Length 263;
 Best Local Similarity 100.0%; Pred. No. 8.5e-117;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HBETLVKYNADQAGAVGYIELDNLNSGKILSPREPERPFWMTFKVLCGAVLSRID 60
 DB 1 HBETLVKYNADQAGAVGYIELDNLNSGKILSPREPERPFWMTFKVLCGAVLSRID 60
 QY 61 AGQEBOLGRIRIHSQNDLYEYSPVTEKHLTDGNTVRELCSAATMGSNDTANLITTTGGP 120
 DB 61 AGQEBOLGRIRIHSQNDLYEYSPVTEKHLTDGNTVRELCSAATMGSNDTANLITTTGGP 120
 QY 121 KSLTAPLHNMGDHVTRLDRWEPENLEALPNDERDTTVPVAMATTIRKLTGELTLASRQ 180
 DB 121 KSLTAPLHNMGDHVTRLDRWEPENLEALPNDERDTTVPVAMATTIRKLTGELTLASRQ 180

QY 181 QUIDMMEADKVAGPILRSALPAGWFIADKSGAGERSRGIITAAIGPDG 228
 DB 181 QUIDMMEADKVAGPILRSALPAGWFIADKSGAGERSRGIITAAIGPDG 228

RESULT 4
 AAW16634
 ID AAW16634 standard; protein; 264 AA.
 XX
 AC AAW16634;
 XX
 DT 09-AUG-1997 (first entry)
 XX
 DE Beta-lactamase (including signal peptide).
 XX
 KM Gene directed enzyme prodnrg therapy; GDEPT;
 KM virus directed enzyme prodnrg therapy; VDEPT; beta-lactamase; cancer;
 KM HIV; inflammation.
 XX
 OS Escherichia coli.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..23
 FT /label= Sig_peptide
 XX
 PN MO9719180-A2.
 XX
 PD 29-MAY-1997.
 XX
 PF 19-NOV-1996; 96WO-GB002845.
 XX
 PR 20-NOV-1995; 95GB-00023703.
 XX
 PA (GLAX) GLAXO GROUP LTD.
 PI Dev I, Moore JT, Ohmstede C;
 XX
 DR WPI; 1997-298117/27.
 DR N-PSDB; AAT66736.
 XX
 PT Molecular chimera for gene or virus directed enzyme prodnrg therapy -
 PT useful for treatment of cancer, viral infection or inflammation.
 XX
 PS Example; Page 28; 38bp; English.
 CC Escherichia coli beta-lactamase (AAW16634), including the signal peptide,
 CC is the expression product of a molecular chimera, designated pCMV-BL
 CC (AAT66737), in which the beta-lactamase gene is under control of the CMV
 CC intermediate/early promoter. Vectors consisting of a transcriptional

CC regulatory DNA sequence linked to a beta-lactamase gene can be used for
 CC enzyme producing therapy. Expression of the beta-lactamase in a targeted
 CC cell allows conversion of a prodrug into an agent toxic to the cell for
 CC treatment of cancer. viral (e.g. HIV) infection or inflammation.
 CC Secretion of the enzyme has the advantage of increasing neighbouring cell
 CC kill

XX Sequence 264 AA;

Query Match 100.0%; Score 1170; DB 2; Length 264;
 Best Local Similarity 100.0%; Pred. No. 8.5e-117;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGARVGYIELDINSKLTLESFPERPERPMMSTFKVLLCGAVLSRID 60

Db 2 HPEITLVKVKADBDQAGARVGYIELDINSKLTLESFPERPERPMMSTFKVLLCGAVLSRID 61

QY 61 AGOGLGRRIHYSQNDLVEYSPVTEKHLTDGATVRELCSAAITMSDNTAANLLTTIGCP 120

Db 62 AGOGLGRRIHYSQNDLVEYSPVTEKHLTDGATVRELCSAAITMSDNTAANLLTTIGCP 121

QY 121 KELTAFLHMGDHYTRLDRWEPELNEALPNDERDTMPVAMATTLRKLLTGELTLASRQ 180

Db 122 KELTAFLHMGDHYTRLDRWEPELNEALPNDERDTMPVAMATTLRKLLTGELTLASRQ 181

QY 181 QLIDMMEADKVAAPLRSALPAGWFIADKSGAGERSGRTIAALGPDG 228

Db 182 QLIDMMEADKVAAPLRSALPAGWFIADKSGAGERSGRTIAALGPDG 229

RESULT 5

AAW18680
 ID AAW18680 standard; protein; 264 AA.

XX AAW18680;

DT 13-AUG-1997 (first entry)

XX Intracellularly-expressed beta-lactamase.

XX Producing therapy; gene directed enzyme producing therapy; GDEPT;

KM virus directed enzyme producing therapy; VDEPT; lung cancer;

XX beta-lactamase; PCMV-delIBL.

XX Escherichia coli.

XX MO9719183-A2.

XX 29-MAY-1997.

XX 19-NOV-1996; 96WO-GB002846.

XX 20-NOV-1995; 95GB-00023703.

XX (GLAXO) GLAXO GROUP LTD.

XX Dev I, Moore JT, Sethna PB;

XX WPI; 1997-298118/27.

XX N-PSDB; AAT70311.

XX DNA construct for gene-directed enzyme producing therapy of lung cancer -

XX comprises lung- or neuroendocrine-specific promoter controlling

XX expression of prodrug-converting enzyme.

XX Example 811; Page 32-34; 53pp; English.

XX The intracellular form (AAW18680) of TEM beta-lactamase is expressed by

XX PCMV-delIBL (AAT70311) in which a PCR-amplified beta-lactamase coding

XX sequence, minus the signal sequence, is placed under control of the

XX intermediate/early promoter of cytomegalovirus. Intracellular beta-

XX lactamase constructs, placed under control of promoter/enhancer elements

XX of lung-associated protein or neuroendocrine marker protein genes, can be

CC used in novel chimaeric molecules for use in prodrug therapy of lung

CC cancer

XX Sequence 264 AA;

Query Match 100.0%; Score 1170; DB 2; Length 264;
 Best Local Similarity 100.0%; Pred. No. 8.5e-117;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGARVGYIELDINSKLTLESFPERPERPMMSTFKVLLCGAVLSRID 60

Db 2 HPEITLVKVKADBDQAGARVGYIELDINSKLTLESFPERPERPMMSTFKVLLCGAVLSRID 61

QY 61 AGOGLGRRIHYSQNDLVEYSPVTEKHLTDGATVRELCSAAITMSDNTAANLLTTIGCP 120

Db 62 AGOGLGRRIHYSQNDLVEYSPVTEKHLTDGATVRELCSAAITMSDNTAANLLTTIGCP 121

QY 121 KELTAFLHMGDHYTRLDRWEPELNEALPNDERDTMPVAMATTLRKLLTGELTLASRQ 180

Db 122 KELTAFLHMGDHYTRLDRWEPELNEALPNDERDTMPVAMATTLRKLLTGELTLASRQ 181

QY 181 QLIDMMEADKVAAPLRSALPAGWFIADKSGAGERSGRTIAALGPDG 228

Db 182 QLIDMMEADKVAAPLRSALPAGWFIADKSGAGERSGRTIAALGPDG 229

RESULT 6

AAW18680
 ID AAW18680 standard; protein; 286 AA.

XX AAW18680;

DT 10-MAR-2003 (revised)

XX 04-JUN-1993 (first entry)

XX Ampicillin resistance protein.

XX CYP1A1; PRNH127; PRNH155; xeroderma pigmentosum group A; XPA;

KM xenobiotics; circular; chimeric cytochrome P4501A1.

XX Homo sapiens.

XX US5180666-A.

XX 19-JAN-1993.

XX 27-JUN-1991; 91US-00721775.

XX 27-JUN-1991; 91US-00721775.

XX (UYWA-) UNIV WAYNE STATE.

XX States JC, Hines RM, Novak RF;

XX WPI; 1993-052845/06.

XX N-PSDB; AAQ36498.

XX In vitro method for testing mutagenicity of a chemical - by metabolising

XX chemical cell line consisting of transformed fibroblasts having

XX detectable cytochrome P450 mixed function oxidase activity and detecting

XX gene damage.

XX Disclosure; Col 21-24; 24pp; English.

XX The expression constructs PRNH127 and PRNH155 contain identical sequences

XX but were constructed using different strategies (see AAQ36498). The

XX constructs comprise exons 2-7 of human CYP1A1 gene under the control of

XX the inducible mouse metallothionein (MMT-1) promoter. The constructs also

XX contain an open reading frame in the opposite orientation to the

XX cytochrome P450 exons. This ORF encodes ampicillin resistance. The

XX constructs are suitable for transformation of human fibroblasts derived

XX from the xeroderma pigmentosum group A. Cultures of the transformed

XX fibroblasts can be used to test substances for mutagenicity. The presence

CC of the inducible cytochrome P450 gene allows metabolism of the substance
CC to mutagenic metabolites. (Updated on 10-MAR-2003 to add missing OS
CC field.)

XX Sequence 286 AA;

Query Match 100.0%; Score 1170; DB 2; Length 286;

Best Local Similarity 100.0%; Pred. No. 9.5e-117; Mismatches 0; Indels 0; Gaps 0;

Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKDADQAGAVGYIELDLSGKILSFPRPERPPMSTFKYLCGAVLSRID 60
DB 24 HPEITLVKVKDADQAGAVGYIELDLSGKILSFPRPERPPMSTFKYLCGAVLSRID 83
QY 61 AGQEBQGRIRIHVSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQEBQGRIRIHVSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDITMPVAMATTIRKLLTGELTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDITMPVAMATTIRKLLTGELTLASRQ 203
QY 181 QLIDWMEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDG 228
DB 204 QLIDWMEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDG 251

RESULT 7
AAR97619 ID AAR97619 standard; protein; 286 AA.

XX AAR97619;

DT 20-AUG-1996 (first entry)

DE Secretory beta-lactamase.

KM Gene therapy; gene directed enzyme prodnug therapy; GDEPT;

KM virus directed enzyme prodnug therapy; VDEPT; prodnug activation;

KM cytotoxic; cytostatic; cancer; tumour; retrovirus; vector;

KW beta-lactamase; cephalosporin.

OS Synthetic.

PN WO9616179-A1.

PD 30-MAY-1996.

PF 20-NOV-1995; 95WO-GB002716.

PR 18-NOV-1994; 94GB-00023367.

PA (WELL) WELLCOME FOUND LTD.

PI Dev IK, Moore JT, Ohmsted C;

DR WPI; 1996-268615/27.

DR N-PSDB; AAT29220.

PT Molecular chimera for use in enzyme gene therapy - is activated in a

PT target cell to express a secretible enzyme which cleaves a prodnug

PT outside the cell into a cytotoxic or cytostatic agent.

XX Example 3; Page 57-58; 73pp; English.

CC A secretory beta-lactamase (AAR97619) is expressed from DNA construct
CC PCMV-BL (AAT29220), in which the beta-lactamase coding sequence is under
CC the control of the intermediate/early cytomegalovirus promoter. Beta-
CC lactamase delivery to mammalian cells confers sensitivity to
CC cephalosporin prodnugs. Liposomal DNA/5-fluorouracil prodnug combinations
CC resulted in s.c. tumour regression in mice bearing A549 tumours. Survival
CC of mice bearing human large cell lung H460 intrathoracic (i.t.) tumours
CC was increased upon i.t. injection of the secretory beta-lactamase DNA

CC construct

XX Sequence 286 AA;

Query Match 100.0%; Score 1170; DB 2; Length 286;

Best Local Similarity 100.0%; Pred. No. 9.5e-117; Mismatches 0; Indels 0; Gaps 0;

Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKDADQAGAVGYIELDLSGKILSFPRPERPPMSTFKYLCGAVLSRID 60
DB 24 HPEITLVKVKDADQAGAVGYIELDLSGKILSFPRPERPPMSTFKYLCGAVLSRID 83
QY 61 AGQEBQGRIRIHVSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQEBQGRIRIHVSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDITMPVAMATTIRKLLTGELTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDITMPVAMATTIRKLLTGELTLASRQ 203
QY 181 QLIDWMEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDG 228
DB 204 QLIDWMEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDG 251

RESULT 8
AAR96423 ID AAR96423 standard; protein; 286 AA.

XX AAR96423;

DT 25-MAR-2003 (revised)

DT 25-NOV-1996 (first entry)

DE Cytochrome P450 (CYP1A1 construct).

KM cytochrome; P450; metallothionein; mouse; human; cytotoxicity; assay;

KW metabolism.

OS Homo sapiens.

PN US5525482-A.

PD 11-JUN-1996.

PF 15-NOV-1994; 94US-00339658.

PR 27-JUN-1991; 91US-00721775.

PR 09-DEC-1992; 92US-00990295.

PA (UYWA-) UNIV WAYNE STATE.

PI Hines RN, Novak RF, States JC;

DR WPI; 1996-286397/29.

DR N-PSDB; AAT30354.

PT Testing chemicals for cytotoxicity to human by detecting gene damage -

PT using recombinant fibroblasts transformed with cytochrome P450 gene under

PT control of inducible promoter.

XX Disclosure; Col 17-24; 26pp; English.

CC The present sequence is encoded by a chimeric mouse metallothionein-
CC cytochrome P450IA1 (CYP1A1) expression construct. Two clones, pRNM127 and
CC pRNM15, were isolated by different methods and which both had the same
CC sequence. The CYP1A1 construct is used in assays to test for cytotoxicity
CC of humans to a chemical. The method comprises exposing human fibroblast
CC cells normally not including any cytochrome P450 activity to potentially
CC toxic chemicals. The cells having been transformed to express cytochrome
CC P450, under the control of a controllable promoter through the CYP1A1
CC gene, upon exposure to the chemical in vitro. The chemical is metabolised
CC intracellularly into a cytochrome metabolite by oxidation within the

fibroblasts through the intracellular cytochrome P450 mixed function oxidase enzymes expressed by the cells. Gene damage in the test cells is detected as an indication of cytotoxicity of the chemical. (Updated on 25 -MAR-2003 to correct PF field.)

Sequence 286 AA;

Query Match 100.0%; Score 1170; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 9.5e-117;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 HPEITLVKXKDADQIGARVGYIEIDLNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60

24 HPEITLVKXKDADQIGARVGYIEIDLNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83

61 AGQOLGRIRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAAILLTTIGSP 120

84 AGQOLGRIRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAAILLTTIGSP 143

121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDTTTPVAAVATTLRKLLTGBELLTLASRQ 180

144 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDTTTPVAAVATTLRKLLTGBELLTLASRQ 203

181 QLIDMMEADKVAAGPLRSALPAGWFIADKSGAGRGSRGIIAALGPDG 228

204 QLIDMMEADKVAAGPLRSALPAGWFIADKSGAGRGSRGIIAALGPDG 251

RESULT 9

AAW16635

ID AAW16635 standard; protein; 286 AA.

AAW16635;

09-AUG-1997 (first entry)

Beta-lactamase (no signal peptide).

Gene directed enzyme prodng therapy; GDEPT;

virus directed enzyme prodng therapy; VDEPT; beta-lactamase; cancer;

HIV; inflammation.

Escherichia coli.

WO9719180-A2.

29-MAY-1997.

19-NOV-1996; 96WO-GB002845.

20-NOV-1995; 95GB-00023703.

(GLAX) GLAXO GROUP LTD.

Dev I, Moore JT, Ohmstede C;

WPI; 1997-298117/27.

N-PSDB; AAT66737.

Molecular chimera for gene or virus directed enzyme prodng therapy -

useful for treatment of cancer, viral infection or inflammation.

Example; Page 26; 38pp; English.

Sequence 286 AA;

Query Match 100.0%; Score 1170; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 9.5e-117;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 HPEITLVKXKDADQIGARVGYIEIDLNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60

24 HPEITLVKXKDADQIGARVGYIEIDLNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83

61 AGQOLGRIRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAAILLTTIGSP 120

84 AGQOLGRIRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAAILLTTIGSP 143

121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDTTTPVAAVATTLRKLLTGBELLTLASRQ 180

144 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDTTTPVAAVATTLRKLLTGBELLTLASRQ 203

181 QLIDMMEADKVAAGPLRSALPAGWFIADKSGAGRGSRGIIAALGPDG 228

204 QLIDMMEADKVAAGPLRSALPAGWFIADKSGAGRGSRGIIAALGPDG 251

RESULT 10

AAW18679

ID AAW18679 standard; protein; 286 AA.

AAW18679;

13-AUG-1997 (first entry)

Secretory beta-lactamase.

Prodng therapy; gene directed enzyme prodng therapy; GDEPT;

virus directed enzyme prodng therapy; VDEPT; lung cancer;

beta-lactamase; PCMV-BL.

Escherichia coli.

WO9719183-A2.

29-MAY-1997.

19-NOV-1996; 96WO-GB002846.

20-NOV-1995; 95GB-00023703.

(GLAX) GLAXO GROUP LTD.

Dev I, Moore JT, Sethna PB;

WPI; 1997-298118/27.

N-PSDB; AAT70309.

DNA construct for gene-directed enzyme prodng therapy of lung cancer -

comprises lung- or neuroendocrine-specific promoter controlling

expression of prodng-converting enzyme.

Example 8ii; Page 26-27; 53pp; English.

The secreted form (AAW18679) of TEM beta-lactamase is expressed by PCMV-BL (AAT70309) in which a PCR-amplified beta-lactamase coding sequence is placed under control of the intermediate/early promoter of

cytomegalovirus. Secretory beta-lactamase constructs, placed under

control of promoter/enhancer elements of lung- associated protein or

neuroendocrine marker protein genes, can be used in novel chimeric

CC molecules for use in prodrg therapy of lung cancer
XX
SQ Sequence 286 AA;

Query Match 100.0%; Score 1170; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 9.5e-117;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 HPELVKVDADDOIGARVGYIELDNGSKILESFRPERPFPMSTFKYLGGAVLSRID 60
DB 24 HPELVKVDADDOIGARVGYIELDNGSKILESFRPERPFPMSTFKYLGGAVLSRID 83
OY 61 AGEOUGRRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANILLTTIGSP 120
DB 84 AGEOUGRRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANILLTTIGSP 143
OY 121 KELTAFLNMGDHTRLDRWEPBELNEALPNDERDTTTPVAMATTIRKLLTGELTLASRQ 180
DB 144 KELTAFLNMGDHTRLDRWEPBELNEALPNDERDTTTPVAMATTIRKLLTGELTLASRQ 203
OY 181 QUIDMWEADKVAGPILRSALPAGWFIADKSGAGERSRGIIAALGPDG 228
DB 204 QUIDMWEADKVAGPILRSALPAGWFIADKSGAGERSRGIIAALGPDG 251
```

RESULT 11

AAV08529

ID AAV08529 standard; protein; 286 AA.

XX AC AAV08529;

DT 03-AUG-1999 (first entry)

DE Vector pASK75 beta-1a protein.

XX Firefly; luciferase; tetracycline; transcriptional control; TetR; TetA;
KW tetracycline repressor; tetracycline promoter; luminescence; luxCDABE;
KW insect; Tn10; medicine; dosage; cheese production; antibiotic; foodstuff;
KW allergy.

OS Synthetic.

XX MO3925866-A1.

XX 27-MAY-1999.

XX 11-NOV-1998; 98WO-FI000873.

XX 14-NOV-1997; 97FI-00004235.

XX (KORP/) KORPELA M.

XX (KARP/) KARP M.

XX (KURIT/) KURITTU J.

XX Korpele M, Karp M, Kurittu J;

XX MPI; 1999-338015/28.

XX N-PSDB; AAV72418.

XX Assaying for tetracycline using recombinant prokaryotic cells.

XX Discloure; Page 47-48; 67pp; English.

XX This invention describes a novel tetracycline assay that uses recombinant
CC prokaryotic cells comprising a luciferase gene under the transcriptional
CC control of a tetracycline repressor and tetracycline promoter and
CC involves the detection of luminescence emitted from the cells. The assay
CC can be used to distinguish tetracycline form other microbial agents. The
CC invention also describes a novel plasmid comprising either the luxCDABE
CC genes, a tetracycline repressor (TetR) and a tetracycline promoter (TetA)
CC from Tn10, or the insect luciferase gene, a tetracycline repressor (TetR)
CC and a tetracycline promoter (TetA) from Tn10. The tetracycline assay
CC method can be used for the determination of tetracycline in a sample,

CC e.g. to study the dosage and penetration of the medicine. The method can
CC also be used to test cheese production, as cheese making bacteria are not
CC able to work in the presence of tetracycline. The method can also be used
CC to determine the presence or concentration of antibiotics in foodstuffs,
CC e.g. for allergic people. The present assay method does not rely on the
CC growth of microbes as do conventional tests, and so is much more rapid.
CC The present assay is also more sensitive, as even a small amount of
CC luminescence can be detected

XX
SQ Sequence 286 AA;
Query Match 100.0%; Score 1170; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 9.5e-117;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 HPELVKVDADDOIGARVGYIELDNGSKILESFRPERPFPMSTFKYLGGAVLSRID 60
DB 24 HPELVKVDADDOIGARVGYIELDNGSKILESFRPERPFPMSTFKYLGGAVLSRID 83
OY 61 AGEOUGRRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANILLTTIGSP 120
DB 84 AGEOUGRRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANILLTTIGSP 143
OY 121 KELTAFLNMGDHTRLDRWEPBELNEALPNDERDTTTPVAMATTIRKLLTGELTLASRQ 180
DB 144 KELTAFLNMGDHTRLDRWEPBELNEALPNDERDTTTPVAMATTIRKLLTGELTLASRQ 203
OY 181 QUIDMWEADKVAGPILRSALPAGWFIADKSGAGERSRGIIAALGPDG 228
DB 204 QUIDMWEADKVAGPILRSALPAGWFIADKSGAGERSRGIIAALGPDG 251
```

RESULT 12

AAV10442

ID AAV10442 standard; protein; 286 AA.

XX AAV10442;

DT 01-DEC-2000 (first entry)

DE Expression vector pSEX15G2 bla protein.

XX Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
KW B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.

OS Synthetic.

XX DE19900635-A1.

XX 13-JUL-2000.

XX 11-JAN-1999; 99DE-01000635.

XX 11-JAN-1999; 99DE-01000635.

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX Breitling F, Pouscka A, Moldenhauer G;

XX MPI; 2000-499832/45.

XX N-PSDB; AAV71430.

XX Selecting monoclonal antibodies, by expressing them on the surface of
PT hybridomas attached to antibody-binding protein, then reaction with
PT antibody library.

PS Claim 16; Fig 3; 22pp; German.

XX This invention describes a novel method for the selection of monoclonal
CC antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma
CC cells to produce antibody-producing hybridomas such that the antibodies
CC are presented at the surface of the hybridomas by an antibody-binding
CC protein (I); and (ii) binding the antibody to antigens (Ag). The

invention also describes antibody-binding proteins (I) that comprise a combination of the signal peptide of a murine immunoglobulin (Ig) kappa chain or a murine MHC (major histocompatibility complex) Class I k(k) molecule; an antibody-binding site of proteins A, G, L or Ig, and the transmembrane domain of PDGFR (platelet-derived growth factor receptor) or CD52. The method is used to select Mab with specificity for particular antigens. Mab can be selected without separate culture of hybridomas, and selection can be made against many antigens in a library, optionally on the basis of strength of affinity for a particular antigen. Complex mixtures of hybridomas can be used for selection, reducing the time and cost involved in Mab selection. This sequence represents the bla protein contained in the expression vector pSEX1162 which contains the bla protein, Neo-R and protein G described in the method of the invention

Query Match 100.0%; Score 1170; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 9.5e-117; Mismatches 0; Indels 0; Gaps 0;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 HPETLVKVAADADQAGVGYIELDLSGKILSFPRPERPMPSTFKVLLCGAVLSRID 60
24 HPETLVKVAADADQAGVGYIELDLSGKILSFPRPERPMPSTFKVLLCGAVLSRID 83
61 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGWTARELCSAATWSDNTAANLLTTTGGP 120
84 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGWTARELCSAATWSDNTAANLLTTTGGP 143
121 KETLAFINMGDHTRLDRMEPELNEALPNDERDTTVPVAAATTKLLTSELTLASRQ 180
144 KETLAFINMGDHTRLDRMEPELNEALPNDERDTTVPVAAATTKLLTSELTLASRQ 203
181 QLIDWMEADKVAAGPLLRGALPAGWFIADKSGAGERSGRTIAALGPDG 228
204 QLIDWMEADKVAAGPLLRGALPAGWFIADKSGAGERSGRTIAALGPDG 251

RESULT 13
AAB10438
ID AAB10438 standard; protein; 286 AA.

AC AAB10438;
DT 01-DEC-2000 (first entry)
XX Expression vector pSEX1162 bla protein.

XX Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
KM B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.

OS Synthetic.

PN DE19900635-A1.

PD 13-JUL-2000.

PF 11-JAN-1999; 99DE-01000635.

PR 11-JAN-1999; 99DE-01000635.

PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

PI Breitling F, Poustka A, Moldenhauer G;

DR WPI: 2000-499832/45.

DR N-PSDB; AAA71428.

PT Selecting monoclonal antibodies, by expressing them on the surface of
XX hybridomas attached to antibody-binding protein, then reaction with
XX antibody library.

XX Claim 16; Fig 1; 22pp; German.

This invention describes a novel method for the selection of monoclonal antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma cells to produce antibody-producing hybridomas such that the antibodies are presented at the surface of the hybridomas by an antibody-binding protein (I); and (ii) binding the antibody to antigens (Ag). The invention also describes antibody-binding proteins (I) that comprise a combination of the signal peptide of a murine immunoglobulin (Ig) kappa chain or a murine MHC (major histocompatibility complex) Class I k(k) molecule; an antibody-binding site of proteins A, G, L or Ig, and the transmembrane domain of PDGFR (platelet-derived growth factor receptor) or CD52. The method is used to select Mab with specificity for particular antigens. Mab can be selected without separate culture of hybridomas, and selection can be made against many antigens in a library, optionally on the basis of strength of affinity for a particular antigen. Complex mixtures of hybridomas can be used for selection, reducing the time and cost involved in Mab selection. This sequence represents the Neo-R protein contained in the expression vector pSEX1162 which contains the bla protein, Neo-R and protein G described in the method of the invention

Query Match 100.0%; Score 1170; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 9.5e-117; Mismatches 0; Indels 0; Gaps 0;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 HPETLVKVAADADQAGVGYIELDLSGKILSFPRPERPMPSTFKVLLCGAVLSRID 60
24 HPETLVKVAADADQAGVGYIELDLSGKILSFPRPERPMPSTFKVLLCGAVLSRID 83
61 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGWTARELCSAATWSDNTAANLLTTTGGP 120
84 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGWTARELCSAATWSDNTAANLLTTTGGP 143
121 KETLAFINMGDHTRLDRMEPELNEALPNDERDTTVPVAAATTKLLTSELTLASRQ 180
144 KETLAFINMGDHTRLDRMEPELNEALPNDERDTTVPVAAATTKLLTSELTLASRQ 203
181 QLIDWMEADKVAAGPLLRGALPAGWFIADKSGAGERSGRTIAALGPDG 228
204 QLIDWMEADKVAAGPLLRGALPAGWFIADKSGAGERSGRTIAALGPDG 251

RESULT 14
AAB10440
ID AAB10440 standard; protein; 286 AA.

AC AAB10440;

DT 01-DEC-2000 (first entry)

XX Expression vector pSEX1162 bla protein.

XX Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
KM B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.

OS Synthetic.

PN DE19900635-A1.

PD 13-JUL-2000.

PF 11-JAN-1999; 99DE-01000635.

PR 11-JAN-1999; 99DE-01000635.

PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

PI Breitling F, Poustka A, Moldenhauer G;

DR WPI: 2000-499832/45.

DR N-PSDB; AAA71429.

PT Selecting monoclonal antibodies, by expressing them on the surface of

PT hybridomas attached to antibody-binding protein, then reaction with
PT antibody library.

PS Claim 16; Fig 2; 22pp; German.

CC This invention describes a novel method for the selection of monoclonal
CC antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma
CC cells to produce antibody-producing hybridomas such that the antibodies
CC are presented at the surface of the hybridomas by an antibody-binding
CC protein (I); and (ii) binding the antibody to antigens (Ag). The
CC invention also describes antibody-binding proteins (I) that comprise a
CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa
CC chain or a murine MHC (major histocompatibility complex) Class I K(IK)
CC molecule; an antibody-binding site of proteins A, G, L or Ig; and the
CC transmembrane domain of PDGFR (platelet-derived growth factor receptor)
CC or CD53. The method is used to select Mab with specificity for particular
CC antigens. Mab can be selected without separate culture of hybridomas, and
CC selection can be made against many antigens in a library, optionally on
CC the basis of strength of affinity for a particular antigen. Complex
CC mixtures of hybridomas can be used for selection, reducing the time and
CC cost involved in Mab selection. This sequence represents the bla protein
CC protein contained in the expression vector pSEX102 which contains the
CC bla protein, Neo-R and protein G described in the method of the invention
CC
SQ Sequence 286 AA;

Query Match 100.0%; Score 1170; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 9.5e-117;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVDADQAGVGYIELDINSKILSFPRPERPMMSTFVLLCGAVLSRID 60
DB 24 HPELVKVDADQAGVGYIELDINSKILSFPRPERPMMSTFVLLCGAVLSRID 83
QY 61 AGQQLGRIRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAIIWSDNTAAILLTTIGCP 120
DB 84 AGQQLGRIRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAIIWSDNTAAILLTTIGCP 143
QY 121 KELTAFLLNMGDHVTRLDRWEPELNEAIPNDERDTTVPVAAATTLRKLLTSELTLASRQ 180
DB 144 KELTAFLLNMGDHVTRLDRWEPELNEAIPNDERDTTVPVAAATTLRKLLTSELTLASRQ 203
QY 181 QLIDMMEADKVAAGPLLSALPAGWFIADKSGAGERSGRTIALLGPDG 228
DB 204 QLIDMMEADKVAAGPLLSALPAGWFIADKSGAGERSGRTIALLGPDG 251

RESULT 15
AAB50898
ID AAB50898 standard; protein; 286 AA.

XX AAB50898;

XX 20-MAR-2001 (first entry)

DE Protein encoded by bla resistance marker of integration vector pLO12306.

XX bla resistance marker; recombinant host cell; saccharification;
KW fermentation; polysaccharase; oligosaccharide degradation; cel2 gene;
KW glucanase; integration vector; pLO12306.

XX Unidentified.

OS WO200071729-A2.

XX 30-NOV-2000.

XX 26-MAY-2000; 2000WO-US014773.

XX 26-MAY-1999; 99US-0136376P.

XX (UYFL) UNIV FLORIDA RES FOUND.

PI Ingram LO, Zhou S;
XX
DR MPI: 2001-032043/04.
DR N-PSDB; AAC91455.

PT Recombinant host cells useful for producing polysaccharase for degrading
PT oligosaccharides, comprises a first heterologous polynucleotide encoding
PT polysaccharase under control of surrogate promoter.

PS Disclosure: Page 82-83; 87pp; English.

CC The present sequence is given in a specification relating to a
CC recombinant host cell suitable for simultaneous saccharification and
CC fermentation. The host cell contains at least one heterologous
CC polynucleotide encoding a polysaccharase under the transcriptional
CC control of a surrogate promoter capable of increasing expression of the
CC polysaccharase. The host cell also contains a second heterologous
CC polynucleotide encoding a secretory polypeptide to facilitate the
CC secretion of the expressed polysaccharase. The recombinant host cell is
CC useful for producing polysaccharase which is useful for enzymatically
CC degrading oligosaccharides such as lignocellulose, hemicellulose,
CC cellulose, pectin or their combinations, and fermenting the product to
CC ethanol, by simultaneous saccharification and fermentation processes. The
CC present sequence is encoded by an integration vector which was introduced
CC into cells to generate recombinant host cells. The vector contains a
CC surrogate promoter from *Zymomonas mobilis*, the *cel2* gene from *Erwinia*
CC chrysanthemi, resistance markers bla and tet, and *Klebsiella oxytoca*
CC target sequence

SQ Sequence 286 AA;

Query Match 100.0%; Score 1170; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 9.5e-117;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVDADQAGVGYIELDINSKILSFPRPERPMMSTFVLLCGAVLSRID 60
DB 24 HPELVKVDADQAGVGYIELDINSKILSFPRPERPMMSTFVLLCGAVLSRID 83
QY 61 AGQQLGRIRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAIIWSDNTAAILLTTIGCP 120
DB 84 AGQQLGRIRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAIIWSDNTAAILLTTIGCP 143
QY 121 KELTAFLLNMGDHVTRLDRWEPELNEAIPNDERDTTVPVAAATTLRKLLTSELTLASRQ 180
DB 144 KELTAFLLNMGDHVTRLDRWEPELNEAIPNDERDTTVPVAAATTLRKLLTSELTLASRQ 203
QY 181 QLIDMMEADKVAAGPLLSALPAGWFIADKSGAGERSGRTIALLGPDG 228
DB 204 QLIDMMEADKVAAGPLLSALPAGWFIADKSGAGERSGRTIALLGPDG 251

Search completed: June 10, 2005, 10:49:14
Job time : 89.4014 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:35:06 ; Search time 16.6267 Seconds
(without alignments)
1319.408 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_228
Perfect score: 1170

Sequence: 1 HPEITLVKVKDAEDQIGARVGV...KSGAGERSGRTIALGPDG 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1170	100.0	286	2	TS1301	beta-lactamase (EC
2	1170	100.0	286	2	S47061	beta-lactamase (EC
3	1170	100.0	286	4	S41975	beta-lactamase (EC
4	1165	99.6	286	1	PNECP	beta-lactamase (EC
5	1165	99.6	286	4	I40905	beta-lactamase (EC
6	1152	98.5	286	2	S60312	extended spectrum
7	1151	98.4	286	2	S30113	beta-lactamase (EC
8	1145	97.9	286	2	S60310	extended spectrum
9	1143	97.7	286	2	S60311	beta-lactamase (EC
10	1139	97.4	286	2	J01546	Bla protein - Salm
11	828	70.8	265	2	S00464	beta-lactamase (EC
12	826	70.6	286	2	S16146	beta-lactamase (EC
13	826	70.6	286	2	A60679	beta-lactamase (EC
14	822	70.3	265	2	S02434	beta-lactamase (EC
15	822	70.3	286	1	A44998	beta-lactamase (EC
16	819	70.0	286	2	A37200	beta-lactamase (EC
17	818	69.9	286	2	A60632	beta-lactamase (EC
18	815	69.7	265	2	A60448	beta-lactamase (EC
19	813	69.5	279	2	A24469	beta-lactamase (EC
20	803.5	68.7	287	1	A44996	beta-lactamase (EC
21	768	65.6	286	1	A44958	beta-lactamase (EC
22	610	52.1	298	2	A41381	beta-lactamase (EC
23	484.5	41.4	302	2	S35188	beta-lactamase (EC
24	483.5	41.3	291	2	S42075	beta-lactamase (EC
25	483	41.3	281	2	D95395	probable beta lact
26	480.5	41.1	293	2	S04649	beta-lactamase (EC
27	479.5	41.0	263	2	A54543	beta-lactamase (EC
28	477.5	40.8	306	2	G69674	beta-lactamase (EC
29	476.5	40.7	306	2	S47330	penicillinase - Ba

30	475.5	40.6	294	2	S16553	beta-lactamase (EC
31	474.5	40.6	288	2	J01136	beta-lactamase (EC
32	470.5	40.2	304	2	A49789	beta-lactamase (EC
33	470.5	40.2	304	2	A35001	beta-lactamase (EC
34	467.5	40.0	306	1	B45822	beta-lactamase (EC
35	467.5	40.0	314	2	S06967	beta-lactamase (EC
36	463.5	39.6	288	2	J50755	beta-lactamase (EC
37	462	39.5	305	2	A61156	beta-lactamase (EC
38	462	39.5	305	2	A57002	beta-lactamase (EC
39	462	39.5	305	2	A60680	beta-lactamase (EC
40	456.5	39.0	311	2	U00520	beta-lactamase (EC
41	455	38.9	276	2	JH0268	beta-lactamase (EC
42	452.5	38.7	291	2	JP0074	beta-lactamase (EC
43	449.5	38.4	263	2	S23929	beta-lactamase (EC
44	448.5	38.3	294	2	S19006	beta-lactamase (EC
45	445.5	38.1	307	1	PNEBL	beta-lactamase (EC

ALIGNMENTS

```
RESULT 1
TS1301
beta-lactamase (EC 3.5.2.6) - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C/Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C/Accession: TS1301
R/WACH, A.; BRACHAT, A.; ALBERTISSEUIL, C.; REBISCHUNG, C.; PHILIPSEN, P.
Yeast 13, 1065-1075, 1997
A/Title: Heterologous His3 marker and GFP reporter modules for PCR-targeting in Saccharom
A/Reference number: Z09587
A/Accession: TS1301
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-286 <WAC>
A/Cross-references: EMBL:AJ002683; PIDN:CAA05686.1
C/Genetics:
A/Gene: bla
C/Superfamily: beta-lactamase I
C/Keywords: hydrolase

Query Match          100.0%; Score 1170; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 8e+94;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HPEITLVKVKDAEDQIGARVGVYIELDNSGKILSFRRPFRPMNSTFYVLGAVLSRID 60
        |||
DB      24 HPEITLVKVKDAEDQIGARVGVYIELDNSGKILSFRRPFRPMNSTFYVLGAVLSRID 83

QY      61 AGQEQIGRRIRHSQNDLYEVSPTVEKHLTDGWTVEICSAATMSDNTAANLLTTIGSP 120
        |||
DB      84 AGQEQIGRRIRHSQNDLYEVSPTVEKHLTDGWTVEICSAATMSDNTAANLLTTIGSP 143

QY      121 KELTAFILNMGDVTRLDREPELNEAIPNDERDITMVAATTIRKLLTGELTLTASRQ 180
        |||
DB      144 KELTAFILNMGDVTRLDREPELNEAIPNDERDITMVAATTIRKLLTGELTLTASRQ 203

QY      161 QIIDMEADKVAQPIILRSALPGWFIADKSGAGERSGRTIALGPDG 228
        |||
DB      204 QIIDMEADKVAQPIILRSALPGWFIADKSGAGERSGRTIALGPDG 251

RESULT 2
S47061
beta-lactamase (EC 3.5.2.6) - phage phi-X174
C/Species: phage phi-X174
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S47061
R/Henrich, B.; Schmidtberger, B.
submitted to the EMBL Data Library, July 1994
A/Description: A variant of phix174 gene B-based positive selection vectors with enhanced
A/Reference number: S47060
A/Accession: S47061
```


RESULT 5
I40905
beta-lactamase (EC 3.5.2.6) - synthetic
C:Species: synthetic
A:Note: Cloning vector pCG1408 engineered and expressed in *Clavibacter xyli* subsp. cynod
C:Date: 15-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Oct-2000
C:Accession: I40905
R:Taylor, J.; Stearman, R.S.; Uratani, B.B.
Plasmid 29, 241-244, 1993
A:Title: Development of a native plasmid as a cloning vector in *Clavibacter xyli* subsp.
A:Reference number: 140904; MUID:93361581; PMID:7689234
A:Accession: I40905
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-286 <RES>
A:Cross-references: EMBL:U21228; NID:g885956; PIDN:AAA70411.1; PID:g885958
C:Keywords: hydrolase

Query Match 99.6%; Score 1165; DB 4; Length 286;
Best Local Similarity 99.1%; Pred. No. 2.2e-93;
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPELVKVDADQAGRVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVDADQAGRVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 83

QY 61 AGQEOIGRIHYSQNDLYEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQEOIGRIHYSQNDLYEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143

QY 121 KELTAFIHNMGDHTVRLDRWBEPLNEAIPNDRDITMPVAMATTIRKLITGELLTLASRQ 180
DB 144 KELTAFIHNMGDHTVRLDRWBEPLNEAIPNDRDITMPVAMATTIRKLITGELLTLASRQ 203

QY 181 QUIDMMEADKXVAGPILRSALPAGWFIADKSGAGERSGIIAALGPDG 228
DB 204 QUIDMMEADKXVAGPILRSALPAGWFIADKSGAGERSGIIAALGPDG 251

RESULT 6
S60312
extended spectrum beta-lactamase CAZ-7 - *Klebsiella pneumoniae*
C:Species: *Klebsiella pneumoniae*
C:Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 22-Jun-1999
C:Accession: S60312
R:Chanai, C.; Poupart, M.C.; Siroc, D.; Labia, R.; Siroc, J.; Cluzel, R.
Antimicrob. Agents Chemother. 36, 1817-1820, 1992
A:Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.
A:Reference number: S60310; MUID:93037315; PMID:1416873
A:Accession: S60312
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <CHAS>
A:Cross-references: EMBL:X65254; NID:g296955; PIDN:CAA46346.1; PID:g296956
C:Superfamily: beta-lactamase I

Query Match 98.5%; Score 1152; DB 2; Length 286;
Best Local Similarity 97.8%; Pred. No. 2.9e-92;
Matches 223; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPELVKVDADQAGRVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVDADQAGRVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 83

QY 61 AGQEOIGRIHYSQNDLYEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQEOIGRIHYSQNDLYEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143

QY 121 KELTAFIHNMGDHTVRLDRWBEPLNEAIPNDRDITMPVAMATTIRKLITGELLTLASRQ 180
DB 144 KELTAFIHNMGDHTVRLDRWBEPLNEAIPNDRDITMPVAMATTIRKLITGELLTLASRQ 203

181 QUIDMMEADKXVAGPILRSALPAGWFIADKSGAGERSGIIAALGPDG 228

DB 204 QUIDMMEADKXVAGPILRSALPAGWFIADKSGAGERSGIIAALGPDG 251

RESULT 7
S30113
beta-lactamase (EC 3.5.2.6) TEM-3 - *Klebsiella pneumoniae* plasmid pCFE04
C:Species: *Klebsiella pneumoniae*
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: S30113
R:Abillat, C.; Lourenco-Vital, J.; Goussard, S.; Courvallin, P.
Mol. Gen. Genet. 235, 113-121, 1992
A:Title: A new example of physical linkage between Tn1 and Tn21: the antibiotic multiple-
A:Reference number: S30112; MUID:93062798; PMID:1331747
A:Accession: S30113
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <MAB>
A:Cross-references: UNIPROT:P00810; EMBL:X64523; NID:g43797; PIDN:CAA45828.1; PID:g43798
C:Genetics:
A:Gene: bla(TEM-3)
A:Genome: plasmid
C:Superfamily: beta-lactamase I
C:Keywords: antibiotic resistance; hydrolase

Query Match 98.4%; Score 1151; DB 2; Length 286;
Best Local Similarity 97.8%; Pred. No. 3.5e-92;
Matches 223; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPELVKVDADQAGRVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVDADQAGRVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 83

QY 61 AGQEOIGRIHYSQNDLYEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQEOIGRIHYSQNDLYEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143

QY 121 KELTAFIHNMGDHTVRLDRWBEPLNEAIPNDRDITMPVAMATTIRKLITGELLTLASRQ 180
DB 144 KELTAFIHNMGDHTVRLDRWBEPLNEAIPNDRDITMPVAMATTIRKLITGELLTLASRQ 203

QY 181 QUIDMMEADKXVAGPILRSALPAGWFIADKSGAGERSGIIAALGPDG 228
DB 204 QUIDMMEADKXVAGPILRSALPAGWFIADKSGAGERSGIIAALGPDG 251

RESULT 8
S60310
extended spectrum beta-lactamase CAZ-2 - *Klebsiella pneumoniae*
C:Species: *Klebsiella pneumoniae*
C:Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 22-Jun-1999
C:Accession: S60310
R:Chanai, C.; Poupart, M.C.; Siroc, D.; Labia, R.; Siroc, J.; Cluzel, R.
Antimicrob. Agents Chemother. 36, 1817-1820, 1992
A:Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.
A:Reference number: S60310; MUID:93037315; PMID:1416873
A:Accession: S60310
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <CHAS>
A:Cross-references: EMBL:X65252; NID:g296951; PIDN:CAA46344.1; PID:g296952
C:Superfamily: beta-lactamase I

Query Match 97.9%; Score 1145; DB 2; Length 286;
Best Local Similarity 97.4%; Pred. No. 1.2e-91;
Matches 222; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 HPELVKVDADQAGRVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVDADQAGRVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 83

QY 61 AGQEOIGRIHYSQNDLYEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120

Db 84 AGOQOLGRRHHYSONDLVYSPVTEKHLTDGWTVELCSAAITMSDNTAANILLTTTGGP 143
QY 121 KETLAFLLHMGDHYTRLDRWPEPELNEAIPNDERDTTTPVAAATTLRKLLTGSELLTLASRQ 180
Db 144 KETLAFLLHMGDHYTRLDRWPEPELNEAIPNDERDTTTPVAAATTLRKLLTGSELLTLASRQ 203
QY 181 QLIDWMEADKVAAGPLLRSGALPAGWFIADKSGAGERSGGIITAAIGPDG 228
Db 204 QLIDWMEADKVAAGPLLRSGALPAGWFIADKSGAGERSGGIITAAIGPDG 251

RESULT 9

S60311
beta-lactamase (EC 3.5.2.6) TEM-1 - Klebsiella pneumoniae transposon Tn331
C/Species: Klebsiella pneumoniae
C/Date: 12-Apr-1996 #sequence revision 19-Apr-1996 #text_change 09-Jul-2004
C/Accession: S60311; F37392; F00498
R:Chanal, C.; Poupart, M.C.; Siroc, D.; Labia, R.; Siroc, J.; Cluzel, R.
AntiMicrob. Agents Chemother. 36, 1817-1820, 1992
A/Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.
A/Reference number: S60310; MUID:93037315; PMID:1416873
A/Accession: S60311
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-286 <CAN>
A/Cross-references: UNIPROT:Q99224; EMBL:X65253; NID:g236953; PIDN:CAA46345.1; PID:g236953
R:Toimasky, M.E.
Plasmid 24, 218-226, 1990
A/Title: Sequencing and expression of aadA, bla, and tnpR from the multiresistance transposon Tn331.
A/Reference number: A37392; MUID:91172904; PMID:1963948
A/Accession: F37392
A/Molecule type: DNA
A/Residues: 1-32 <TOL>
A/Cross-references: GB:M5547; NID:g155010; PIDN:AAA98408.1; PID:g155016
C/Genetics:
A/Gene: TEM-bla
C/Superfamily: beta-lactamase I
C/Keywords: antibiotic resistance; hydrolase
Query Match 97.7%; Score 1143; DB 2; Length 286;
Best Local Similarity 96.9%; Pred. No. 1.7e-91;
Matches 221; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 HPEITLVKVKADQDQAGRVGYIELDLSNGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
Db 24 HPEITLVKVKADQDQAGRVGYIELDLSNGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
QY 61 AGOQOLGRRHHYSONDLVYSPVTEKHLTDGWTVELCSAAITMSDNTAANILLTTTGGP 120
Db 84 AGOQOLGRRHHYSONDLVYSPVTEKHLTDGWTVELCSAAITMSDNTAANILLTTTGGP 143
QY 121 KETLAFLLHMGDHYTRLDRWPEPELNEAIPNDERDTTTPVAAATTLRKLLTGSELLTLASRQ 180
Db 144 KETLAFLLHMGDHYTRLDRWPEPELNEAIPNDERDTTTPVAAATTLRKLLTGSELLTLASRQ 203
QY 181 QLIDWMEADKVAAGPLLRSGALPAGWFIADKSGAGERSGGIITAAIGPDG 228
Db 204 QLIDWMEADKVAAGPLLRSGALPAGWFIADKSGAGERSGGIITAAIGPDG 251

RESULT 10

QJ01546
Bla protein - Salmonella typhimurium plasmid NTP16
N/Alternate names: beta lactamase homolog
C/Species: Salmonella typhimurium
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: QJ01546
R:Canon, P.M.; Strike, P.
Plasmid 27, 220-230, 1992
A/Title: Complete nucleotide sequence and gene organization of plasmid NTP16.
A/Reference number: QJ01548; MUID:92383313; PMID:1325061
A/Accession: QJ01546
A/Status: translation not shown

A/Molecule type: DNA
A/Residues: 1-286 <CAN>
A/Cross-references: UNIPROT:Q8L2F9
C/Genetics:
A/Genome: plasmid
C/Superfamily: beta-lactamase I

Query Match 97.4%; Score 1139; DB 2; Length 286;
Best Local Similarity 97.4%; Pred. No. 3.9e-91;
Matches 222; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADQDQAGRVGYIELDLSNGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
Db 24 HPEITLVKVKADQDQAGRVGYIELDLSNGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
QY 61 AGOQOLGRRHHYSONDLVYSPVTEKHLTDGWTVELCSAAITMSDNTAANILLTTTGGP 120
Db 84 AGOQOLGRRHHYSONDLVYSPVTEKHLTDGWTVELCSAAITMSDNTAANILLTTTGGP 143
QY 121 KETLAFLLHMGDHYTRLDRWPEPELNEAIPNDERDTTTPVAAATTLRKLLTGSELLTLASRQ 180
Db 144 KETLAFLLHMGDHYTRLDRWPEPELNEAIPNDERDTTTPVAAATTLRKLLTGSELLTLASRQ 203
QY 181 QLIDWMEADKVAAGPLLRSGALPAGWFIADKSGAGERSGGIITAAIGPDG 228
Db 204 QLIDWMEADKVAAGPLLRSGALPAGWFIADKSGAGERSGGIITAAIGPDG 251

RESULT 11

S00464
beta-lactamase (EC 3.5.2.6) class A - Escherichia coli plasmid p453
N/Alternate names: beta-lactamase PIT-2; beta-lactamase SHV-1
C/Species: Escherichia coli
C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1993
C/Accession: S00464
R:Barthelmy, M.; Peduzzi, J.; Labia, R.
Biochem. J. 251, 73-79, 1988
A/Title: Complete amino acid sequence of p453-plasmid-mediated PIT-2 beta-lactamase (SHV-1).
A/Reference number: S00464; MUID:88268817; PMID:3260490
A/Accession: S00464
A/Molecule type: protein
A/Residues: 1-265 <BAR>
C/Genetics:
A/Genome: plasmid
C/Superfamily: beta-lactamase I
C/Keywords: antibiotic resistance; hydrolase
Query Match 70.8%; Score 828; DB 2; Length 265;
Best Local Similarity 69.0%; Pred. No. 3.1e-64;
Matches 156; Conservative 33; Mismatches 37; Indels 0; Gaps 0;

QY 2 PETLVKVKADQDQAGRVGYIELDLSNGKILSFRRPFRPMMSTFKVLLCGAVLSRID 61
Db 2 PETLVKVKADQDQAGRVGYIELDLSNGKILSFRRPFRPMMSTFKVLLCGAVLSRID 61
QY 62 GQEQOLGRRHHYSONDLVYSPVTEKHLTDGWTVELCSAAITMSDNTAANILLTTTGGP 121
Db 62 GQEQOLGRRHHYSONDLVYSPVTEKHLTDGWTVELCSAAITMSDNTAANILLTTTGGP 121
QY 122 ELTAFLLHMGDHYTRLDRWPEPELNEAIPNDERDTTTPVAAATTLRKLLTGSELLTLASRQ 181
Db 122 ELTAFLLHMGDHYTRLDRWPEPELNEAIPNDERDTTTPVAAATTLRKLLTGSELLTLASRQ 181
QY 182 LIDWMEADKVAAGPLLRSGALPAGWFIADKSGAGERSGGIITAAIGPD 227
Db 182 LIDWMEADKVAAGPLLRSGALPAGWFIADKSGAGERSGGIITAAIGPD 227

RESULT 12

S16146
beta-lactamase (EC 3.5.2.6) 2A precursor - Klebsiella pneumoniae plasmids
N/Alternate names: beta-lactamase SHV2A
C/Species: Klebsiella pneumoniae

A/Accession: S12703
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-286 <POD>
A/Cross-references: EMBL:X53433; NID:g43789; PIDN:CAA37524.1; PID:g43790
C/Genetics:
A/Genome: plasmid
C/Superfamily: Beta-lactamase I
C/Keywords: antibiotic resistance; hydrolase

Query Match 70.3%; Score 822; DB 1; Length 286;
Best Local Similarity 68.6%; Pred. No. 1.1e-63;
Matches 155; Conservative 33; Mismatches 38; Indels 0; Gaps 0;

```
QY      2 PETLVKVDADQDLGARVGYIELDINSKILSFRRERFPMMSTFKYLLCGAVLSRIDA 61
      23 PQLPEQITLSQSLSGRVGMTEMDLASGRTLTAWRADERFPMSTFKYVLCGAVLARVDA 82
      QY      62 GQEQIGRRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTANILLTTGGPK 121
      Db      83 GDEQLERKIHRYQDLDVYSPVSEKHLADGMTVGELCAAITMSDNSANILLLATVGGPA 142
      QY      122 ELTAFILHMGDHVTRLDDWPEELNEAIPNDERDPTMPYMATTLRKLLTGELTLASRQ 181
      Db      143 GLTAPLRQIGDVTRLDDWETELNEALPGDARDTTTPASMAATLRLKLLTSQRLSARSQRQ 202
      QY      182 LIDWWEADKVGAPLRSALPAGWFIADKSGAGERSGRIIAALGPD 227
      Db      203 LIGMMVDNRVAGPLRSVLPAGWFIADKTKGASERGARGIVALLGPN 248
```

Search completed: June 10, 2005, 10:58:49
Job time : 17.6267 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:23:36 ; Search time 76.3841 Seconds
(without alignments)
1528.512 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_228

Perfect score: 1170
Sequence: 1 HPEITLVKVKADMDQLGARVG.....KSGAGERSRGIIALGPDG 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03: *
1: uniprot_sprot: *
2: uniprot_crembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1170	100.0	229	2	Q6WVY5 Klebsiella
2	1170	100.0	232	2	Q6WVY4 hafiaia alve
3	1170	100.0	241	2	Q6WVY8 Klebsiella
4	1170	100.0	242	2	Q6WVY3 escherichia
5	1170	100.0	285	2	Q6KB67 hordeum vul
6	1170	100.0	286	2	Q38058 bacterioph
7	1170	100.0	286	2	Q00626 staphylococ
8	1170	100.0	286	2	Q79CL6 methylobact
9	1170	100.0	286	2	Q79DR3 escherichia
10	1165	99.6	255	2	Q84H50 escherichia
11	1165	99.6	261	2	Q84H49 Klebsiella
12	1165	99.6	264	2	Q6PRU6 acinetobact
13	1165	99.6	281	2	Q6OIV0 serratia ma
14	1165	99.6	282	2	Q6OIV1 serratia ma
15	1165	99.6	286	1	BLAT_ECOLI
16	1165	99.6	286	1	BLAT_SALTI
17	1165	99.6	286	1	BLAT_SALTI
18	1165	99.6	286	2	Q8V433 Klebsiella
19	1165	99.6	286	2	Q8V433 Klebsiella
20	1165	99.6	286	2	Q93A77 escherichia
21	1165	99.6	286	2	Q6A253 haemophilus
22	1165	99.6	286	2	Q6LBN9 pseudomonas
23	1165	99.6	286	2	Q6LBN9 pseudomonas
24	1165	99.6	286	2	Q6LBN9 pseudomonas
25	1165	99.6	286	2	Q6LBN9 pseudomonas
26	1165	99.6	286	2	Q6LBN9 pseudomonas
27	1165	99.6	286	2	Q6LBN9 pseudomonas
28	1165	99.6	286	2	Q6LBN9 pseudomonas
29	1165	99.6	286	2	Q6LBN9 pseudomonas
30	1165	99.6	286	2	Q6LBN9 pseudomonas
31	1165	99.6	286	2	Q6LBN9 pseudomonas

32	1165	99.6	286	2	Q7BP57 shigella fl
33	1165	99.6	286	2	Q7BR75 neisseria m
34	1165	99.6	286	2	Q7BRY3 salmonella
35	1165	99.6	286	2	Q7BHD3 serratia ma
36	1165	99.6	286	2	Q7B9Y1 plasmid ppy
37	1165	99.6	286	2	Q7BVP8 Klebsiella
38	1162	99.3	234	2	Q6WVY6 citrobacter
39	1162	99.3	286	2	P78144 escherichia
40	1162	99.3	286	2	Q8KSD2 escherichia
41	1161	99.2	274	2	Q6Q4T6 pseudomonas
42	1161	99.2	277	2	Q9XHC0 escherichia
43	1161	99.2	286	2	Q32372 capnocytoph
44	1161	99.2	286	2	Q8RPY9 enterobacter
45	1161	99.2	286	2	Q932Y6 pseudomonas

ALIGNMENTS

RESULT 1	ID	Q6WVY5	PRELIMINARY;	PRT;	229 AA.
AC	Q6WVY5				
DT	05-JUL-2004 (TREMBlrel. 27, Created)				
DT	05-JUL-2004 (TREMBlrel. 27, Last sequence update)				
DT	05-JUL-2004 (TREMBlrel. 27, Last annotation update)				
DE	Beta-lactamase (Fragment).				
GN	Name=BLATEM;				
OS	Klebsiella oxyloca.				
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;				
OC	Enterobacteriaceae; Klebsiella.				
OX	NCBI_Taxid=571;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=MISC126;				
RA	Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;				
RL	Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AY265885; AAP93843.1; --				
DR	HSSP; P00807; 1KGE.				
DR	Interpro; IPR000871; Beta_lactamase_A.				
DR	PRINTS; PR00118; BLACTAMASEA.				
DR	PROSITE; PS00146; BETA_LACTAMASE_A; 1.				
FT	NON_TER	1	1		
FT	NON_TER	229	229		
SQ	SEQUENCE	229 AA; 25067 MW; C85582C2617F4467 CRC64;			
Query Match		100.0%; Score 1170; DB 2; Length 229;			
Best Local Similarity		100.0%; Pred. No. 8.7e-87;			
Matches 228; Conservative		0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	HPEITLVKVKADMDQLGARVGYIELDLNSGKIIESTFRPEERPFPMSTFKYLLCGAVLSRID			60
DB	2	HPEITLVKVKADMDQLGARVGYIELDLNSGKIIESTFRPEERPFPMSTFKYLLCGAVLSRID			61
QY	61	AGQOLGRIRHYSQNDLVYSPVTEKHLTDGWTVEILCSAATITMSDNTNANLLTTIGSP			120
DB	62	AGQOLGRIRHYSQNDLVYSPVTEKHLTDGWTVEILCSAATITMSDNTNANLLTTIGSP			121
QY	121	KEITLFLNMGDHVRRLDRMBELNEALPNDERDTTPVANAATTIKLITGELITLASRQ			180
DB	122	KEITLFLNMGDHVRRLDRMBELNEALPNDERDTTPVANAATTIKLITGELITLASRQ			181
QY	181	QIIDMNEADKVAEPILRSALPAGWFIADKSGAGERSRGIIALGPDG 228			
DB	182	QIIDMNEADKVAEPILRSALPAGWFIADKSGAGERSRGIIALGPDG 229			
RESULT 2					
QY	Q6WVY4	PRELIMINARY;	PRT;	232 AA.	
AC	Q6WVY4				
DT	05-JUL-2004 (TREMBlrel. 27, Created)				
DT	05-JUL-2004 (TREMBlrel. 27, Last sequence update)				

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DT 05-JUL-2004 (TreeBLrel. 27, Last annotation update)
DE Beta-lactamase (Fragment).
GN Name=blatm;
OS Hafnia alvei.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Hafnia.
OX NCBI_TaxID=569;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MISC198;
RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
RL Submitted (APR-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY255886; AAP93844.1; -.
DR HSSP; P00807; IKGE.
DR InterPro; IPR000871; Beta_lactamase_A.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A, 1.
FT NON_TER 1
FT TER 232
SQ SEQUENCE 232 AA; 25380 MW; 3D5DFD885582C261 CRC64;

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Query Match	100.0%;	Score 1170;	DB 2;	Length 232;
Best Local Similarity	100.0%;	Pred. No. 8.8e-87;		
Matches 228; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

Qy	1	HPETLVKKAQEDDQGAHVGIETLIDNSGKLTLESRRPREERPMMSSTFVLLCGAVLSRID	60
Db	2	HPETLVKKAQEDDQGAHVGIETLIDNSGKLTLESRRPREERPMMSSTFVLLCGAVLSRID	61
Qy	61	AGQEGQGRRIHYSONDLVEYSPVTEKHLTDGKTVRELCSAIIITMSDNTAAAILTTIGCP	120
Db	62	AGQEGQGRRIHYSONDLVEYSPVTEKHLTDGKTVRELCSAIIITMSDNTAAAILTTIGCP	121
Qy	121	KELTAFILHMGDHYTRLDLWMEPELNEALPNDERDITVMVAATTLRKLLTGELLTLASRQ	180
Db	122	KELTAFILHMGDHYTRLDLWMEPELNEALPNDERDITVMVAATTLRKLLTGELLTLASRQ	181
Qy	181	QLIDIMEDDKVAGPLLRSLPAGWFIADKSGAGRGSGIIITAAIGPDD	228
Db	182	QLIDIMEDDKVAGPLLRSLPAGWFIADKSGAGRGSGIIITAAIGPDD	229

Q6MWT8	Q6MWT8	PRELIMINARY;	PRT;	241 AA.
AC	Q6MWT8;			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	Beta-lactamase (Fragment).			
GN	Name=blatEM;			
OS	Klebsiella pneumoniae.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Klebsiella.			
OX	NCBI_TaxID=573;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MISC12;			
RA	Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;			
RL	Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AY265882; AAP3840.1; -.			
DR	HSSP; P00807; 1KGE.			
DR	InterPro; IPR001466; Beta_lactamase.			
DR	InterPro; IPR000871; Beta_lactamase_A.			
DR	Pfam; PF00144; Beta-lactamase; 1.			
DR	PRINTS; PR00118; BLACTAMASA.			
DR	PROSITE; PS00146; BETA_LACTAMASE_A; 1.			
FT	NOV_TER	1	1	
FT	NOV_TER	241	241	
Q0	SEQUENCE	241 AA;	26407 MW;	36DF2AFDF0C5807D CRC64;

Query Match	100.0%;	Score 1170;	DB 2;	Length 241;
Best Local Similarity	100.0%;	Pred. No. 9.2e-87;		

Matches	228	Conservative	0	Mismatches	0	Indels	0	Gaps	0																																					
QY	1	HPEFLVVKVKAEDQ	GA	RVGI	IELD	LN	SG	KIL	FS	FP	EE	RP	PM	M	ST	K	V	L	C	G	A	V	L	S	R	I	D	60																		
Db	7	HPEFLVVKVKAEDQ	GA	RVGI	IELD	LN	SG	KIL	FS	FP	EE	RP	PM	M	ST	K	V	L	C	G	A	V	L	S	R	I	D	66																		
QY	61	AGGEOGGRIRHS	QND	LV	ES	PV	TE	KE	KL	TQ	GM	T	RE	L	C	S	A	I	T	M	S	D	T	A	N	L	L	T	T	IG	120															
Db	67	AGGEOGGRIRHS	QND	LV	ES	PV	TE	KE	KL	TQ	GM	T	RE	L	C	S	A	I	T	M	S	D	T	A	N	L	L	T	T	IG	126															
QY	121	KELTAFLHNNGD	H	T	R	L	D	R	M	E	P	E	L	N	E	A	I	P	N	D	E	R	T	T	P	V	A	M	A	T	T	L	R	K	L	T	G	E	L	I	T	L	S	R	Q	180
Db	127	KELTAFLHNNGD	H	T	R	L	D	R	M	E	P	E	L	N	E	A	I	P	N	D	E	R	T	T	P	V	A	M	A	T	T	L	R	K	L	T	G	E	L	I	T	L	S	R	Q	186
QY	181	QLIDIMWADK	V	A	G	G	L	N	S	A	L	P	A	G	E	F	I	A	D	K	S	G	A	G	R	G	S	R	G	I	A	A	L	G	P	G	228									
Db	187	QLIDIMWADK	V	A	G	L	N	S	A	L	P	A	G	E	F	I	A	D	K	S	G	A	G	R	G	S	R	G	I	A	A	L	G	P	G	234										

RESULT 4	
Q6WWY3	
ID Q6WWY3	PRELIMINARY; PRT; 242 AA.

RC		Gemini;
DT	05-JUL-2004	(TIREMBLrel_27, Created)
DT	05-JUL-2004	(TIREMBLrel_27, Last sequence update)
DT	05-JUL-2004	(TIREMBLrel_27, Last annotation update)
D8	Beta-lactamase (Fragment).	
GN	Name=blatEM;	
OS	Escherichia coli.	
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	
OC	Enterobacteriaceae; Escherichia.	
OX	NCB1_TaxID=562;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=TAO05;	
RA	Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;	
RL	Submitted (JAPR-2004) to the EMBL/GenBank/DDBB databases.	
DR	EMBL; AY265867; AAP93845.1; -.	
DR	HSSP; P00807; IKGE.	
DR	InterPro; IPR001466; Beta_lactamase.	
DR	InterPro; IPR000871; Beta_lactamase_A.	
DR	Pfam; PF00144; Beta_lactamase_1.	
DR	PRINTS; PR00118; BLACTAMASEA.	
DR	PROSITE; PS00146; BETA_LACTAMASE_A; 1.	
FT	NON_TER	
LT	NON_TER	
SQ	SEQUENCE	242 AA; 26554 MW; 38C3DFDA6A53807D CRC64;

Query Match	100.0%	Score 1170;	DB 2;	Length 242;
Best Local Similarity	100.0%	Pred. No. 9.3e-87;		
Matches 228; Conservative	0;	Mismatches	0;	Gaps 0;

Qy	1	HPELVVKAEDQGLGARVYIELDNSGKILISFPREERFPMMSPFKVLCCGVLSRID	60
Db	8	HPELVVKAEDQGLGARVYIELDNSGKILISFPREERFPMMSPFKVLCCGVLSRID	67
Qy	61	AGEQQLGRRIHYSQNDLVEKSPYTEKILTGQMTVRELCSAIIQMSDNTAANLLTTIGCP	120
Db	68	AGEQQLGRRIHYSQNDLVEKSPYTEKILTGQMTVRELCSAIIQMSDNTAANLLTTIGCP	127
Qy	121	KEITAFLLHNGDHYTRLDRWEPEINAEIIPNDEKDTTPVAMATTLRLTGLLELTLASRQ	180
Db	128	KEITAFLLHNGDHYTRLDRWEPEINAEIIPNDEKDTTPVAMATTLRLTGLLELTLASRQ	187
Qy	181	QLIDWMDADKYAGPILRSALPAGCFIADKSGAGERSRGIIAALGPDG	228
Db	188	QLIDWMDADKYAGPILRSALPAGCFIADKSGAGERSRGIIAALGPDG	235

RESULT 5		
Q6KB67		
ID Q6KB67	PRELIMINARY;	PRT; 285 AA.
AC Q6KB67;		

DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Hypoetical protein (Fragment).
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Triticeae; Hordeum.
 NC NCB1_Taxid=4513;
 RX [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE-First leaf.
 RC Jansen C., Korell M., Ecker C., Biedenkopf D., Kogel K.H.;
 RA Submitted (May-2004) to the EMBL/Genbank/DDbJ databases.
 RL EMBL; AJ171773; CAG30723.1; -.
 DR HSBP; P08077; IAUQ.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASE.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 KW Hypoetical protein.
 FT NON_TER 285
 SQ SEQUENCE 285 AA; 31371 MW; A2F22753375FA930 CRC64;

Query Match 100.0%; Score 1170; DB 2; Length 285;
 Best Local Similarity 100.0%; Pred. No. 1.1e-86;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HPELVKVKADADQAGVGYIELDLSGKILSFPRPERPFWMTFKVLLCGAVLSRID 60
 DB 24 HPELVKVKADADQAGVGYIELDLSGKILSFPRPERPFWMTFKVLLCGAVLSRID 83
 QY 61 AGQELGRRIRHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGCP 120
 DB 84 AGQELGRRIRHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGCP 143
 QY 121 KELTAFILNMGDHTVRLDRWPELNEALPNDERDTTMAPVAAATTIRKLLTGELTLASRQ 180
 DB 144 KELTAFILNMGDHTVRLDRWPELNEALPNDERDTTMAPVAAATTIRKLLTGELTLASRQ 203
 QY 181 QLIIDMEADKVAGPLLRSGALPAGWFIADKSGAGERSGIIAALGPDG 228
 DB 204 QLIIDMEADKVAGPLLRSGALPAGWFIADKSGAGERSGIIAALGPDG 251
 RESULT 6
 Q38058 PRELIMINARY; PRT; 286 AA.
 ID Q38058;
 AC Q38058;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Beta_lactamase.
 GN Name=bla;
 OS Bacteriophage phi-X174.
 CC Viruses; ssDNA viruses; Microviridae; Microvirinae.
 NC NCB1_Taxid=10847;
 RX [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=95172401; PubMed=7867948; DOI=10.1016/0378-1119(94)00839-K;
 RA Henrich B., Schmidtberger B.;
 RT "A variant of phix174 gene B-based positive selection vectors with
 enhanced lytic potential.";
 RL Gene 154:51-54(1995).
 DR EMBL; Z35638; CAA84692.1; -.
 DR PIR; S47061; S47061.
 DR HSBP; Q9R435; 1HTZ.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASE.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.

SQ SEQUENCE 286 AA; 31557 MW; 5BB2F22753375FA9 CRC64;
 Query Match 100.0%; Score 1170; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 1.1e-86;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HPELVKVKADADQAGVGYIELDLSGKILSFPRPERPFWMTFKVLLCGAVLSRID 60
 DB 24 HPELVKVKADADQAGVGYIELDLSGKILSFPRPERPFWMTFKVLLCGAVLSRID 83
 QY 61 AGQELGRRIRHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGCP 120
 DB 84 AGQELGRRIRHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGCP 143
 QY 121 KELTAFILNMGDHTVRLDRWPELNEALPNDERDTTMAPVAAATTIRKLLTGELTLASRQ 180
 DB 144 KELTAFILNMGDHTVRLDRWPELNEALPNDERDTTMAPVAAATTIRKLLTGELTLASRQ 203
 QY 181 QLIIDMEADKVAGPLLRSGALPAGWFIADKSGAGERSGIIAALGPDG 228
 DB 204 QLIIDMEADKVAGPLLRSGALPAGWFIADKSGAGERSGIIAALGPDG 251

RESULT 7
 Q00626 PRELIMINARY; PRT; 286 AA.
 ID Q00626;
 AC Q00626; Q08022; Q08102; Q09393; Q09396; Q09397; Q09398; Q09399;
 AC Q09400; Q09401; Q09402; Q09403; Q09404; Q09405; Q09406; Q09407;
 AC Q09408; Q09481; Q09482; Q09483; Q09490; Q57339;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Beta_lactamase.
 OS Staphylococcus aureus.
 CC Plasmid J3356/POX7/3, and Plasmid J3356/POX7/1.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCB1_Taxid=1280;
 RX [1]
 RN SEQUENCE FROM N.A.
 RP PLASMID=J3356/POX7/3, and J3356/POX7/1;
 RA MEDLINE=96422755; PubMed=8825372; DOI=10.1006/plas.1995.0005;
 RA Needham C., Noble W.C., Dyke K.G.;
 RT "The staphylococcal insertion sequence IS257 is active.";
 RL Plasmid 34:198-205(1995).
 DR EMBL; U36912; AAB39957.1; -.
 DR EMBL; U36911; AAB39956.1; -.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASE.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 KW Plasmid.
 SQ SEQUENCE 286 AA; 31557 MW; 5BB2F22753375FA9 CRC64;
 Query Match 100.0%; Score 1170; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 1.1e-86;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HPELVKVKADADQAGVGYIELDLSGKILSFPRPERPFWMTFKVLLCGAVLSRID 60
 DB 24 HPELVKVKADADQAGVGYIELDLSGKILSFPRPERPFWMTFKVLLCGAVLSRID 83
 QY 61 AGQELGRRIRHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGCP 120
 DB 84 AGQELGRRIRHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGCP 143
 QY 121 KELTAFILNMGDHTVRLDRWPELNEALPNDERDTTMAPVAAATTIRKLLTGELTLASRQ 180
 DB 144 KELTAFILNMGDHTVRLDRWPELNEALPNDERDTTMAPVAAATTIRKLLTGELTLASRQ 203
 QY 181 QLIIDMEADKVAGPLLRSGALPAGWFIADKSGAGERSGIIAALGPDG 228
 DB 204 QLIIDMEADKVAGPLLRSGALPAGWFIADKSGAGERSGIIAALGPDG 251

RESULT 8

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079CL6 PRELIMINARY; PRT; 286 AA.
ID 079CL6
AC 079CL6;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Beta-lactamase.
GN Name-bia;
OS Methylobacillus flagellatum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Methylotiales;
OC Methylotiales; Methylotiales.
OX NCBI_TaxID=405;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97074643; PubMed=8917070; DOI=10.1016/0378-1119(96)00114-X;
RA Seebrijski I.G., Vassin V.M., Tsygankov Y.D.;
RT "Two new members of the B108 superfamily: cloning, sequencing and
expression of bioB genes of Methylobacillus flagellatum and
Corynebacterium glutamicum."
RL Gene 175:15-22(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Seebrijski I., Vassin V., Tsygankov Y.;
RL Submitted (JUL-1995) to the EMBL/Genbank/DBJ databases.
DR EMBL; U31280; AAC4581.1; -.
DR HSSP; P00807; IALO.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;

Query Match 100.0%; Score 1170; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 1,le-86;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADQDQAGRVGTYIELDLSGKILSFPRPERPPMSTFVLLCGAVLSRID 60
DB HPEITLVKVKADQDQAGRVGTYIELDLSGKILSFPRPERPPMSTFVLLCGAVLSRID 83
QY 61 AGQEGLRRIHYSONDLVEYSPVTEKHLTDGNTVRELCSAIIITSDNTAAILLTTIGP 120
DB AGQEGLRRIHYSONDLVEYSPVTEKHLTDGNTVRELCSAIIITSDNTAAILLTTIGP 143
QY 121 KETLAFILNMGDHVTRLDRWPELNEAIPNDRDITMVPVAMATTLRKLLTGELLTLASRQ 180
DB KETLAFILNMGDHVTRLDRWPELNEAIPNDRDITMVPVAMATTLRKLLTGELLTLASRQ 203
QY 144 KETLAFILNMGDHVTRLDRWPELNEAIPNDRDITMVPVAMATTLRKLLTGELLTLASRQ 203
DB KETLAFILNMGDHVTRLDRWPELNEAIPNDRDITMVPVAMATTLRKLLTGELLTLASRQ 203
QY 181 QLIIMWEADKVAQPLRLSALPAGWFIADKSGAGRGSGIITAAIGPDG 228
DB QLIIMWEADKVAQPLRLSALPAGWFIADKSGAGRGSGIITAAIGPDG 251

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RESULT 9

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079DR3 PRELIMINARY; PRT; 286 AA.
ID 079DR3
AC 079DR3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Mutant extended-spectrum beta-lactamase precursor (EC 3.5.2.6).
GN Name-bia; Synonyms=blatm-116;
OS Escherichia coli.
OC Plasmid pBP4, and Plasmid pCAPS.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=K-12;
RA Maneewannakul K., Maneewannakul S., Ippen-Ihler K.;
RL Submitted (AUG-1991) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12; PLASMID=pBP4;
RA Rondot S., Anthony K., Dubel S., Ida N., Beyreuther K., Frost L.,
RA Little M., Breitling F.;
RL Submitted (APR-1997) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC PLASMID=pCAPS;
RX MEDLINE=96189310; PubMed=9514792; DOI=10.1006/abio.1997.2558;
RA Schlieper D., Von Wilcken-Bergmann B., Schmidt M., Sobek H.,
RA Mueller-Hill B.;
RT "A positive selection vector for cloning of long polymerase chain
reaction fragments based on a lethal mutant of the ctp gene
of Escherichia coli."
RL Anal. Biochem. 257:203-209(1998).
RN [4]
RP SEQUENCE FROM N.A.
RX PubMed=15243036;
RA Jeong S.H., Bae I.K., Lee J.H., Sohn S.G., Kang G.H., Jeon G.J.,
RA Kim Y.H., Jeong B.C., Lee S.H.;
RT "Molecular Characterization of Extended-Spectrum Beta-Lactamases
Produced by Clinical Isolates of Klebsiella pneumoniae and Escherichia
coli from a Korean Nationwide Survey."
RL J. Clin. Microbiol. 42:2902-2906(2004).
DR EMBL; M74750; AAA24057.1; -.
DR EMBL; Y12694; CAA73226.1; -.
DR EMBL; AJ001614; CAA04868.1; -.
DR EMBL; AY425988; AAQ95605.1; -.
DR HSSP; P00807; IALO.
DR GO; GO:0008800; F:beta-lactamase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW Hydrolase; Plasmid; Signal.
FT SIGNAL 1 23 Potential.
SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;

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Query Match 100.0%; Score 1170; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 1,le-86;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 HPEITLVKVKADQDQAGRVGTYIELDLSGKILSFPRPERPPMSTFVLLCGAVLSRID 60
DB HPEITLVKVKADQDQAGRVGTYIELDLSGKILSFPRPERPPMSTFVLLCGAVLSRID 83
QY 61 AGQEGLRRIHYSONDLVEYSPVTEKHLTDGNTVRELCSAIIITSDNTAAILLTTIGP 120
DB AGQEGLRRIHYSONDLVEYSPVTEKHLTDGNTVRELCSAIIITSDNTAAILLTTIGP 143
QY 121 KETLAFILNMGDHVTRLDRWPELNEAIPNDRDITMVPVAMATTLRKLLTGELLTLASRQ 180
DB KETLAFILNMGDHVTRLDRWPELNEAIPNDRDITMVPVAMATTLRKLLTGELLTLASRQ 203
QY 144 KETLAFILNMGDHVTRLDRWPELNEAIPNDRDITMVPVAMATTLRKLLTGELLTLASRQ 203
DB KETLAFILNMGDHVTRLDRWPELNEAIPNDRDITMVPVAMATTLRKLLTGELLTLASRQ 203
QY 181 QLIIMWEADKVAQPLRLSALPAGWFIADKSGAGRGSGIITAAIGPDG 228
DB QLIIMWEADKVAQPLRLSALPAGWFIADKSGAGRGSGIITAAIGPDG 251

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RESULT 10

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084H50 PRELIMINARY; PRT; 255 AA.
ID 084H50
AC 084H50;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE TEM-117 beta-lactamase (Fragment).

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```
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OK NCBI_TaxID=562;
RN
  (1)
  SEQUENCE FROM N.A.
  Box A.T.A., Pauw A., Leverstein-vanHall M.A.;
  Submitted (Jul-2002) to the EMBL/GenBank/DBJ databases.
  DR EMBL; AY130282; AAN05026.1; -.
  DR HSSP; Q9R435; 1HTZ.
  DR InterPro; IPR001466; Beta_lactamase.
  DR InterPro; IPR008711; Beta_lactamase_A.
  DR Pfam; PF00144; Beta-lactamase; 1.
  DR PRINTS; PR00118; BLACTAMASEA.
  DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
  FT NON_TER
  FT NON_TER
  SQ SEQUENCE 255 AA; 27906 MW; DCBB28B65978C3A6 CRC64;

Query Match 99.6%; Score 1165; DB 2; Length 255;
Best Local Similarity 99.1%; Pred. No. 2.5e-86;
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPELVKVKDAEDQAGARVGYIELDLSNGKILSFRRPERPMMSTPFKVLGCAVLSRD 60
DB 12 HPELVKVKDAEDQAGARVGYIELDLSNGKILSFRRPERPMMSTPFKVLGCAVLSRD 71
QY 61 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGVTVELCSAATMSDNTAANLLTTIGSP 120
DB 72 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGVTVELCSAATMSDNTAANLLTTIGSP 131
QY 121 KELTAFILNMGDHVRRLDRWPELNEAI PNDERDTTMAPAAATTARKLITGELLTLASRQ 180
DB 132 KELTAFILNMGDHVRRLDRWPELNEAI PNDERDTTMAPAAATTARKLITGELLTLASRQ 191
QY 181 QLIDWMEADKVA GPILRSALPAGWFIADKSGAGERSGIIAALGPDG 228
DB 192 QLIDWMEADKVA GPILRSALPAGWFIADKSGAGERSGIIAALGPDG 239

RESULT 11
Q84H49 PRELIMINARY; PRT; 261 AA.
AC 084H49:
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DB TEM-110 beta-lactamase (Fragment).
OS Klebsiella oxytoca.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OK NCBI_TaxID=571;
RN
  (1)
  SEQUENCE FROM N.A.
  Box A.T.A., Pauw A., Leverstein-vanHall M.A., Verhoef J., Pluit A.C.;
  Submitted (Jul-2002) to the EMBL/GenBank/DBJ databases.
  DR EMBL; AY130283; AAN05027.1; -.
  DR HSSP; Q9R435; 1HTZ.
  DR InterPro; IPR001466; Beta_lactamase.
  DR InterPro; IPR008711; Beta_lactamase_A.
  DR Pfam; PF00144; Beta-lactamase; 1.
  DR PRINTS; PR00118; BLACTAMASEA.
  DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
  FT NON_TER
  FT NON_TER
  SQ SEQUENCE 261 AA; 28738 MW; 4F748F733A08CB CRC64;

Query Match 99.6%; Score 1165; DB 2; Length 261;
Best Local Similarity 99.1%; Pred. No. 2.6e-86;
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPELVKVKDAEDQAGARVGYIELDLSNGKILSFRRPERPMMSTPFKVLGCAVLSRD 60
|||||
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DB 12 HPELVKVKDAEDQAGARVGYIELDLSNGKILSFRRPERPMMSTPFKVLGCAVLSRD 71
QY 61 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGVTVELCSAATMSDNTAANLLTTIGSP 120
DB 72 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGVTVELCSAATMSDNTAANLLTTIGSP 131
QY 121 KELTAFILNMGDHVRRLDRWPELNEAI PNDERDTTMAPAAATTARKLITGELLTLASRQ 180
DB 132 KELTAFILNMGDHVRRLDRWPELNEAI PNDERDTTMAPAAATTARKLITGELLTLASRQ 191
QY 181 QLIDWMEADKVA GPILRSALPAGWFIADKSGAGERSGIIAALGPDG 228
DB 192 QLIDWMEADKVA GPILRSALPAGWFIADKSGAGERSGIIAALGPDG 239

RESULT 12
Q6PRU6 PRELIMINARY; PRT; 264 AA.
AC 06PRU6:
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DB TEM beta-lactamase (Fragment).
OS Acinetobacter sp. U11.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OK NCBI_TaxID=269266;
RN
  (1)
  SEQUENCE FROM N.A.
  RC STRAIN=U11;
  RA Ghadimi S., Hosseini-Mazinan S.M.;
  Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
  DR EMBL; AY583762; AAS86428.1; -.
  DR HSSP; P00807; 1ALQ.
  DR InterPro; IPR001466; Beta_lactamase.
  DR InterPro; IPR008711; Beta_lactamase_A.
  DR Pfam; PF00144; Beta-lactamase; 1.
  DR PRINTS; PR00118; BLACTAMASEA.
  DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
  FT NON_TER
  FT NON_TER
  SQ SEQUENCE 264 AA; 28986 MW; A4F071CF7489352C CRC64;

Query Match 99.6%; Score 1165; DB 2; Length 264;
Best Local Similarity 99.1%; Pred. No. 2.6e-86;
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPELVKVKDAEDQAGARVGYIELDLSNGKILSFRRPERPMMSTPFKVLGCAVLSRD 60
DB 12 HPELVKVKDAEDQAGARVGYIELDLSNGKILSFRRPERPMMSTPFKVLGCAVLSRD 71
QY 61 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGVTVELCSAATMSDNTAANLLTTIGSP 120
DB 72 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGVTVELCSAATMSDNTAANLLTTIGSP 131
QY 121 KELTAFILNMGDHVRRLDRWPELNEAI PNDERDTTMAPAAATTARKLITGELLTLASRQ 180
DB 132 KELTAFILNMGDHVRRLDRWPELNEAI PNDERDTTMAPAAATTARKLITGELLTLASRQ 191
QY 181 QLIDWMEADKVA GPILRSALPAGWFIADKSGAGERSGIIAALGPDG 228
DB 192 QLIDWMEADKVA GPILRSALPAGWFIADKSGAGERSGIIAALGPDG 239

RESULT 13
Q6OIV0 PRELIMINARY; PRT; 281 AA.
AC 06OIV0:
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DB TEM-1 beta-lactamase (Fragment).
OK Name=blatEM-1;
RN
  (1)
  SEQUENCE FROM N.A.
  Box A.T.A., Pauw A., Leverstein-vanHall M.A., Verhoef J., Pluit A.C.;
  Submitted (Jul-2002) to the EMBL/GenBank/DBJ databases.
  DR EMBL; AY130284; AAN05028.1; -.
  DR HSSP; Q9R435; 1HTZ.
  DR InterPro; IPR001466; Beta_lactamase.
  DR InterPro; IPR008711; Beta_lactamase_A.
  DR Pfam; PF00144; Beta-lactamase; 1.
  DR PRINTS; PR00118; BLACTAMASEA.
  DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
  FT NON_TER
  FT NON_TER
  SQ SEQUENCE 281 AA; 30738 MW; 4F748F733A08CB CRC64;
```


RT coli plasmid R6K.";
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3732-3736 (1978).
 RN [5]
 RN SEQUENCE FROM N.A. (TEM-3).
 RA Sougakoff W., Goussard S., Courvalin P.;
 RT "The TEM-3 beta-lactamase, which hydrolyzes broad-spectrum
 cephalosporins, is derived from the TEM-2 penicillinase by two amino
 acid substitutions.";
 RL FEMS Microbiol. Lett. 56:343-348 (1988).
 RN [6]
 RN SEQUENCE FROM N.A. (TEM-3).
 RP PLASMID=pcpF04;
 RX MEDLINE=93062798; PubMed=1331747;
 RA Mabilat C., Lourencao-Vital J., Goussard S., Courvalin P.;
 RT "A new example of physical linkage between Tnl and Tn21: the
 antibiotic multiple-resistance region of plasmid pcpF04 encoding
 extended-spectrum beta-lactamase TEM-3.";
 RL Mol. Gen. Genet. 235:113-121 (1992).
 RN [7]
 RN SEQUENCE FROM N.A. (TEM-4 AND TEM-5).
 RP STRAIN=CB66134; PLASMID=pcpF04, and pUD16;
 RX MEDLINE=89378760; PubMed=2550326; DOI=10.1016/0378-1119(89)90236-9;
 RA Sougakoff W., Petit A., Goussard S., Siroc D., Bure A., Courvalin P.;
 RT "Characterization of the plasmid gene blaT-4 and blaT-5 which encode
 the broad-spectrum beta-lactamases TEM-4 and TEM-5 in
 enterobacteriaceae.";
 RL Gene 78:339-348 (1989).
 RN [8]
 RN SEQUENCE FROM N.A. (TEM-6).
 RP STRAIN=HB251;
 RX MEDLINE=92166702; PubMed=1655171;
 RA Goussard S., Sougakoff W., Mabilat C., Bauernfeind A., Courvalin P.;
 RT "An ISI-like element is responsible for high-level synthesis of
 extended-spectrum beta-lactamase TEM-6 in Enterobacteriaceae.";
 RL J. Gen. Microbiol. 137:2681-2687 (1991).
 RN [9]
 RN SEQUENCE FROM N.A. (TEM-8; TEM-16 AND TEM-24).
 RP MEDLINE=93037315; PubMed=1416873;
 RA Chanal C., Poupart M.C., Siroc D., Labia R., Siroc J., Cluzel R.;
 RT "Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase
 genes.";
 RL Antimicrob. Agents Chemother. 36:1817-1820 (1992).
 RN [10]
 RN SEQUENCE OF 24-286 (IRT-4).
 RP STRAIN=PEV;
 RX MEDLINE=94333751; PubMed=8056282; DOI=10.1016/0378-1097(94)00186-3;
 RA Brun T., Peduzzi J., Canica M.M., Paul G., Nevot P., Barthelmy M.,
 Labia R.;
 RT "Characterization and amino acid sequence of IRT-4, a novel TEM-type
 enzyme with a decreased susceptibility to beta-lactamase inhibitors.";
 RL FEMS Microbiol. Lett. 120:111-117 (1994).
 RN [11]
 RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF TEM-1.
 RP MEDLINE=92183921; PubMed=154485; DOI=10.1016/0014-5793(92)80232-6;
 RA Jelsch C., Lenfant F., Masson J.-M., Samama J.-P.;
 RT "Beta-lactamase TEM1 of E. coli. Crystal structure determination at
 2.5-A resolution.";
 RL PDBS Lett. 299:135-142 (1992).
 RN [12]
 RN X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF TEM-1.
 RP MEDLINE=93361453; PubMed=8356032;
 RA Jelsch C., Mourey L., Masson J.-M., Samama J.-P.;
 RT "Crystal structure of Escherichia coli TEM1 beta-lactamase at 1.8-A
 resolution.";
 RL Proteins 16:364-383 (1993).
 RN [13]
 RN X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF TEM-1 COMPLEXED WITH BLIP.
 RP MEDLINE=9618652; PubMed=8605632;
 RA Strzemecka N.C.J., Jensen S.E., Alvari P.M., James M.N.G.;
 RT "A potent new mode of beta-lactamase inhibition revealed by the 1.7 A
 X-ray crystallographic structure of the TEM-1-BLIP complex.";
 RL Nat. Struct. Biol. 3:290-297 (1996).
 RN [14]

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF TEM-1.
 RX MEDLINE=98153145; PubMed=9485412; DOI=10.1021/bi97250ub;
 RA Maveyraud L., Pratt R.F., Samama J.-P.;
 RT "Crystal structure of an acylation transition-state analog of the TEM-
 1 beta-lactamase. Mechanistic implications for class A beta-
 lactamases.";
 RL Biochemistry 37:2622-2628 (1998).
 RN [15]
 RN X-RAY CRYSTALLOGRAPHY (2.28 ANGSTROMS) OF TEM-1.
 RP MEDLINE=99352177; PubMed=10423234; DOI=10.1021/bi990758z;
 RA Swaren P., Golemi D., Cabantous S., Bulchev A., Maveyraud L.,
 Wobashery S., Samama J.-P.;
 RT "X-ray structure of the Asn276Asp variant of the Escherichia coli TEM-
 1 beta-lactamase: direct observation of electrostatic modulation in
 resistance to inactivation by clavulanic acid.";
 RL Biochemistry 38:9570-9576 (1999).
 CC -I- FUNCTION: TEM-type are the most prevalent beta-lactamases in
 enterobacteria; they hydrolyze the beta-lactam bond in susceptible
 beta-lactam antibiotics, thus conferring resistance to penicillins
 and cephalosporins. TEM-3 and TEM-4 are capable of hydrolyzing
 cefotaxime and ceftazidime. TEM-5 is capable of hydrolyzing
 ceftazidime. TEM-6 is capable of hydrolyzing ceftazidime and
 aztreonam. TEM-8/CAZ-2, TEM-16/CAZ-7 and TEM-24/CAZ-6 are markedly
 active against ceftazidime. IRT-4 shows resistance to beta-
 lactamase inhibitors.
 CC -I- CATALYTIC ACTIVITY: A beta-lactam + H(2O) = a substituted beta-
 amino acid.
 CC -I- BIOTECHNOLOGY: This protein is used as a marker in many commonly
 used cloning vectors, such as pBR322 and the pUC series.
 CC -I- MISCELLANEOUS: The beta-lactamase present on pBR322 was cloned
 from plasmid B1 (R7268).
 CC -I- SIMILARITY: Belongs to the class-A beta-lactamase family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL, J01749; AAB59737.1; -
 DR EMBL, V00613; CAA23886.1; -
 DR EMBL, X64523; CAA45828.1; -
 DR EMBL, X57972; CAA41038.1; -
 DR EMBL, X65252; CAA46344.1; -
 DR EMBL, X65253; CAA46345.1; -
 DR EMBL, X65294; AAB64386.1; -
 DR EMBL, U89928; AAB64386.1; -
 DR EMBL, U66885; AAC48875.1; -
 DR PIR, A93821; PNECP.
 DR PIR, S30113; S30113.
 DR PDB, 1AXB; X-ray; -
 DR PDB, 1BTV; X-ray; -
 DR PDB, 1BTL; X-ray; -
 DR PDB, 1CK3; X-ray; -
 DR PDB, 1ERM; X-ray; -
 DR PDB, 1ERO; X-ray; -
 DR PDB, 1ESU; X-ray; -
 DR PDB, 1FOG; X-ray; -
 DR PDB, 1JTD; X-ray; -
 DR PDB, 1JTG; X-ray; -
 DR PDB, 1JVP; X-ray; -
 DR PDB, 1JWZ; X-ray; -
 DR PDB, 1LHY; X-ray; -
 DR PDB, 1LIT; X-ray; -
 DR PDB, 1LIX; X-ray; -
 DR PDB, 1LNY; X-ray; -
 DR PDB, 1LNY; X-ray; -
 DR PDB, 1LNY; X-ray; -

DR PDB; ITEM; X-ray; -
DR PDB; IXPB; X-ray; -

Query Match 99.6%; Score 1165; DB 1; Length 286;
Best Local Similarity 99.1%; Pred. No. 2.9e-86;
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	1	HPE TLVVKVKAEDQLGARVGYIELDLSNGKILLESFRPEERFPMMSTFKVLGAVLSRID	60
DB	24	HPE TLVVKVKAEDQLGARVGYIELDLSNGKILLESFRPEERFPMMSTFKVLGAVLSRID	83
QY	61	AGEQLGRRRIHYSNDLVEYSPVTEKHLTDGNTVRELCSAAITWSDNTAANLLTTIGP	120
DB	84	AGEQLGRRRIHYSNDLVEYSPVTEKHLTDGNTVRELCSAAITWSDNTAANLLTTIGP	143
QY	121	KELTAFLHNMGDHTRLDLRLRMEPELNEAIPNDRDPTMPVAMATTLRKLLTGELLTLASRQ	180
DB	144	KELTAFLHNMGDHTRLDLRLRMEPELNEAIPNDRDPTMPVAMATTLRKLLTGELLTLASRQ	203
QY	181	QLIDMMEADKVAQPLRLRSALPAGWFIADKSGAGERSRGIITAAIGPDG	228
DB	204	QLIDMMEADKVAQPLRLRSALPAGWFIADKSGAGERSRGIITAAIGPDG	251

Search completed: June 10, 2005, 10:57:04
Job time : 77.3841 secs